Report

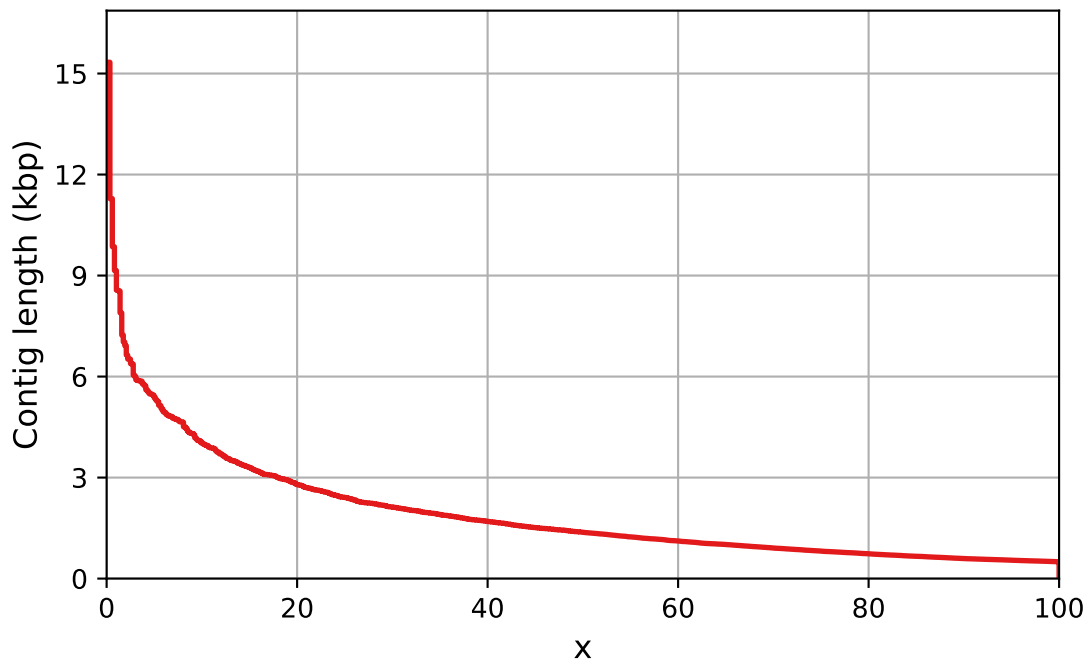|	TELL_Seq_BX10X_NA12878_phased_possorted_bam_filtered.long
# contigs (>= 0 bp)	11373
# contigs (>= 1000 bp)	1524
# contigs (>= 5000 bp)	40
# contigs (>= 10000 bp)	2
# contigs (>= 25000 bp)	0
# contigs (>= 50000 bp)	0
Total length (>= 0 bp)	6727059
Total length (>= 1000 bp)	2918551
Total length (>= 5000 bp)	263156
Total length (>= 10000 bp)	26619
Total length (>= 25000 bp)	0
Total length (>= 50000 bp)	0
# contigs	3761
Largest contig	15334
Total length	4446467
Reference length	45867
GC (%)	54.63
Reference GC (%)	39.17
N50	1372
NG50	11285
N75	817
NG75	9858
L50	927
LG50	2
L75	1986
LG75	3
# misassemblies	0
# misassembled contigs	0
Misassembled contigs length	0
# local misassemblies	0
# scaffold gap ext. mis.	0
# scaffold gap loc. mis.	0
# unaligned mis. contigs	0
# unaligned contigs	3742 + 2 part
Unaligned length	4422115
Genome fraction (%)	49.777
Duplication ratio	1.067
# N's per 100 kbp	0.00
# mismatches per 100 kbp	113.88
# indels per 100 kbp	8.76
Largest alignment	4815
Total aligned length	23435
NGA50	542
LGA50	16

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

	TELL_Seq_BX10X_NA12878_phased_possorted_bam_filtered.long
# 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.	0
# unaligned mis. contigs	0
# mismatches	26
# indels	2
# indels (<= 5 bp)	2
# indels (> 5 bp)	0
Indels length	4

