

Report

	combined.final.contigs
# contigs (>= 0 bp)	334983
# contigs (>= 1000 bp)	58144
# contigs (>= 5000 bp)	3683
# contigs (>= 10000 bp)	1050
# contigs (>= 25000 bp)	195
# contigs (>= 50000 bp)	54
Total length (>= 0 bp)	278184651
Total length (>= 1000 bp)	135786855
Total length (>= 5000 bp)	39091828
Total length (>= 10000 bp)	21401498
Total length (>= 25000 bp)	9214363
Total length (>= 50000 bp)	4393864
# contigs	178912
Largest contig	256554
Total length	217947069
Reference length	103878306
N50	1359
N75	768
L50	34944
L75	89973
# misassemblies	1
# misassembled contigs	1
Misassembled contigs length	513
# local misassemblies	3
# unaligned mis. contigs	3
# unaligned contigs	178707 + 142 part
Unaligned length	217885060
Genome fraction (%)	0.047
Duplication ratio	1.737
# N's per 100 kbp	0.00
# mismatches per 100 kbp	2423.54
# indels per 100 kbp	175.59
Largest alignment	4113
Total aligned length	38092

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

	combined.final.contigs
# misassemblies	1
# relocations	0
# translocations	0
# inversions	0
# interspecies translocations	1
# misassembled contigs	1
Misassembled contigs length	513
# possibly misassembled contigs	0
# possible misassemblies	0
# local misassemblies	3
# unaligned mis. contigs	3
# mismatches	1187
# indels	86
# indels (<= 5 bp)	84
# indels (> 5 bp)	2
Indels length	132

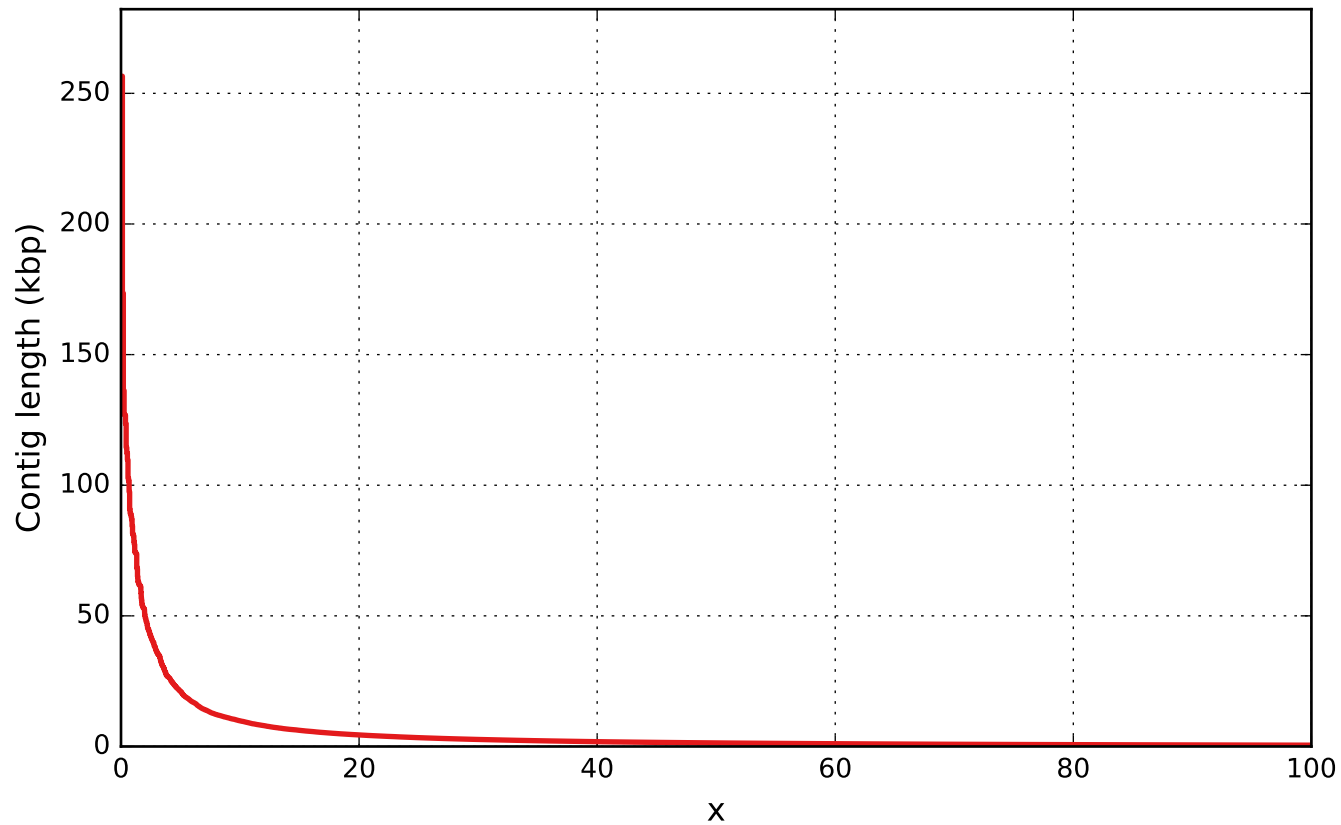
All statistics are based on contigs of size ≥ 500 bp, unless otherwise noted (e.g., "# contigs (≥ 0 bp)" and "Total length (≥ 0 bp)" include all contigs).

