

Report

	SC2297.consensus
# contigs (>= 0 bp)	1
# contigs (>= 1000 bp)	1
# contigs (>= 5000 bp)	1
# contigs (>= 10000 bp)	1
# contigs (>= 25000 bp)	1
# contigs (>= 50000 bp)	0
Total length (>= 0 bp)	29892
Total length (>= 1000 bp)	29892
Total length (>= 5000 bp)	29892
Total length (>= 10000 bp)	29892
Total length (>= 25000 bp)	29892
Total length (>= 50000 bp)	0
# contigs	1
Largest contig	29892
Total length	29892
Reference length	29903
GC (%)	37.97
Reference GC (%)	37.97
N50	29892
NG50	29892
N75	29892
NG75	29892
L50	1
LG50	1
L75	1
LG75	1
# misassemblies	0
# misassembled contigs	0
Misassembled contigs length	0
# local misassemblies	0
# scaffold gap ext. mis.	0
# scaffold gap loc. mis.	1
# unaligned mis. contigs	0
# unaligned contigs	0 + 0 part
Unaligned length	0
Genome fraction (%)	98.432
Duplication ratio	1.016
# N's per 100 kbp	1525.49
# mismatches per 100 kbp	74.74
# indels per 100 kbp	6.79
# genomic features	19 + 4 part
Largest alignment	29424
Total aligned length	29424
NA50	29424
NGA50	29424
NA75	29424
NGA75	29424
LA50	1
LGA50	1
LA75	1
LGA75	1

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

	SC2297.consensus
# misassemblies	0
# contig misassemblies	0
# c. relocations	0
# c. translocations	0
# c. inversions	0
# scaffold misassemblies	0
# s. relocations	0
# s. translocations	0
# s. inversions	0
# misassembled contigs	0
Misassembled contigs length	0
# local misassemblies	0
# scaffold gap ext. mis.	0
# scaffold gap loc. mis.	1
# unaligned mis. contigs	0
# mismatches	22
# indels	2
# indels (<= 5 bp)	1
# indels (> 5 bp)	1
Indels length	10

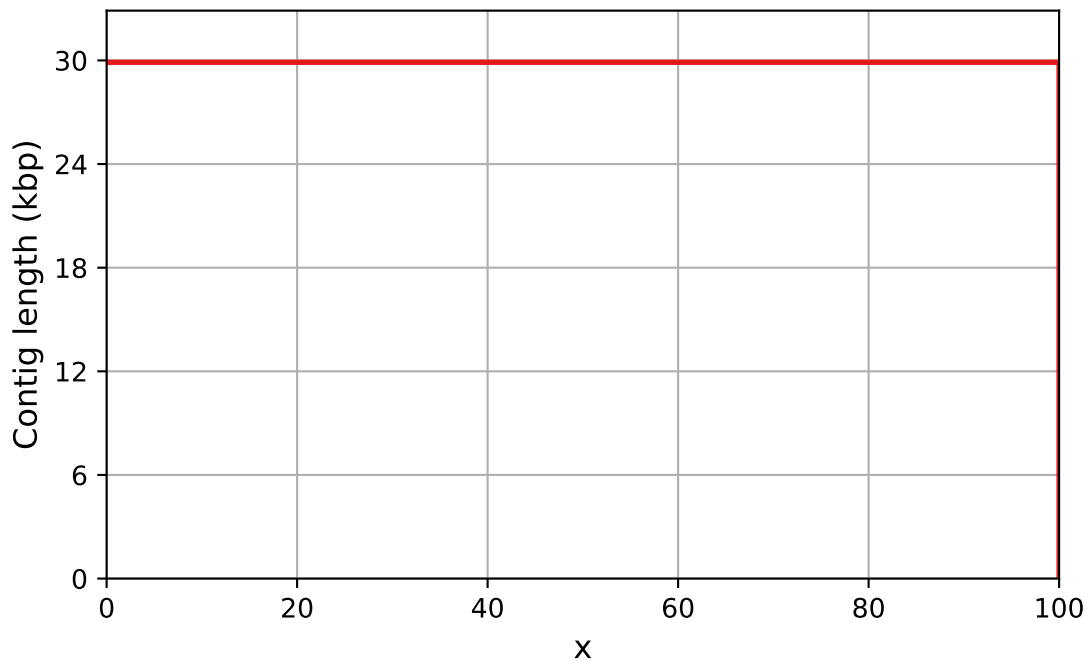
All statistics are based on contigs of size ≥ 500 bp, unless otherwise noted (e.g., "# contigs (≥ 0 bp)" and "Total length (≥ 0 bp)" include all contigs).