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
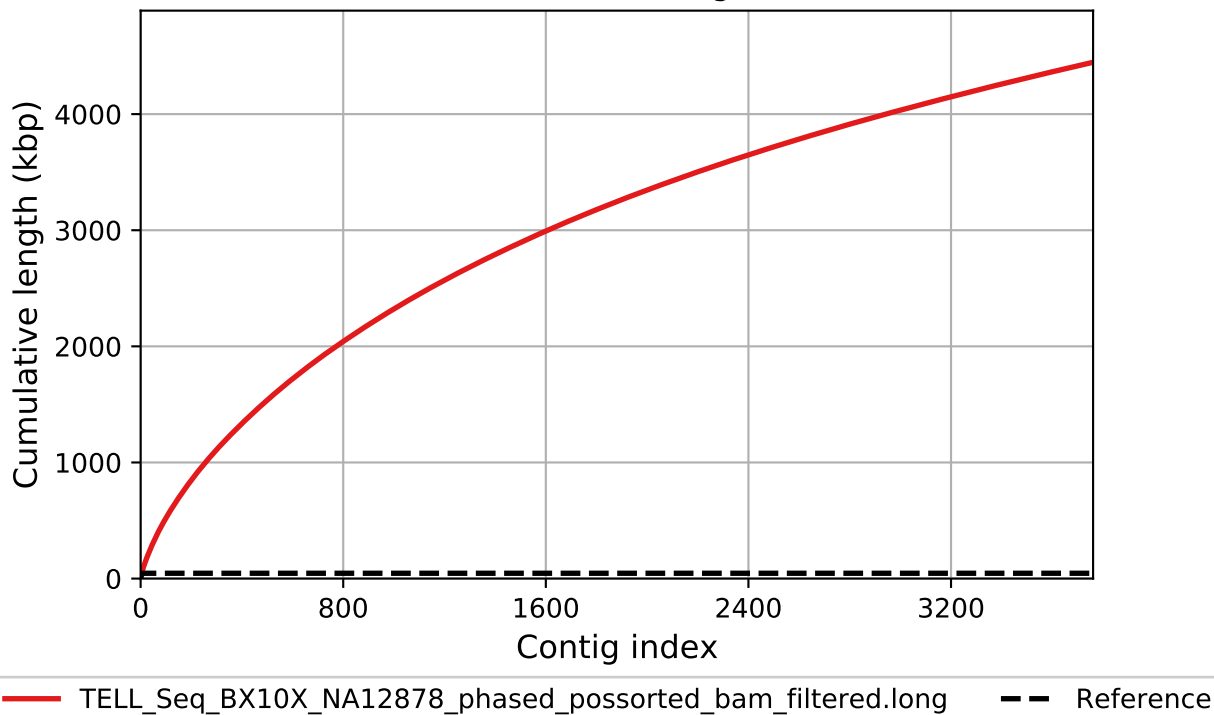
	TELL_Seq_BX10X_NA12878_phased_possorted_bam_filtered.long
# fully unaligned contigs	3742
Fully unaligned length	4415990
# partially unaligned contigs	2
Partially unaligned length	6125
# N's	0

