

Report

	220410_RR4342129_dna_assembly.megahit_asm	220410_RR4342133_dna_assembly.megahit_asm
# contigs (>= 0 bp)	161952	166148
# contigs (>= 1000 bp)	25167	30885
# contigs (>= 5000 bp)	1190	2595
# contigs (>= 10000 bp)	282	826
# contigs (>= 25000 bp)	35	156
# contigs (>= 50000 bp)	9	47
Total length (>= 0 bp)	123859441	150487838
Total length (>= 1000 bp)	51904151	81750948
Total length (>= 5000 bp)	11009046	29811065
Total length (>= 10000 bp)	4897402	17866508
Total length (>= 25000 bp)	1486506	8108978
Total length (>= 50000 bp)	650797	4319914
# contigs	89614	88129
Largest contig	131335	266140
Total length	95542768	120479536
Reference length	2224914	2224914
N50	1095	1702
N75	703	833
L50	21215	13987
L75	49092	40344
# misassemblies	7	0
# misassembled contigs	7	0
Misassembled contigs length	7945	0
# local misassemblies	1	0
# scaffold gap ext. mis.	0	0
# scaffold gap loc. mis.	0	0
# unaligned mis. contigs	2	2
# unaligned contigs	88245 + 46 part	88054 + 46 part
Unaligned length	94245108	120455755
Genome fraction (%)	55.854	0.715
Duplication ratio	1.045	1.630
# N's per 100 kbp	0.00	0.00
# mismatches per 100 kbp	1154.42	2597.32
# indels per 100 kbp	7.73	113.20
Largest alignment	3896	1496
Total aligned length	1280524	19089

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

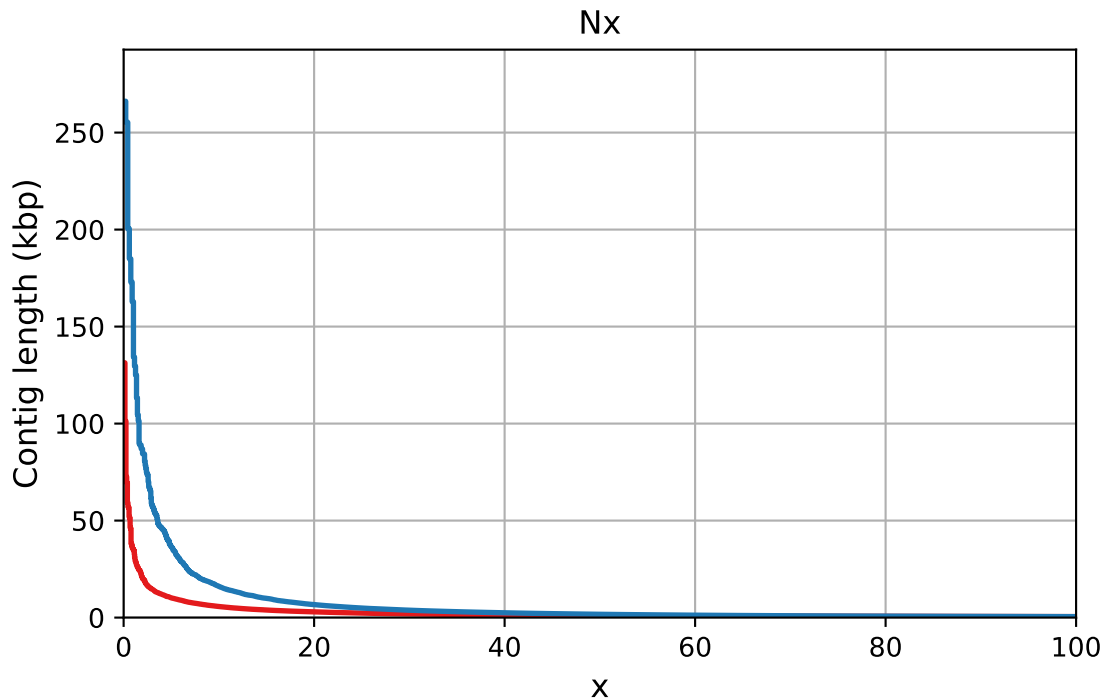
	220410_RR4342129_dna_assembly.megahit_asm	220410_RR4342133_dna_assembly.megahit_asm
# misassemblies	7	0
# contig misassemblies	7	0
# c. relocations	7	0
# c. translocations	0	0
# c. inversions	0	0
# c. interspecies translocations	0	0
# scaffold misassemblies	0	0
# s. relocations	0	0
# s. translocations	0	0
# s. inversions	0	0
# s. interspecies translocations	0	0
# misassembled contigs	7	0
Misassembled contigs length	7945	0
# possibly misassembled contigs	46	44
# possible misassemblies	55	51
# local misassemblies	1	0
# scaffold gap ext. mis.	0	0
# scaffold gap loc. mis.	0	0
# unaligned mis. contigs	2	2
# mismatches	14346	413
# indels	96	18
# indels (<= 5 bp)	88	14
# indels (> 5 bp)	8	4
Indels length	334	112

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

	220410_RR4342129_dna_assembly.megahit_asm	220410_RR4342133_dna_assembly.megahit_asm
# fully unaligned contigs	88245	88054
Fully unaligned length	94184447	120348847
# partially unaligned contigs	46	46
Partially unaligned length	60661	106908
# N's	0	0