Unaligned report

	combined.final.contigs
# fully unaligned contigs	178707
Fully unaligned length	217026444
# partially unaligned contigs	142
Partially unaligned length	858616
# N's	0

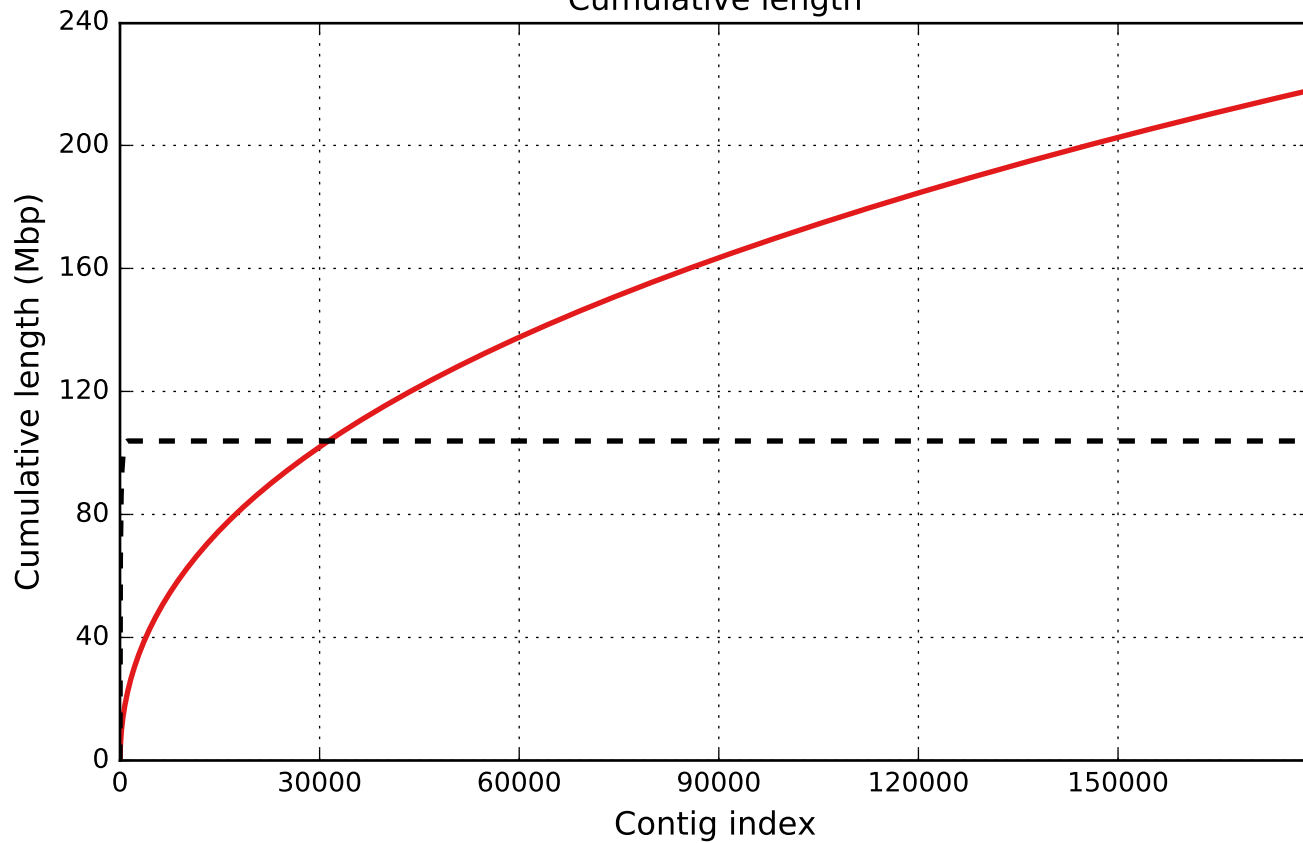
All statistics are based on contigs of size ≥ 500 bp, unless otherwise noted (e.g., "# contigs (≥ 0 bp)" and "Total length (≥ 0 bp)" include all contigs).