Unaligned report

	SC2297.consensus
# fully unaligned contigs	0
Fully unaligned length	0
# partially unaligned contigs	0
Partially unaligned length	0
# N's	456

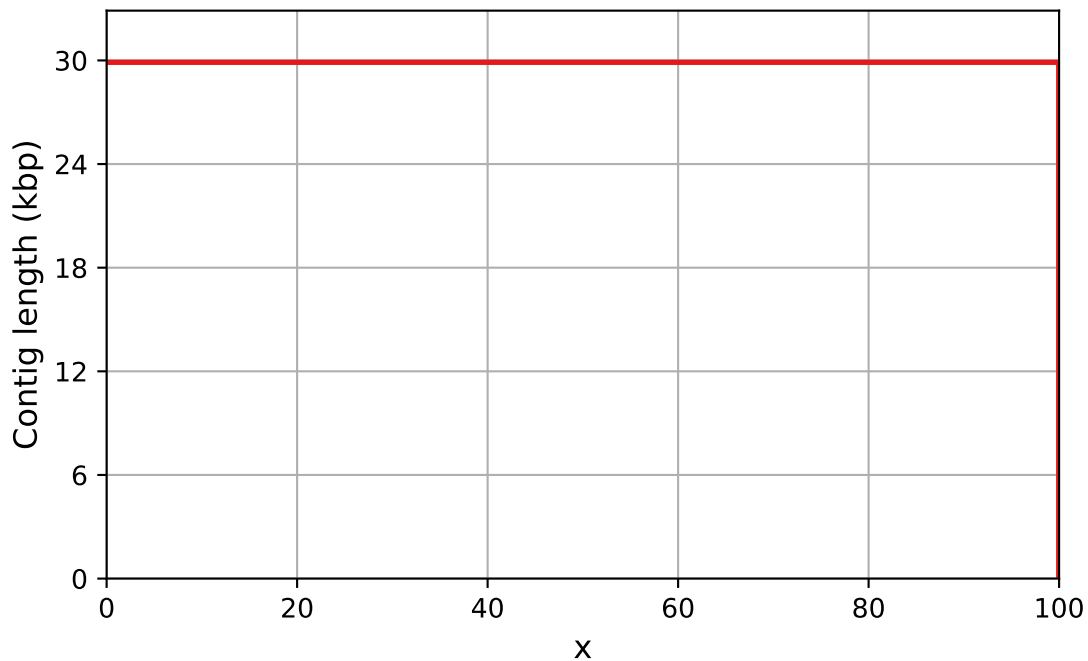
All statistics are based on contigs of size ≥ 500 bp, unless otherwise noted (e.g., "# contigs (≥ 0 bp)" and "Total length (≥ 0 bp)" include all contigs).

