Report

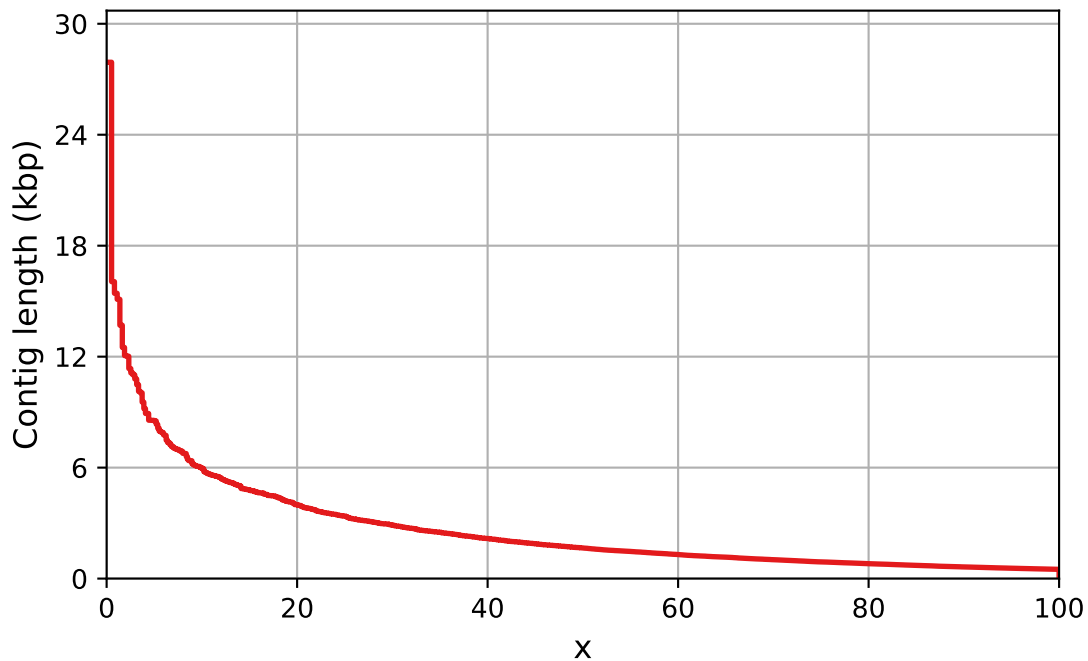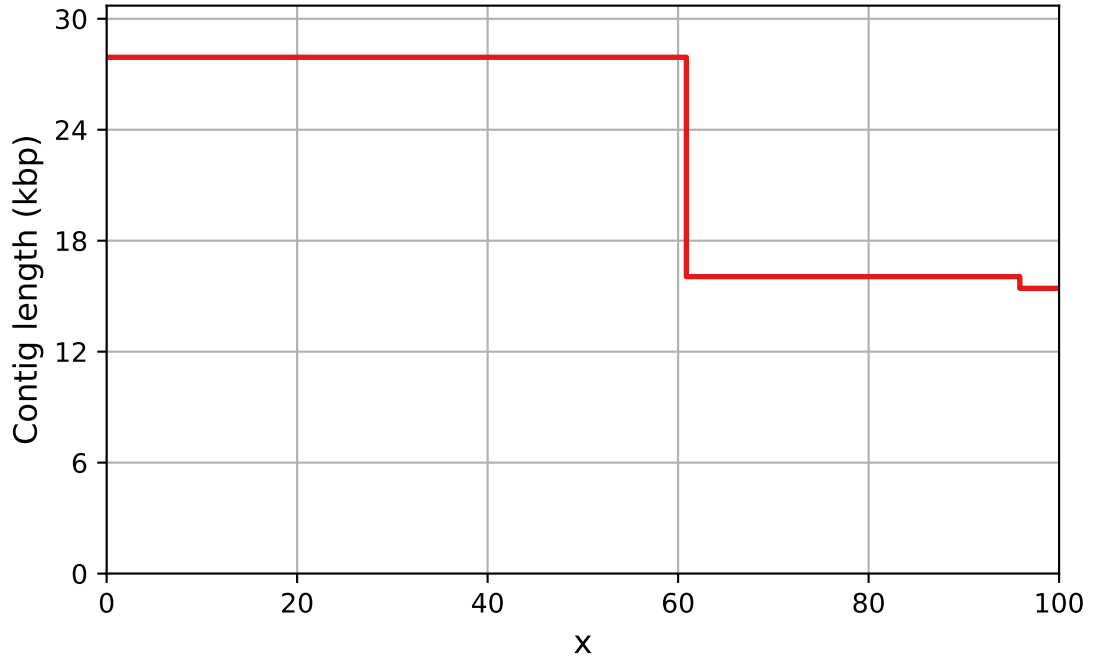|	TELL_Seq_BX10X_NA12878_phased_possorted_bam_filtered.long
# contigs (>= 0 bp)	11147
# contigs (>= 1000 bp)	1716
# contigs (>= 5000 bp)	101
# contigs (>= 10000 bp)	15
# contigs (>= 25000 bp)	1
# contigs (>= 50000 bp)	0
Total length (>= 0 bp)	7517683
Total length (>= 1000 bp)	3799679
Total length (>= 5000 bp)	751032