Nx

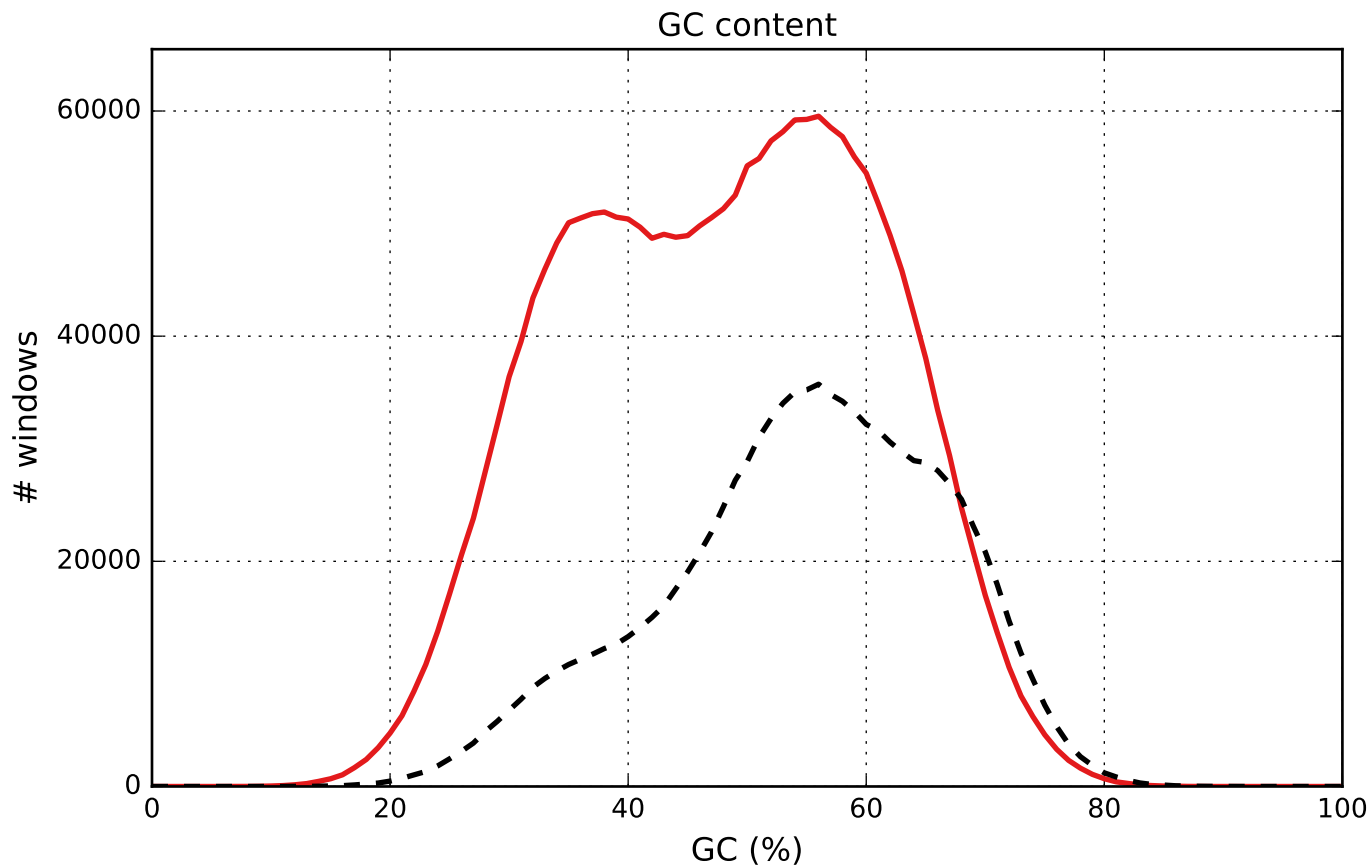


— combined.final.contigs

Cumulative length