Nx



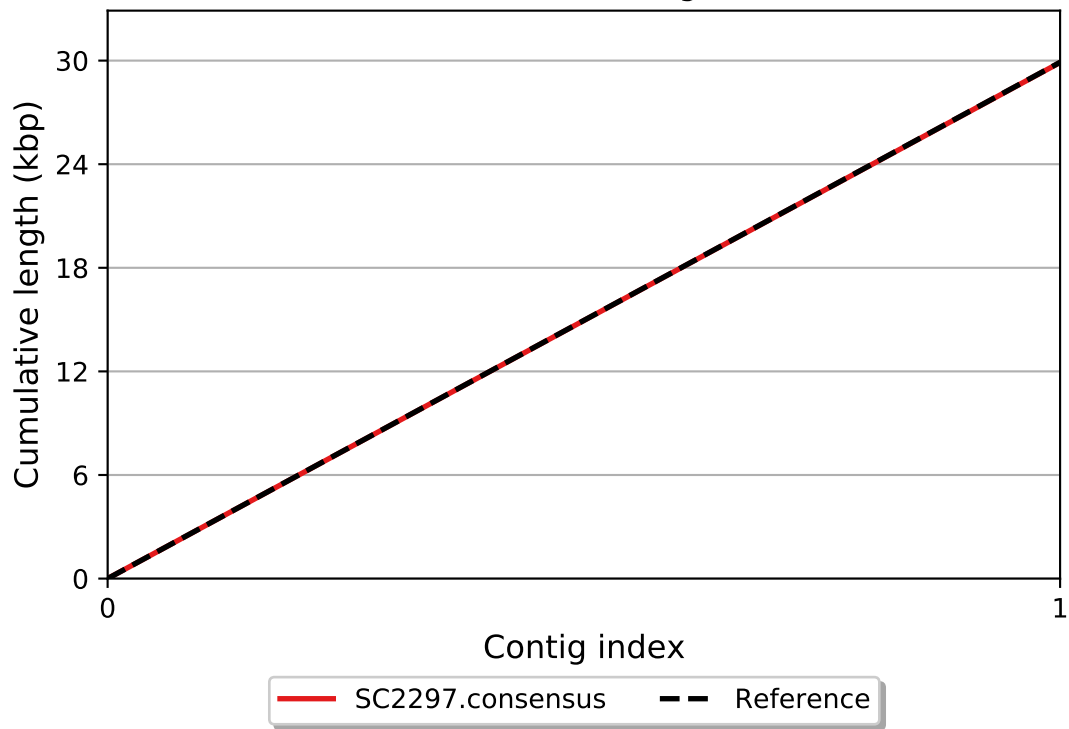
— SC2297.consensus

NGx

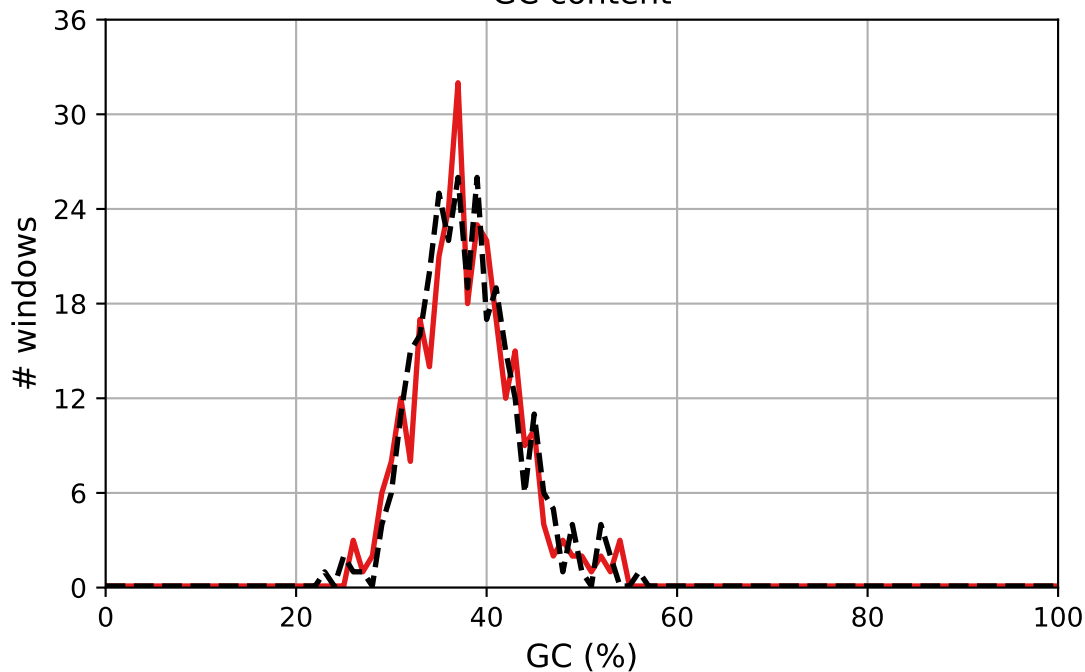