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

TELL_Seq_BX10X_NA12878_phased_possorted_bam_filtered.long

NGx
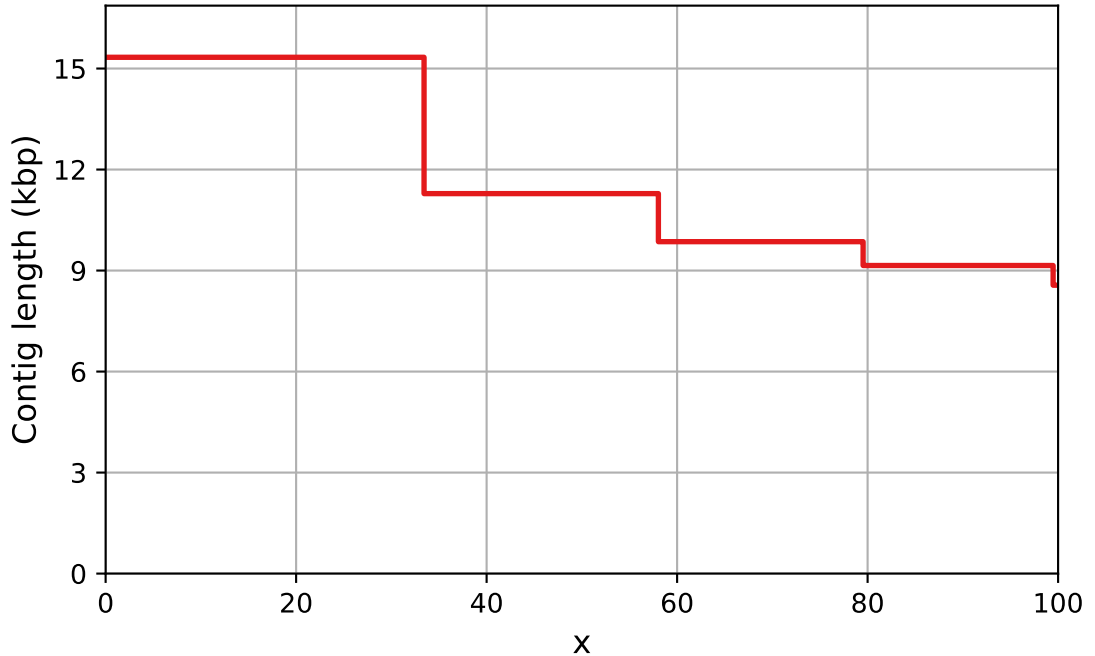
TELL_Seq_BX10X_NA12878_phased_possorted_bam_filtered.long