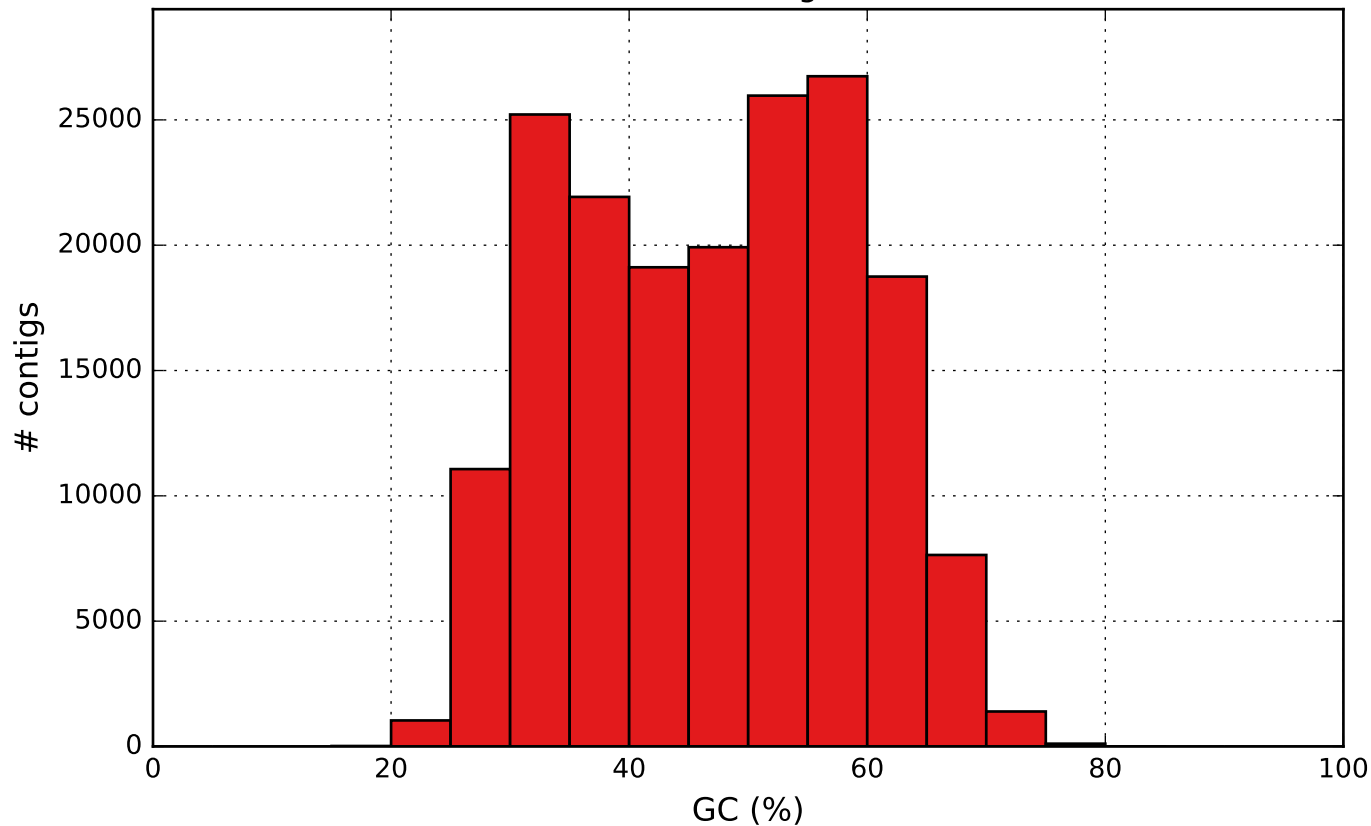


— combined.final.contigs - - Reference