— SC2297.consensus

Cumulative length

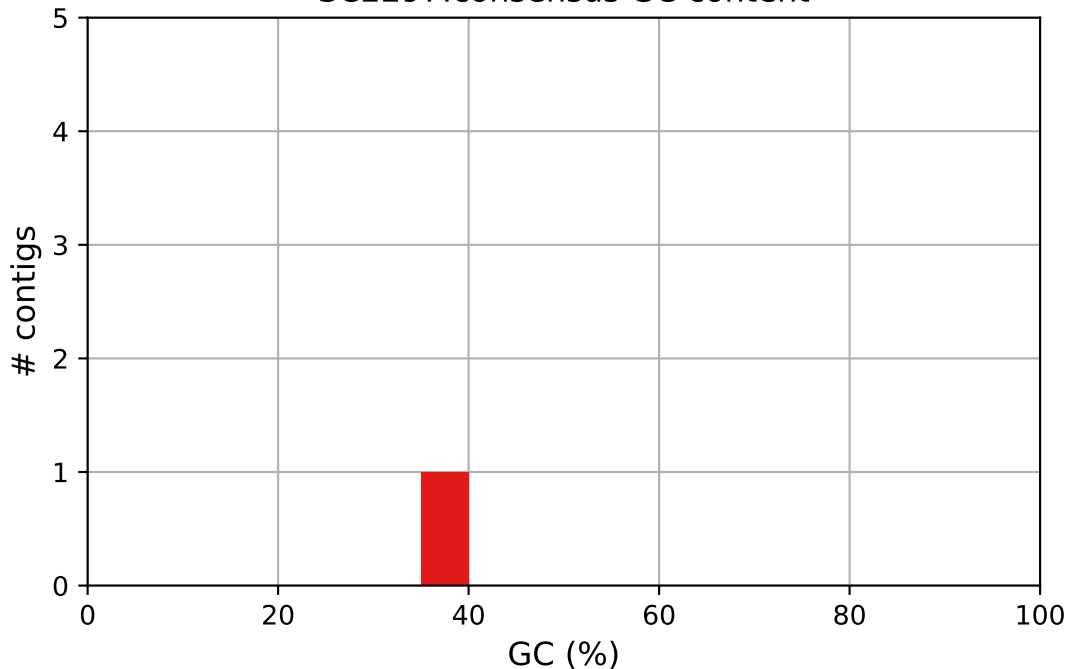


GC content



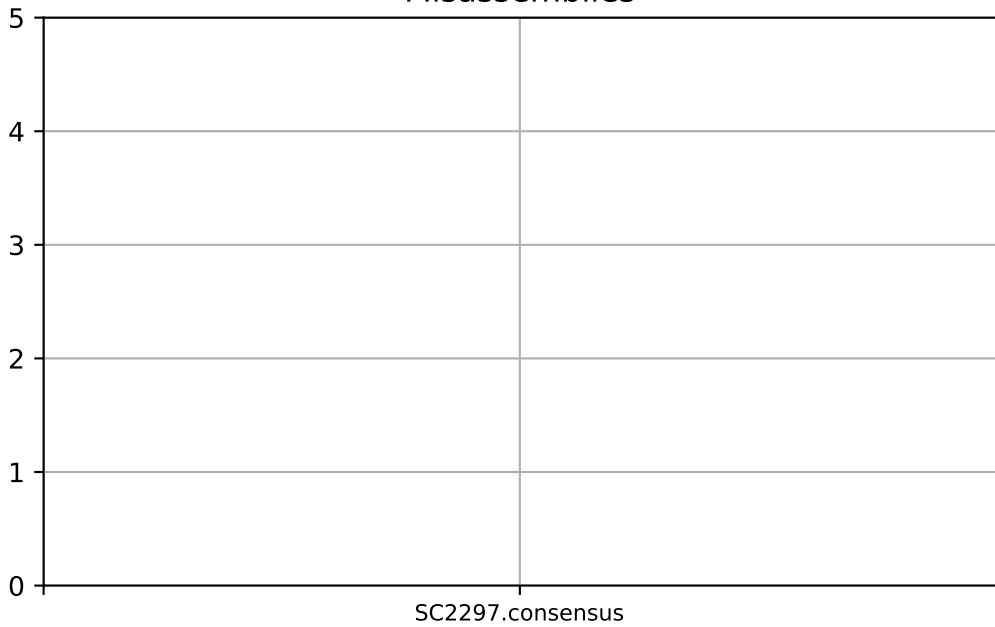