Cumulative length

TELL_Seq_BX10X_NA12878_phased_possorted_bam_filtered.long — — Reference

GC content

TELL_Seq_BX10X_NA12878_phased_possorted_bam_filtered.long — — Reference
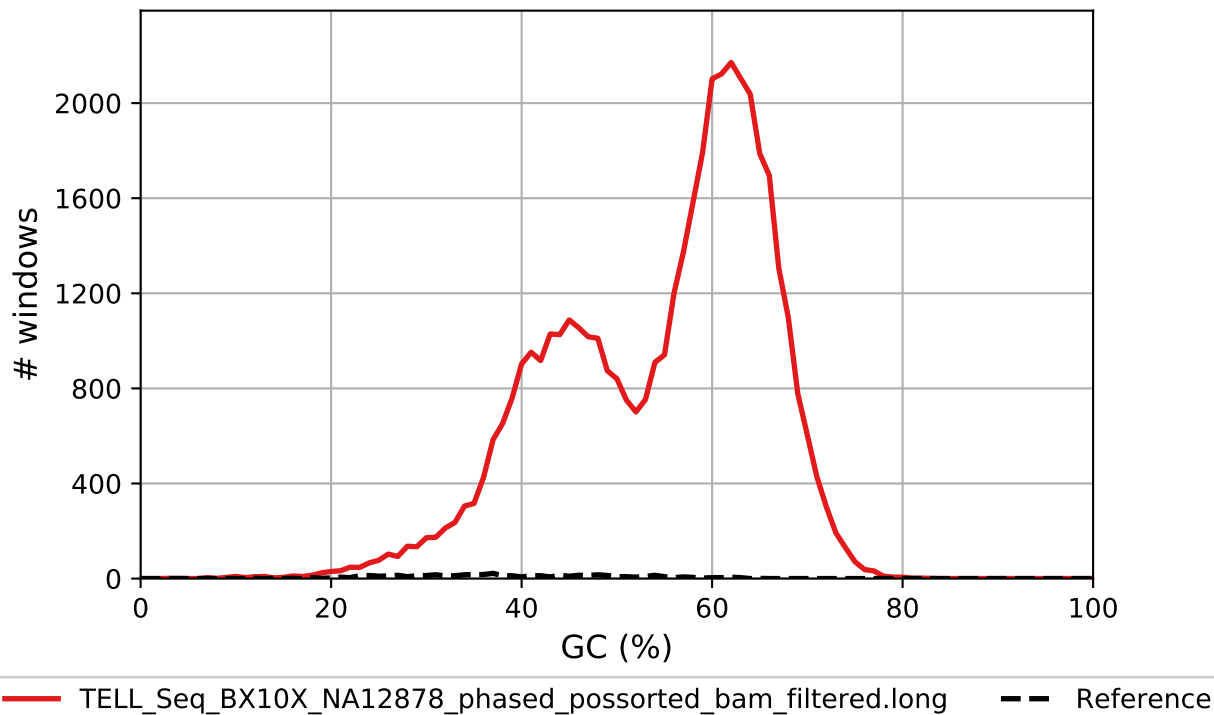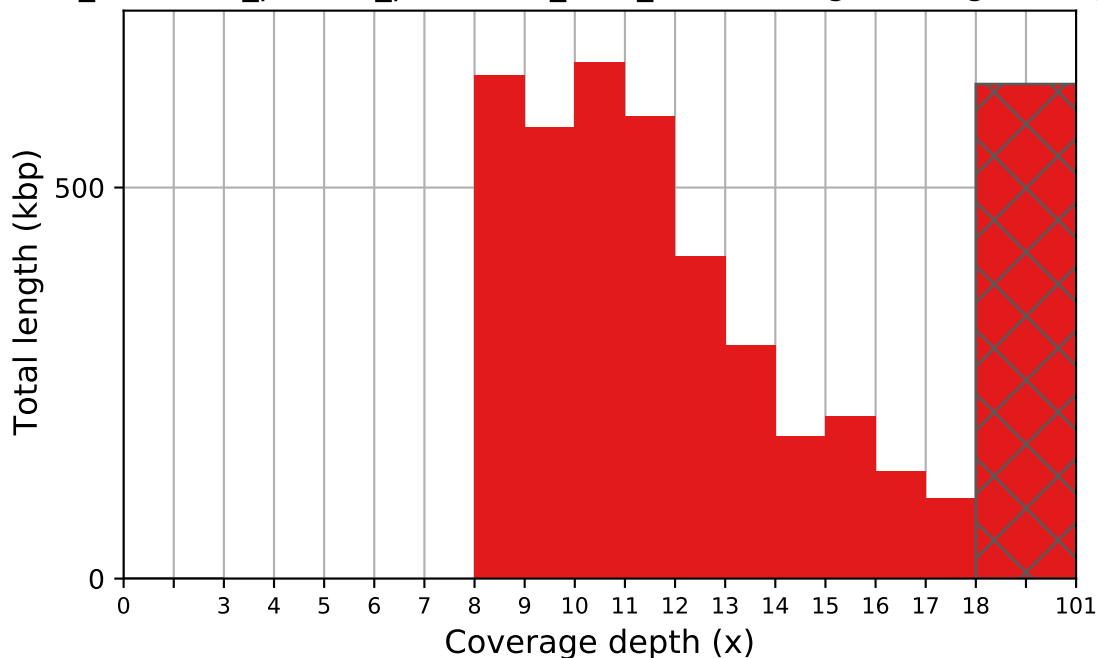
TELL_Seq_BX10X_NA12878_phased_possorted_bam_filtered.long GC content
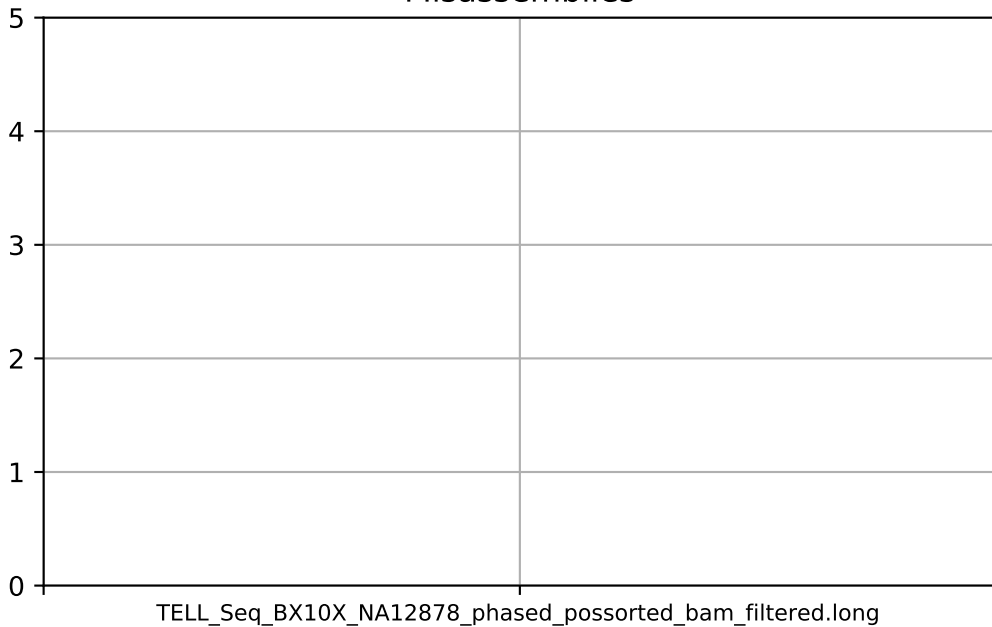