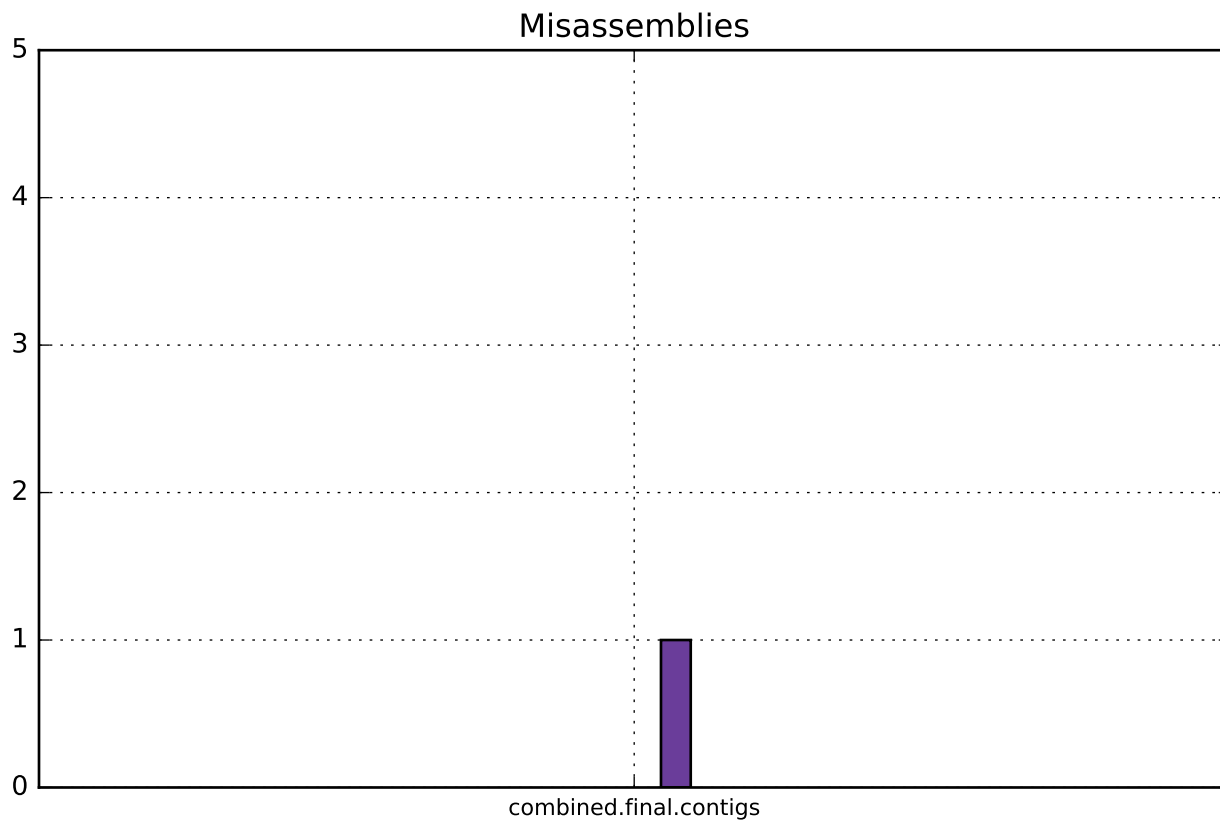



— combined.final.contigs - - Reference

combined.final.contigs