— SC2297.consensus - - Reference

SC2297.consensus GC content



SC2297.consensus

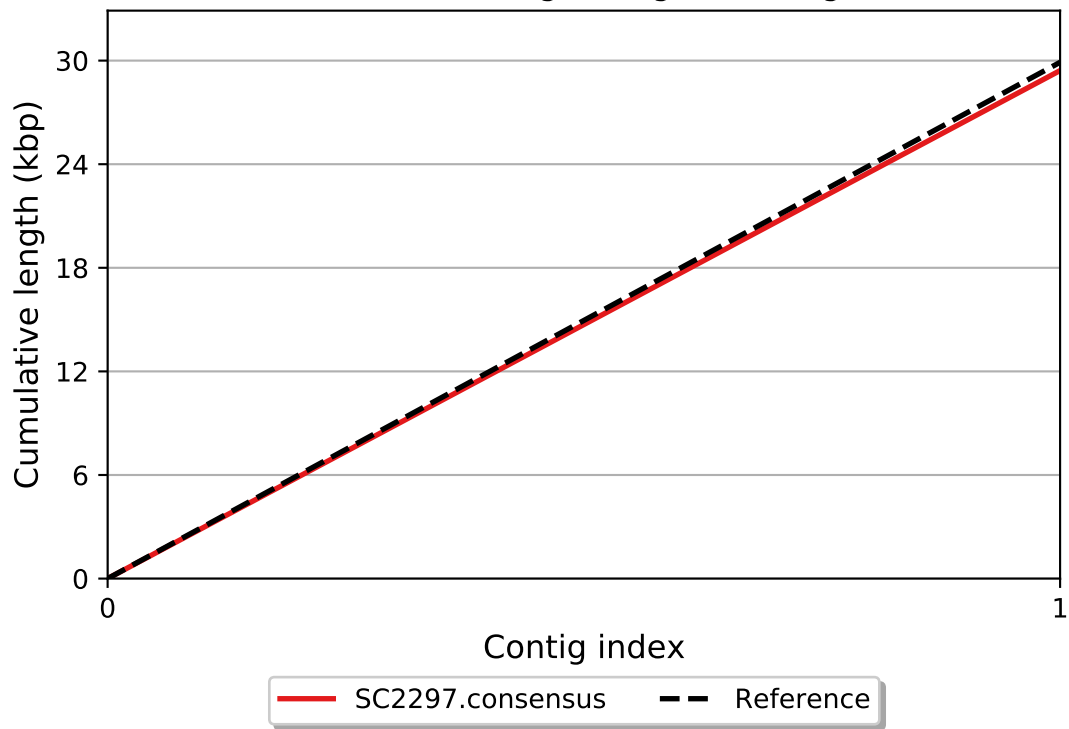