Coverage histogram (bin size: 1x)
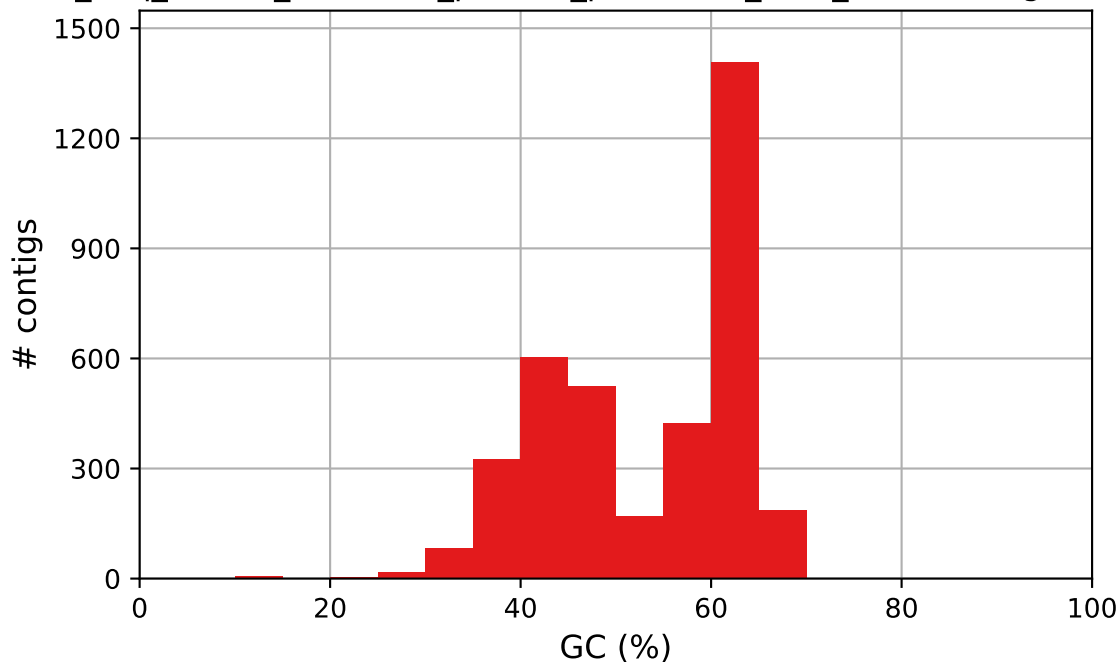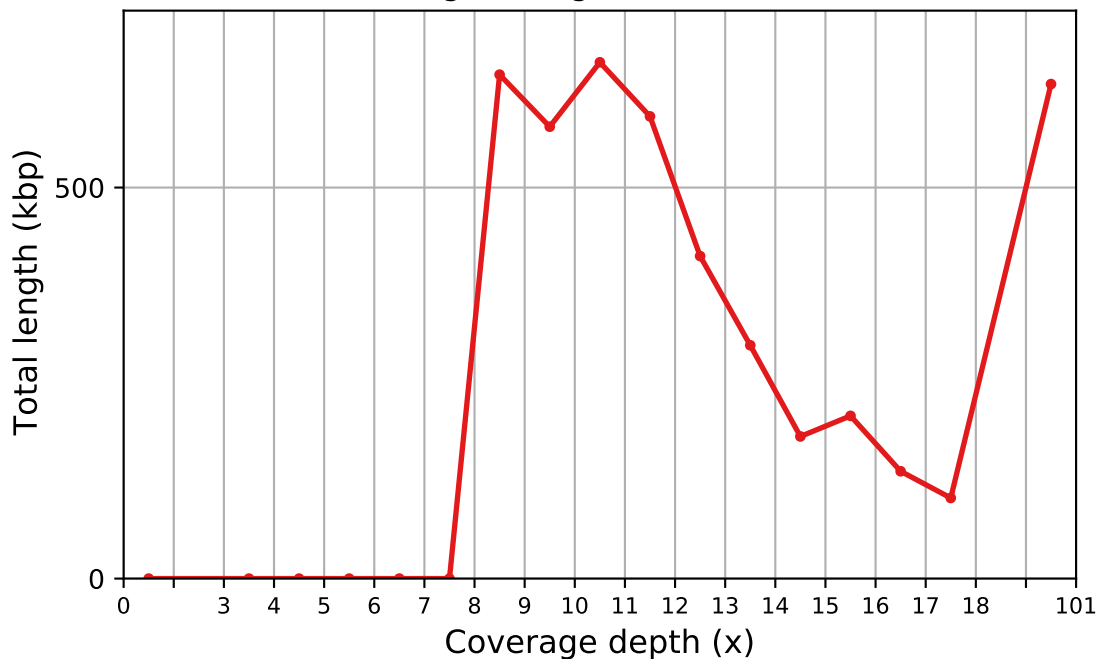
TELL_Seq_BX10X_NA12878_phased_possorted_bam_filtered.long coverage histogram