GC content

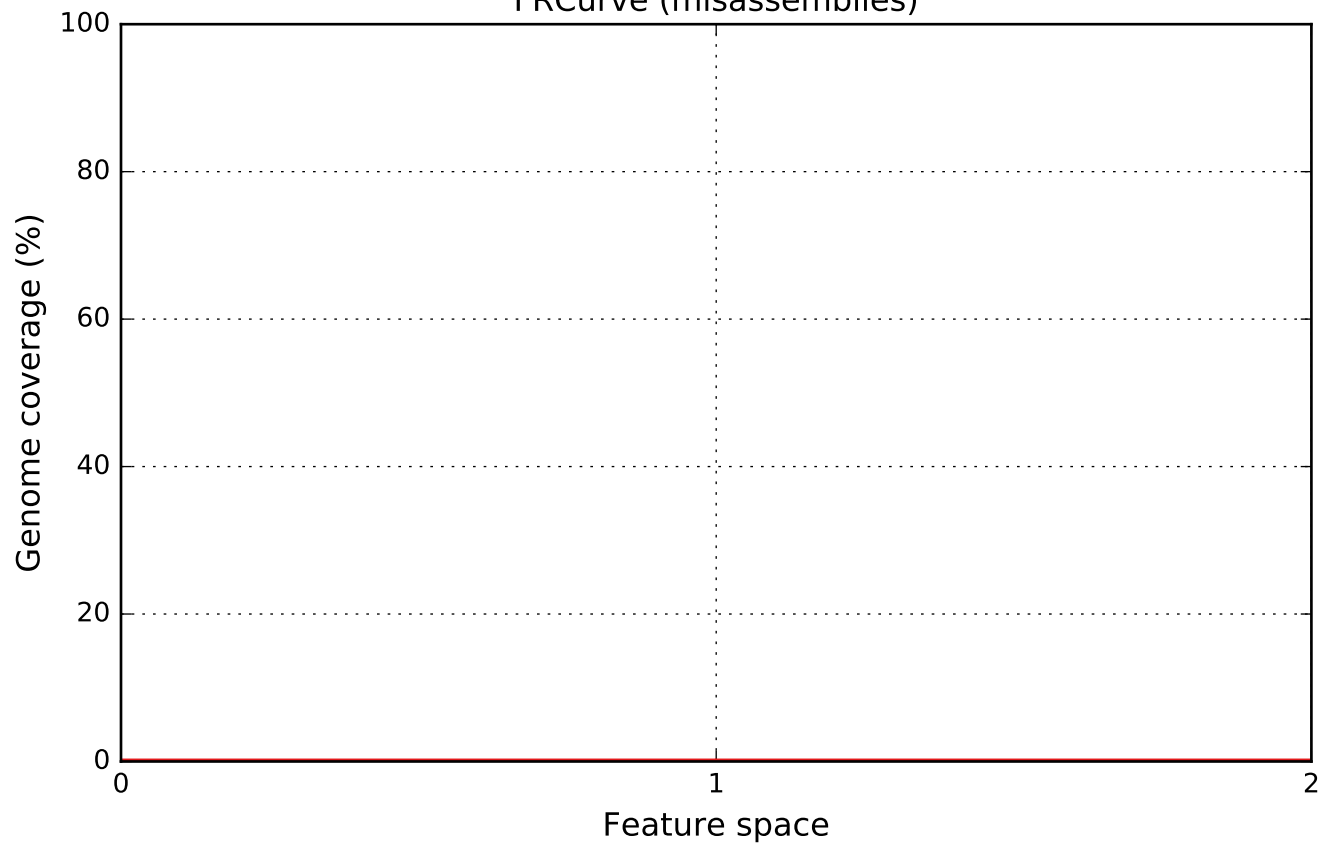


combined.final.contigs