Total length (>= 10000 bp)	199714
Total length (>= 25000 bp)	27918
Total length (>= 50000 bp)	0
# contigs	3969
Largest contig	27918
Total length	5356908
Reference length	45867
GC (%)	56.52
Reference GC (%)	39.17
N50	1659
NG50	27918
N75	903
NG75	16057
L50	834
LG50	1
L75	1946
LG75	2
# 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	3951 + 1 part
Unaligned length	5328445
Genome fraction (%)	59.548
Duplication ratio	1.042
# N's per 100 kbp	0.00
# mismatches per 100 kbp	65.90
# indels per 100 kbp	7.32
Largest alignment	4870
Total aligned length	27520
NGA50	871
LGA50	11

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
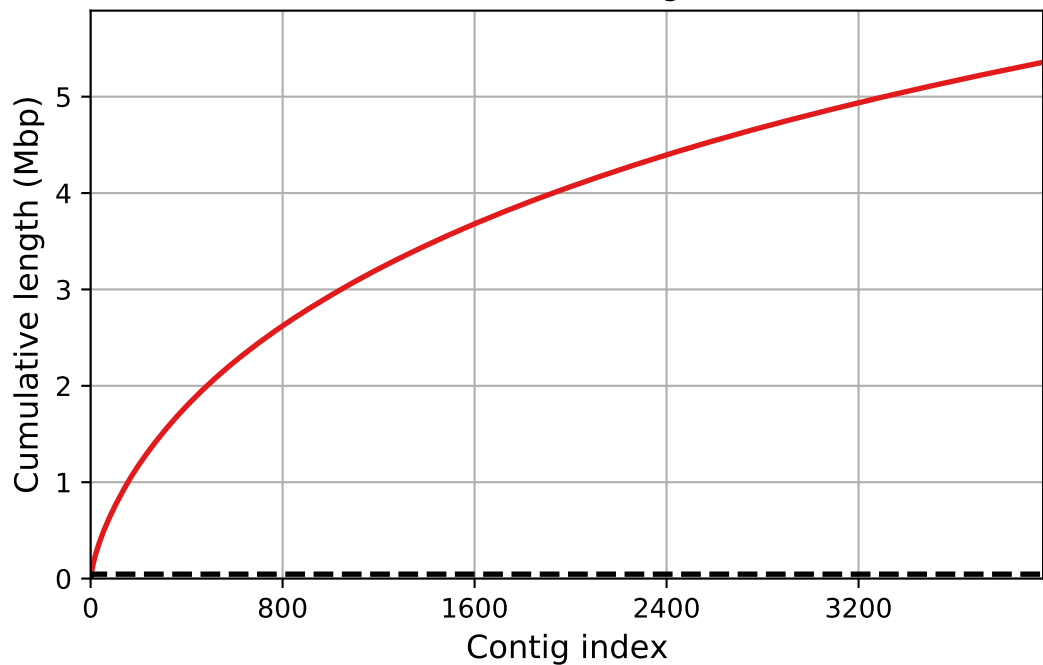
	TELL_Seq_BX10X_NA12878_phased_possorted_bam_filtered.long
# misassemblies	0
# contig misassemblies	0
# c. relocations	0
# c. translocations	0