Misassemblies



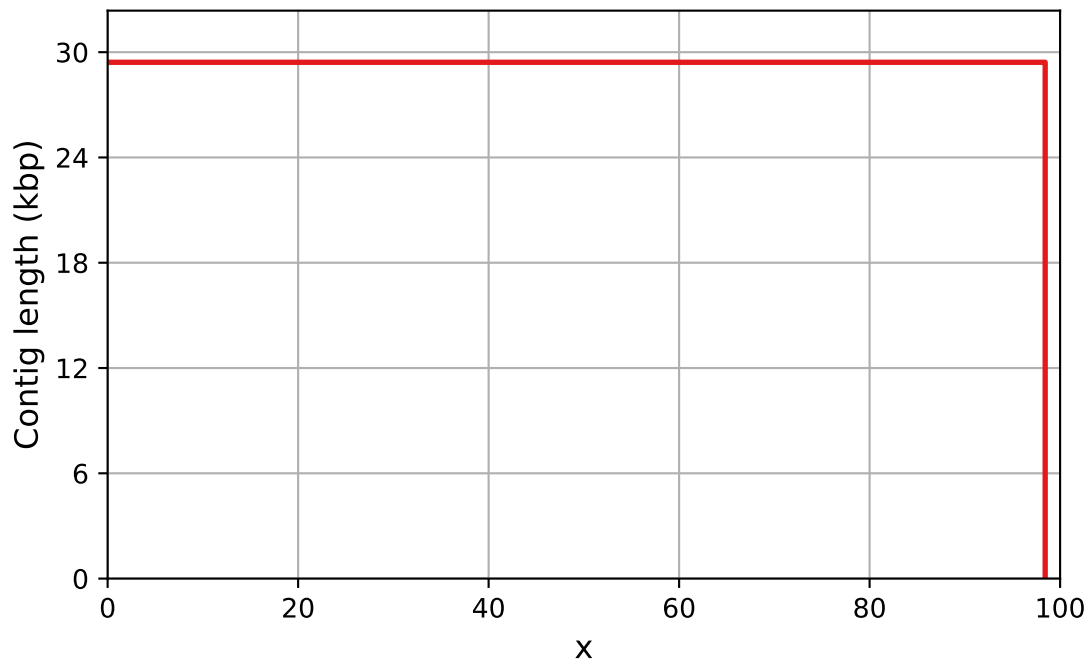
FRCurve (misassemblies)



Cumulative length (aligned contigs)