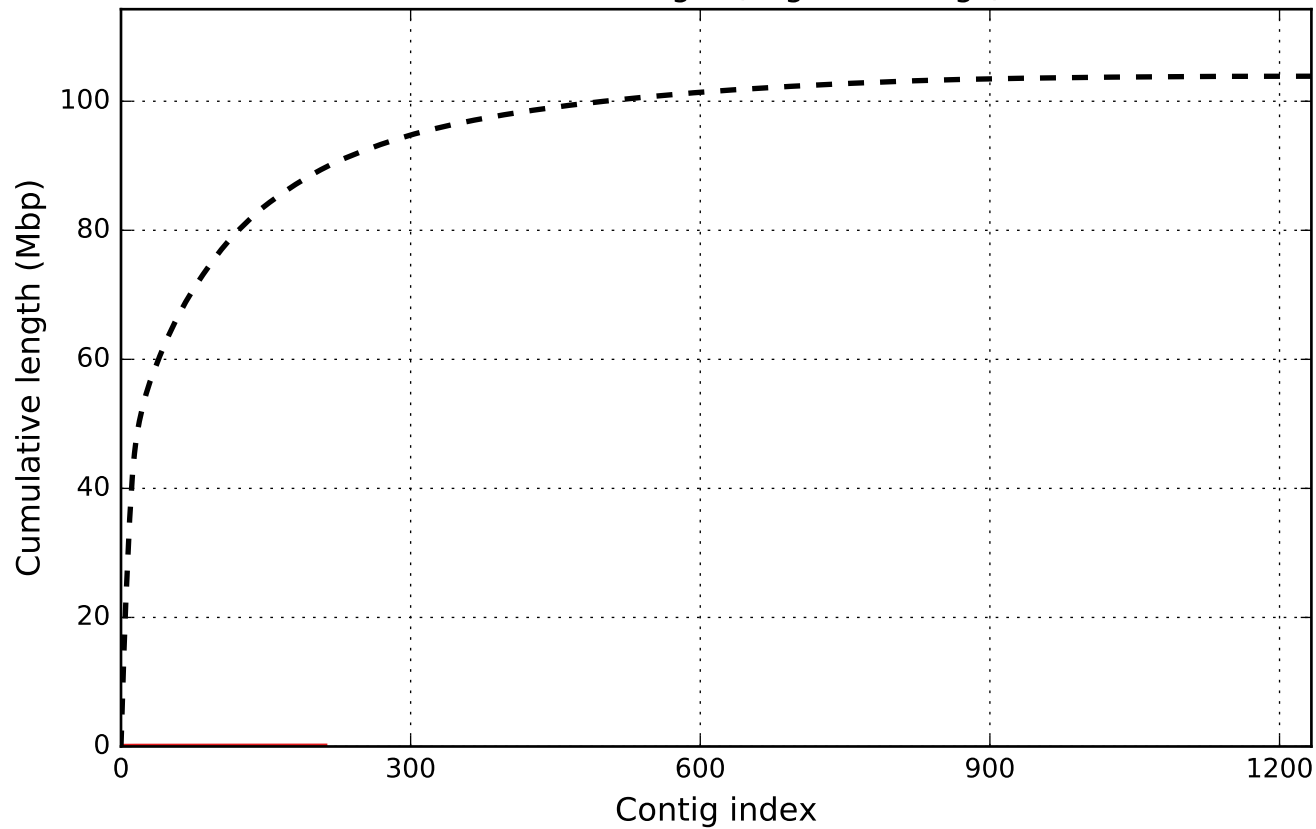
 # interspecies translocations

FRCurve (misassemblies)