# c. inversions	0
# scaffold misassemblies	0
# s. relocations	0
# s. translocations	0
# s. inversions	0
# misassembled contigs	0
Misassembled contigs length	0
# local misassemblies	0
# scaffold gap ext. mis.	0
# scaffold gap loc. mis.	0
# unaligned mis. contigs	0
# mismatches	18
# 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	3951
Fully unaligned length	5327404
# partially unaligned contigs	1
Partially unaligned length	1041
# 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

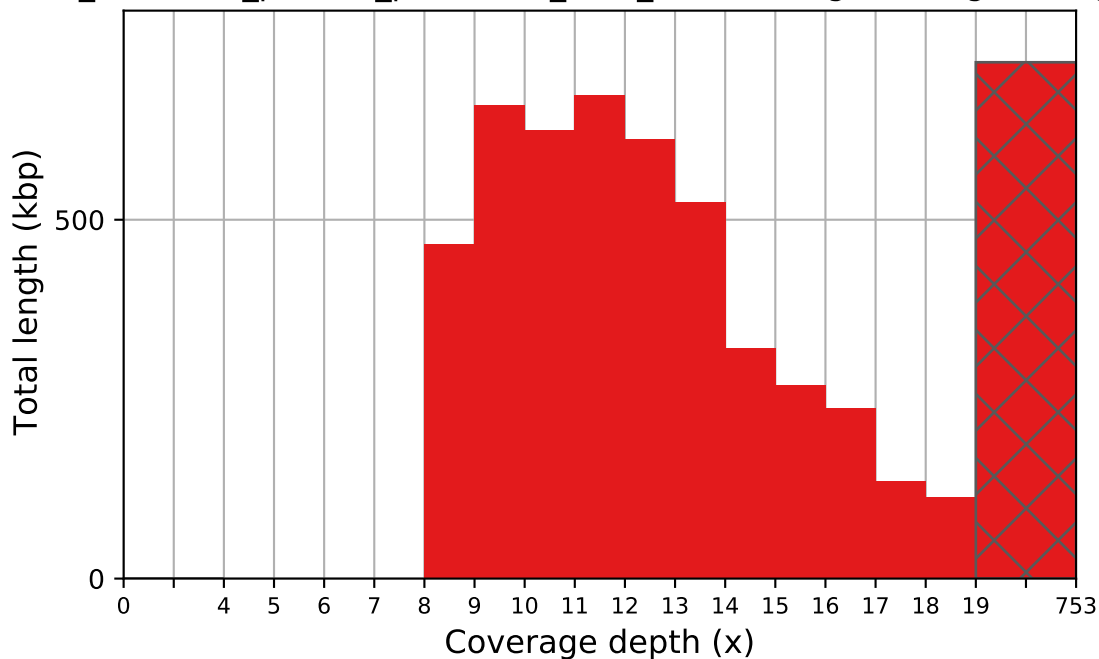TELL_Seq_BX10X_NA12878_phased_possorted_bam_filtered.long GC content
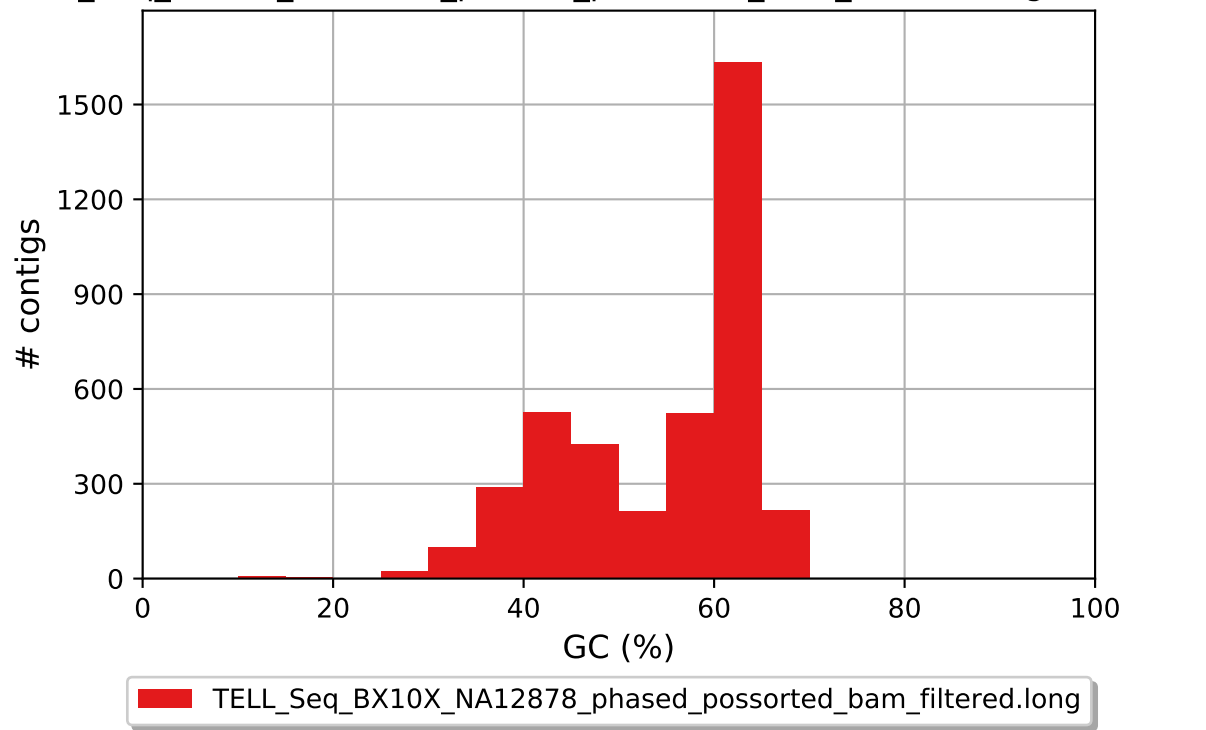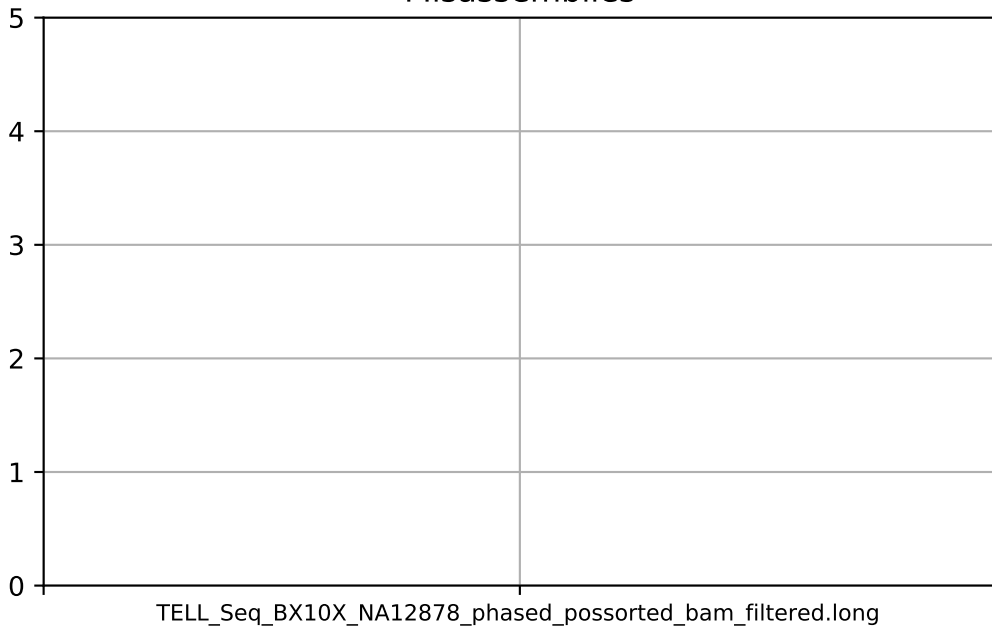
Coverage histogram (bin size: 1x)
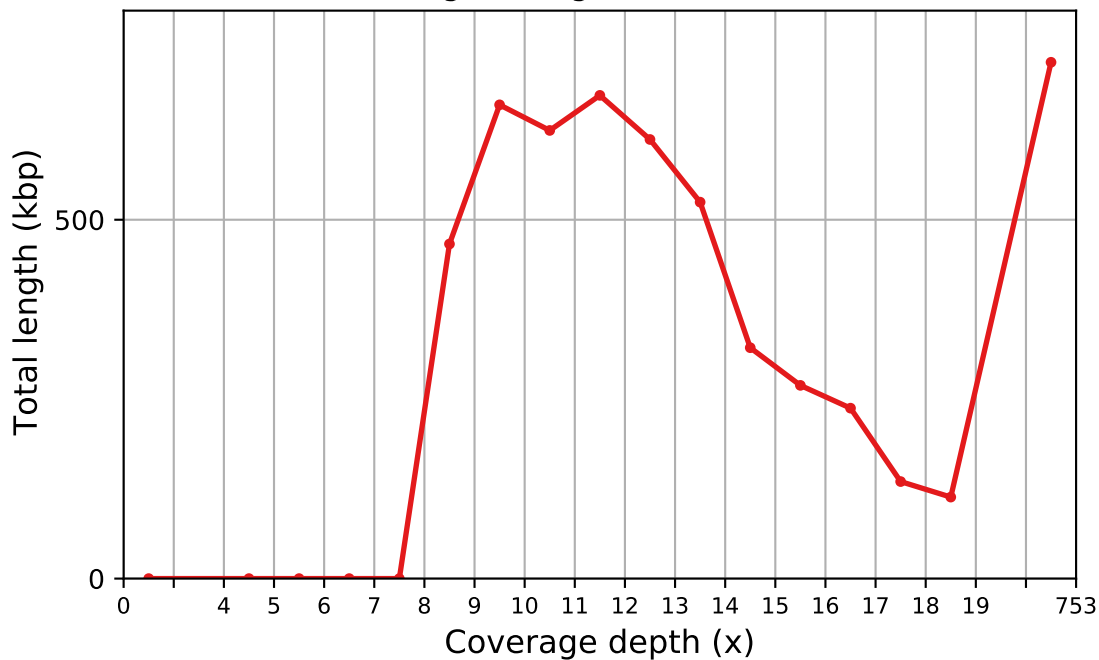
TELL_Seq_BX10X_NA12878_phased_possorted_bam_filtered.long coverage histogram (