Misassemblies

TELL_Seq_BX10X_NA12878_phased_possorted_bam_filtered.long

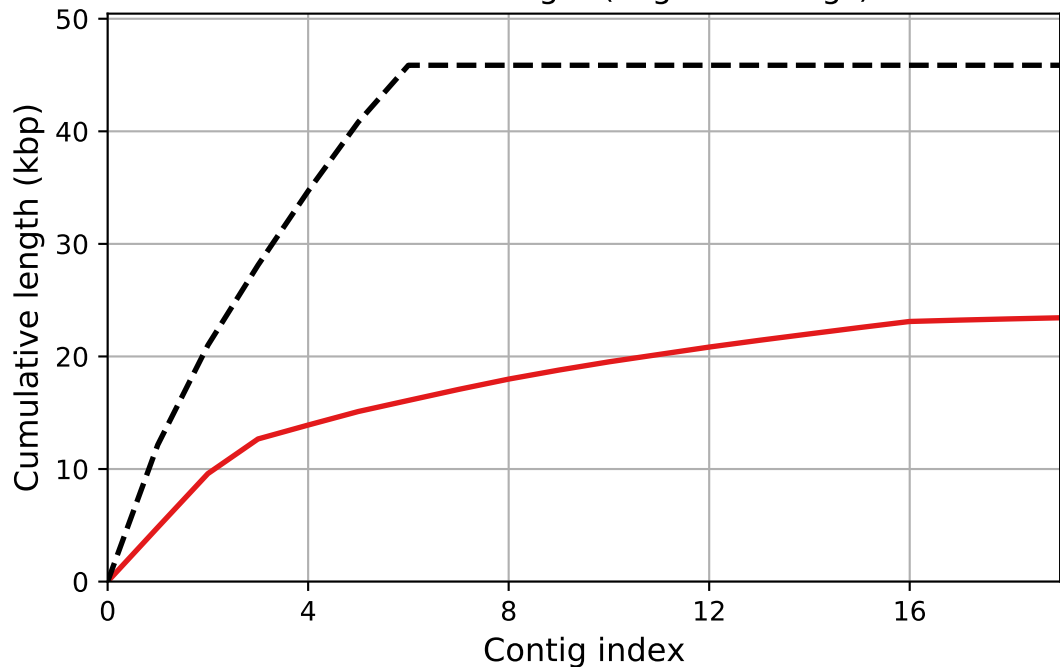FRCurve (misassemblies)
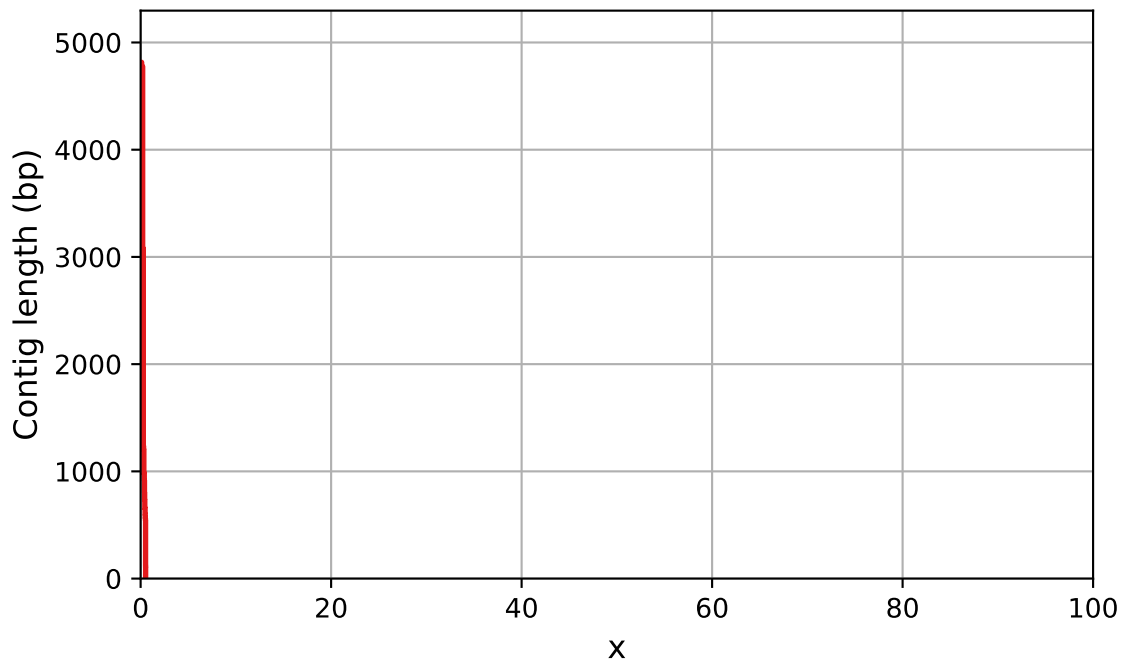
TELL_Seq_BX10X_NA12878_phased_possorted_bam_filtered.long
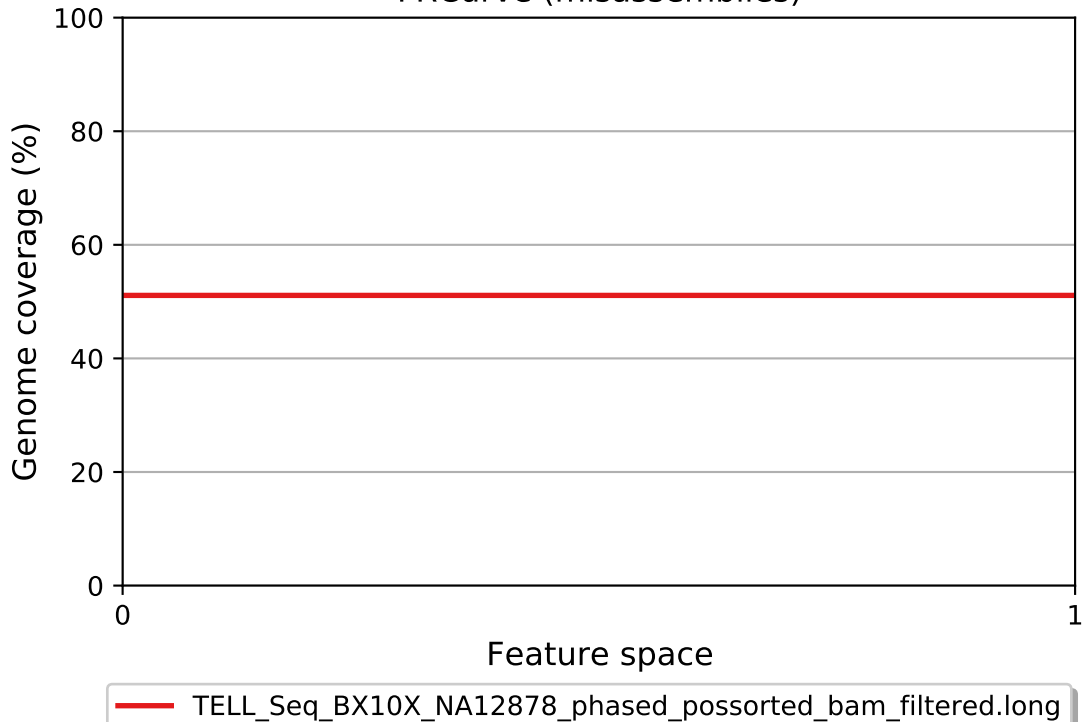