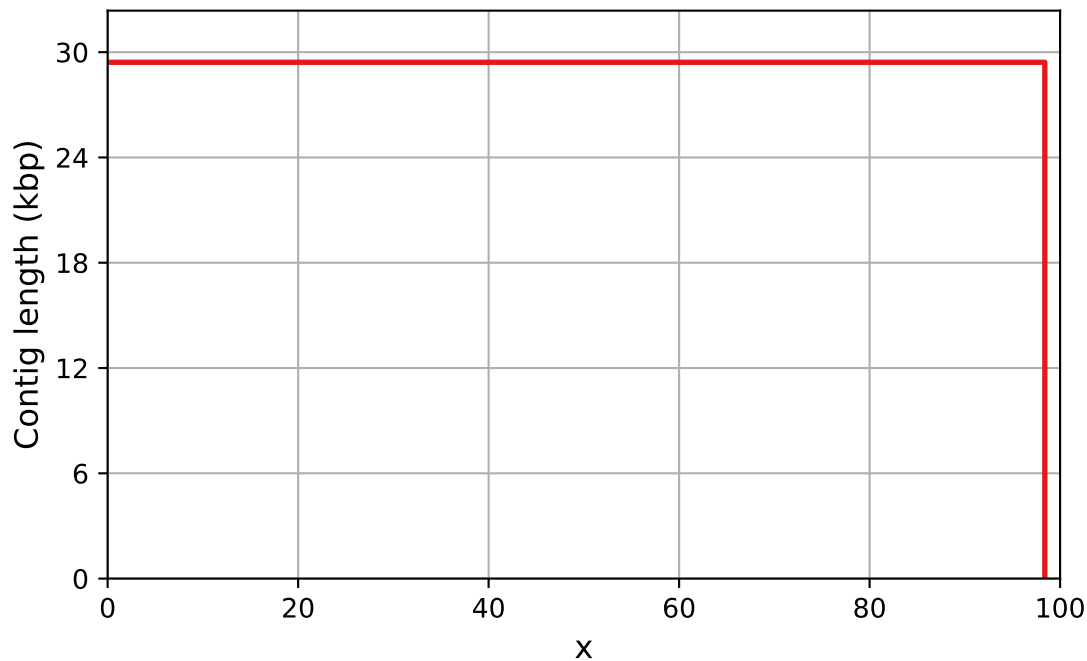


NAx

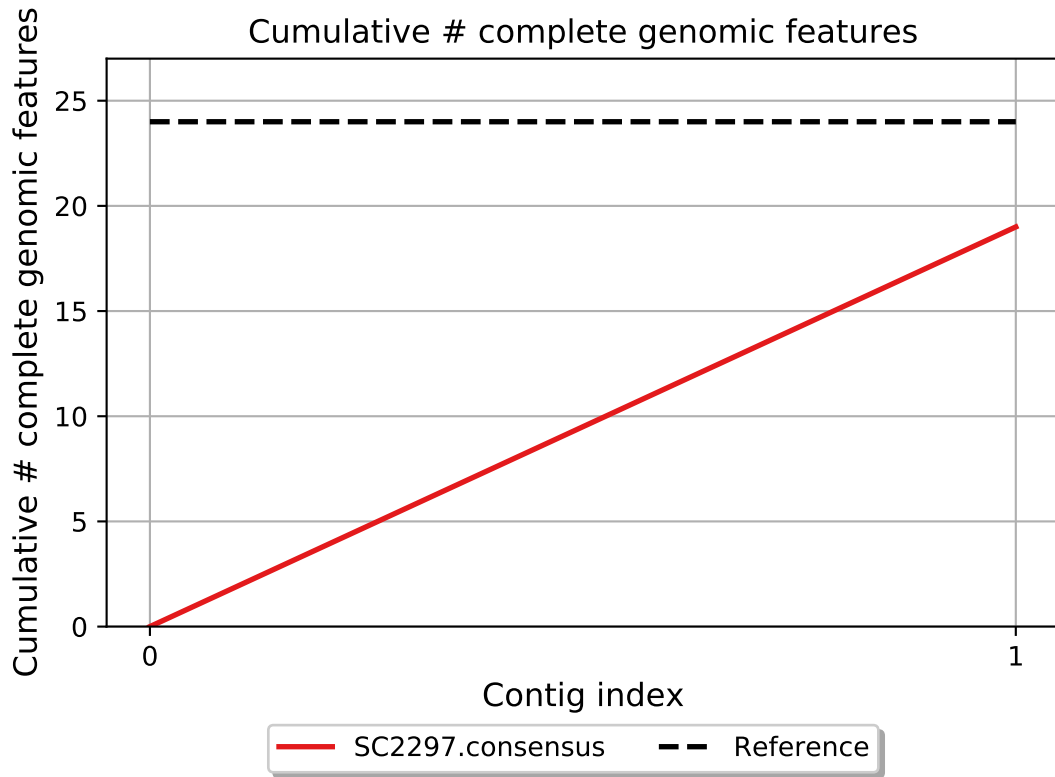


— SC2297.consensus

NGAx



— SC2297.consensus



FRCurve (genomic features)