Misassemblies
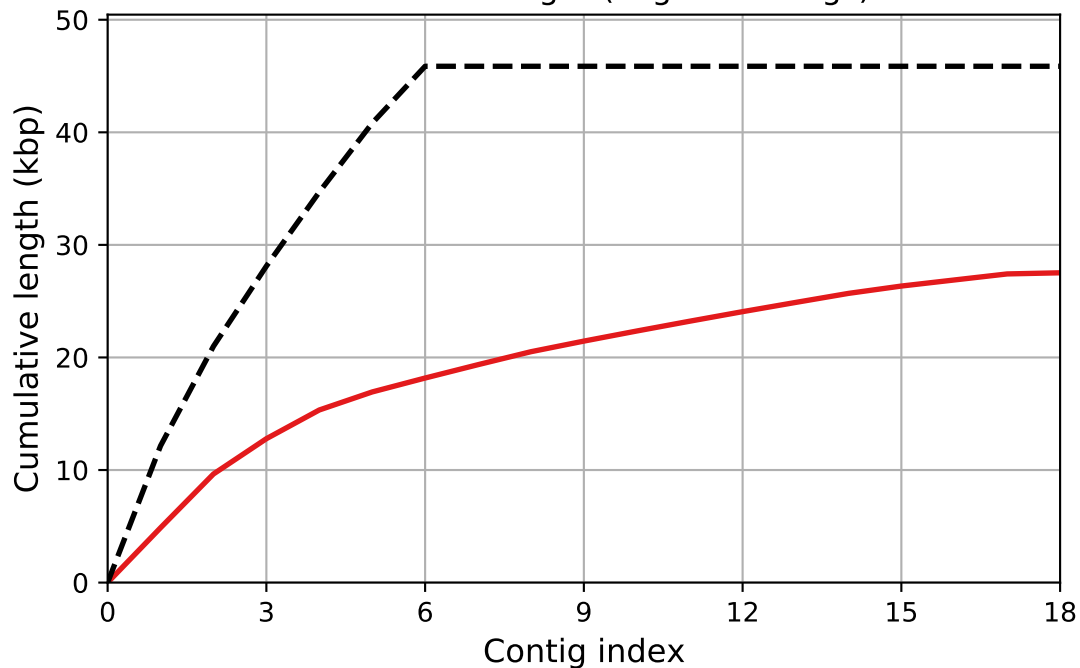
TELL_Seq_BX10X_NA12878_phased_possorted_bam_filtered.long

FRCurve (misassemblies)

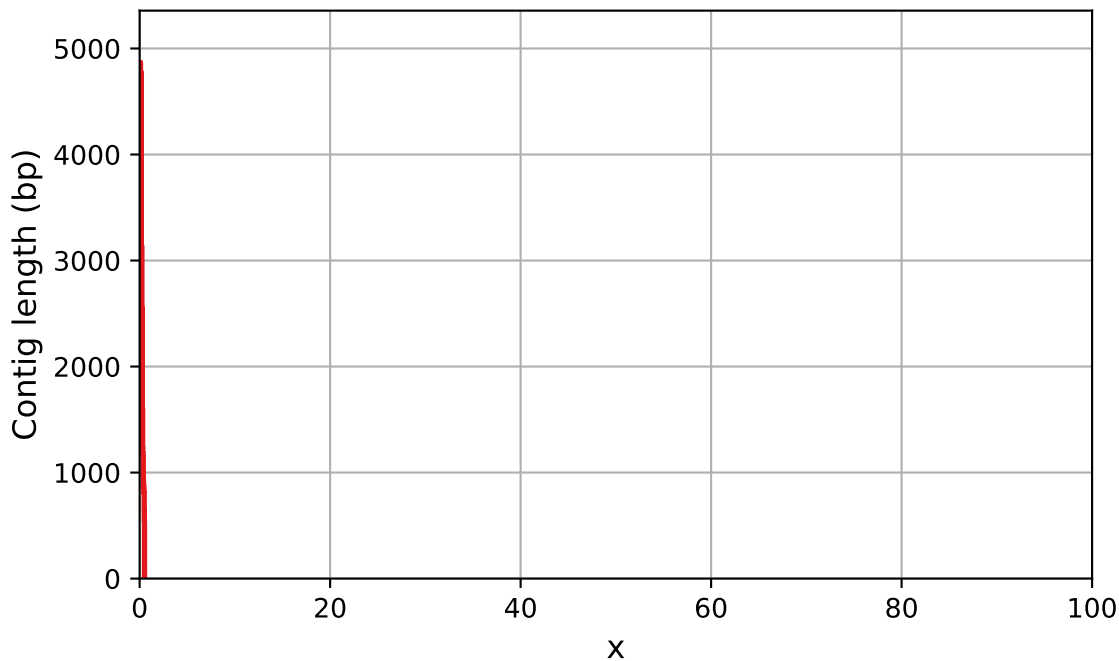TELL_Seq_BX10X_NA12878_phased_possorted_bam_filtered.long
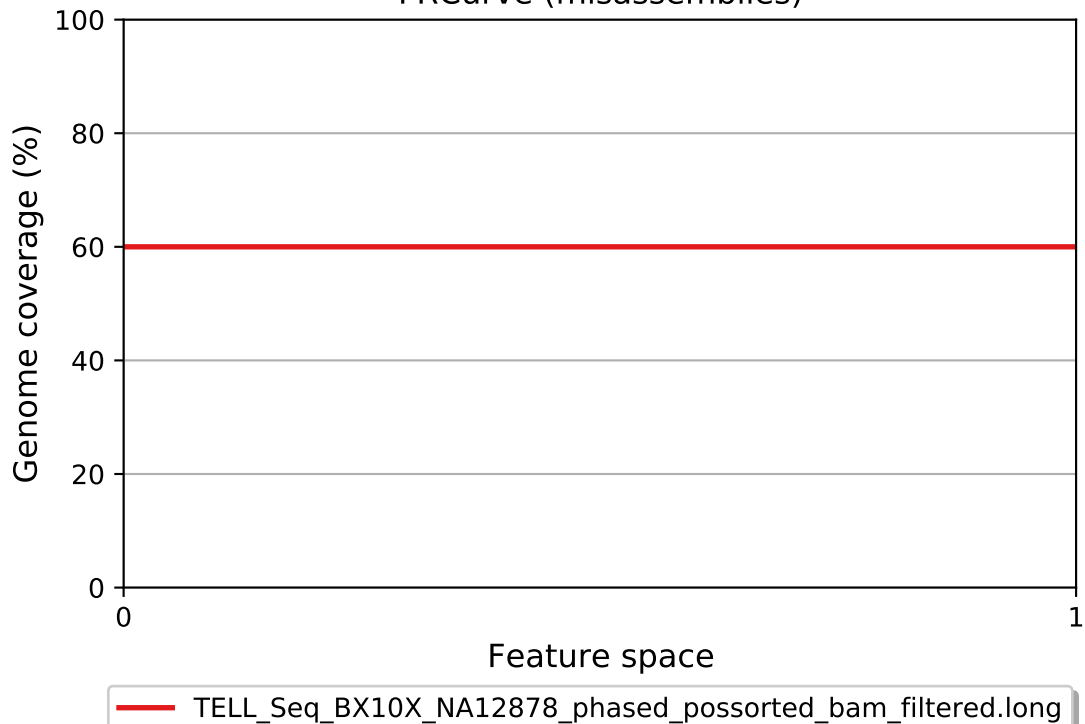
Cumulative length (aligned contigs)

NAx

TELL_Seq_BX10X_NA12878_phased_possorted_bam_filtered.long

NGAx