Cumulative length (aligned contigs)
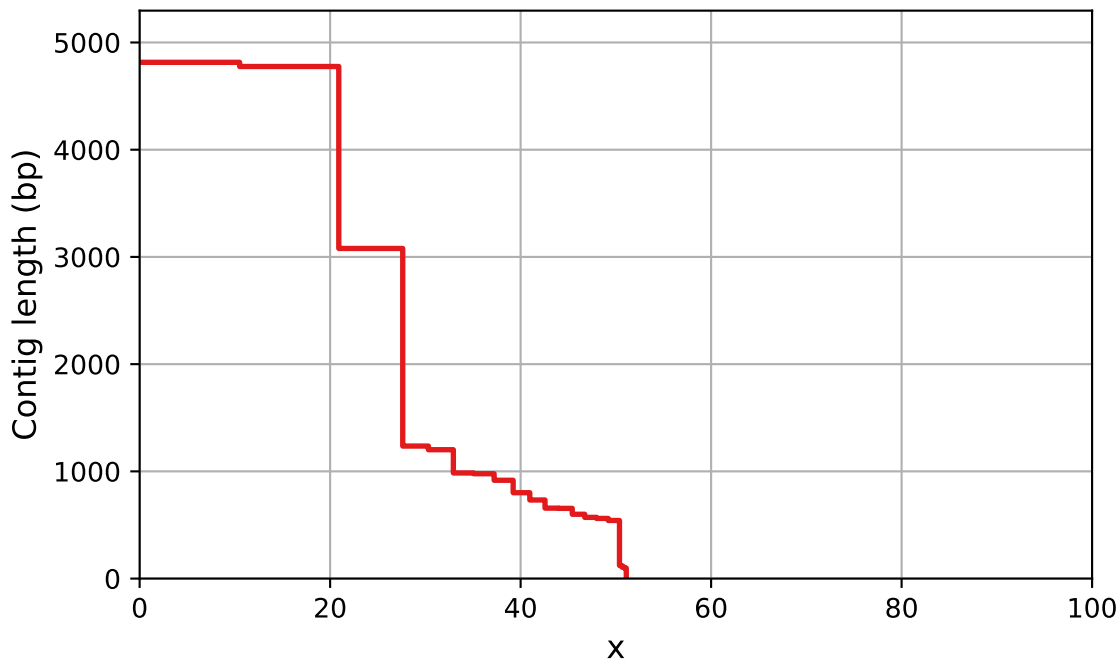
TELL_Seq_BX10X_NA12878_phased_possorted_bam_filtered.long — Reference

NAx

TELL_Seq_BX10X_NA12878_phased_possorted_bam_filtered.long

NGAx

TELL_Seq_BX10X_NA12878_phased_possorted_bam_filtered.long