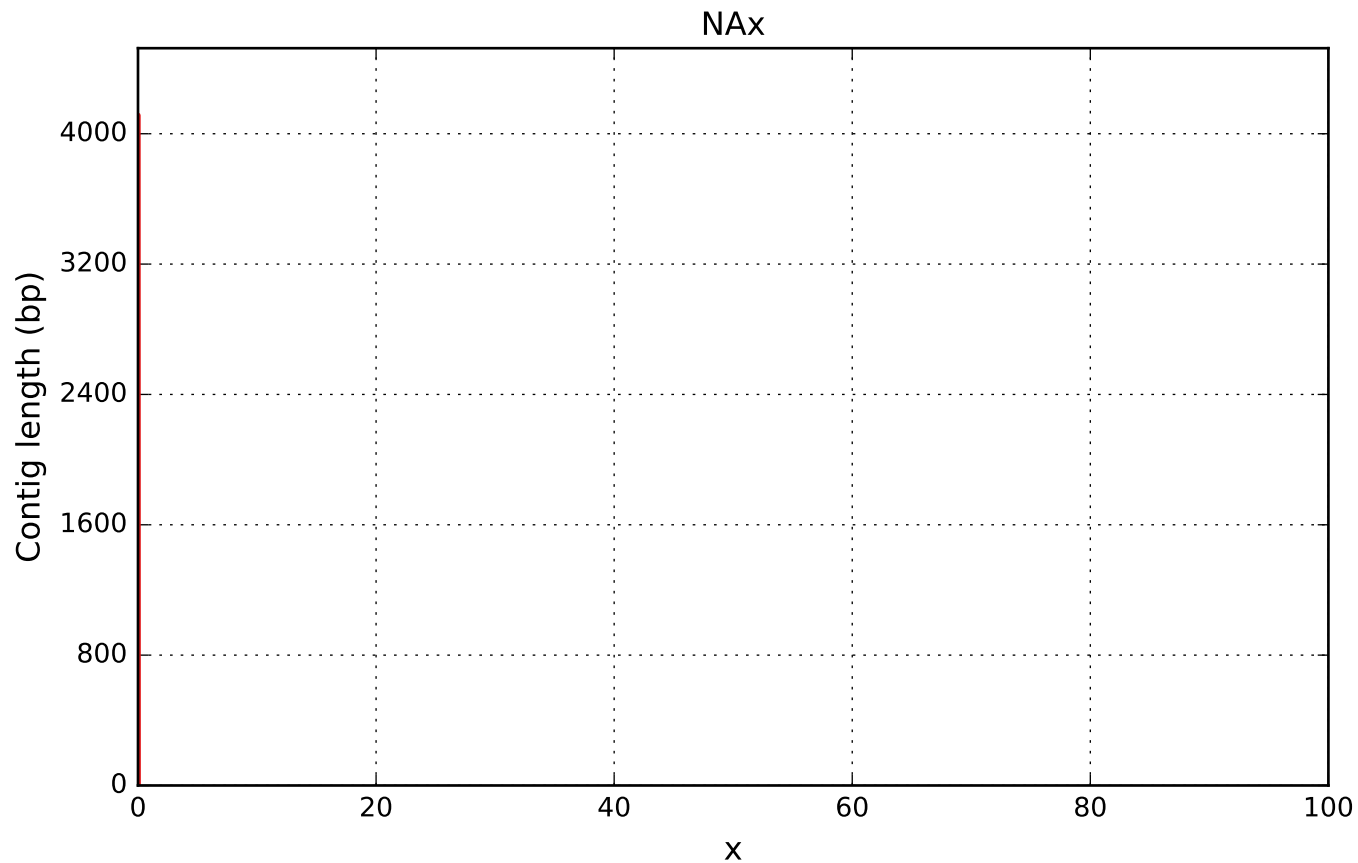


— combined.final.contigs

Cumulative length (aligned contigs)



— combined.final.contigs - - Reference



— combined.final.contigs