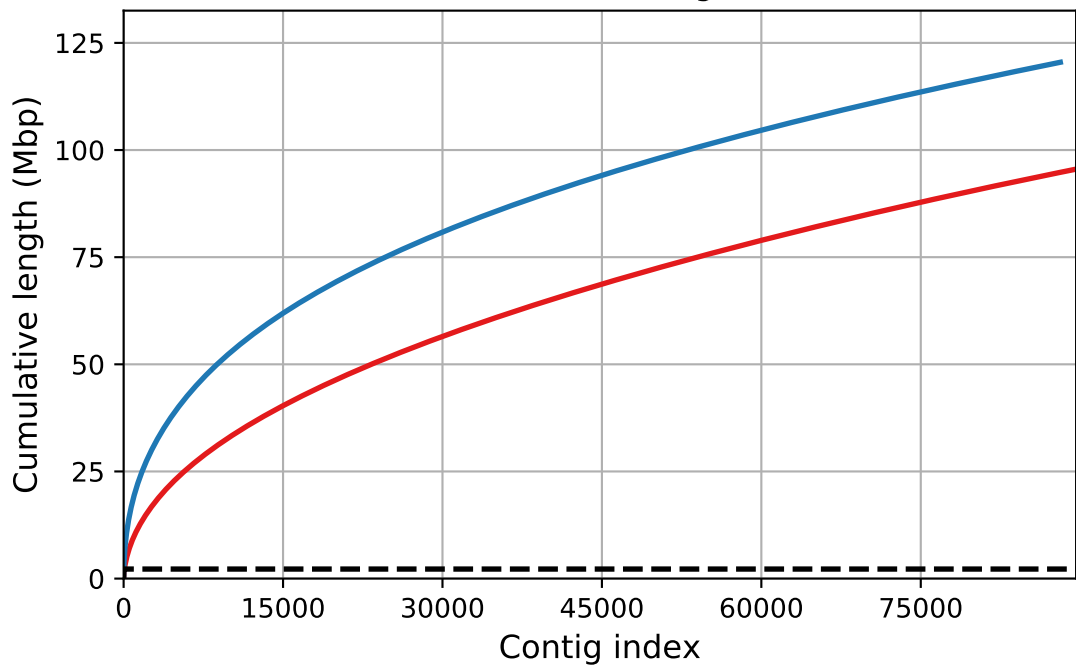
All statistics are based on contigs of size ≥ 500 bp, unless otherwise noted (e.g., "# contigs (≥ 0 bp)" and "Total length (≥ 0 bp)" include all contigs).



10_RR4342129_dna_assembly.megahit_asm

220410_RR4342133_dna_assembly.m

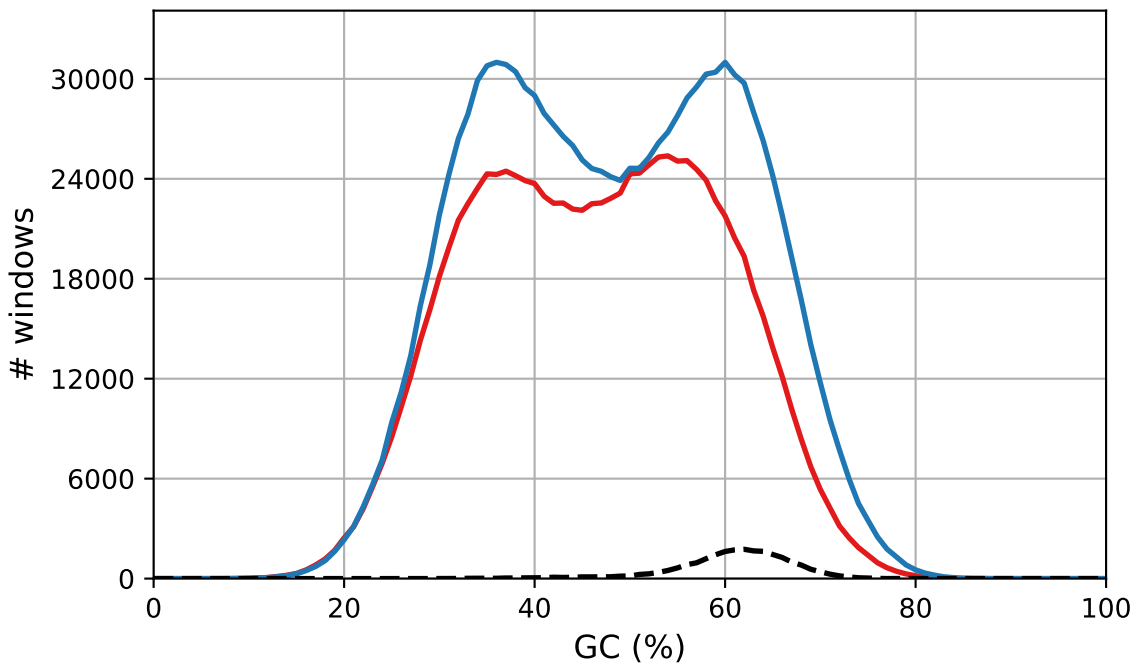
Cumulative length



2129_dna_assembly.megahit_asm

220410_RR4342133_dna_assembly.megahit_as

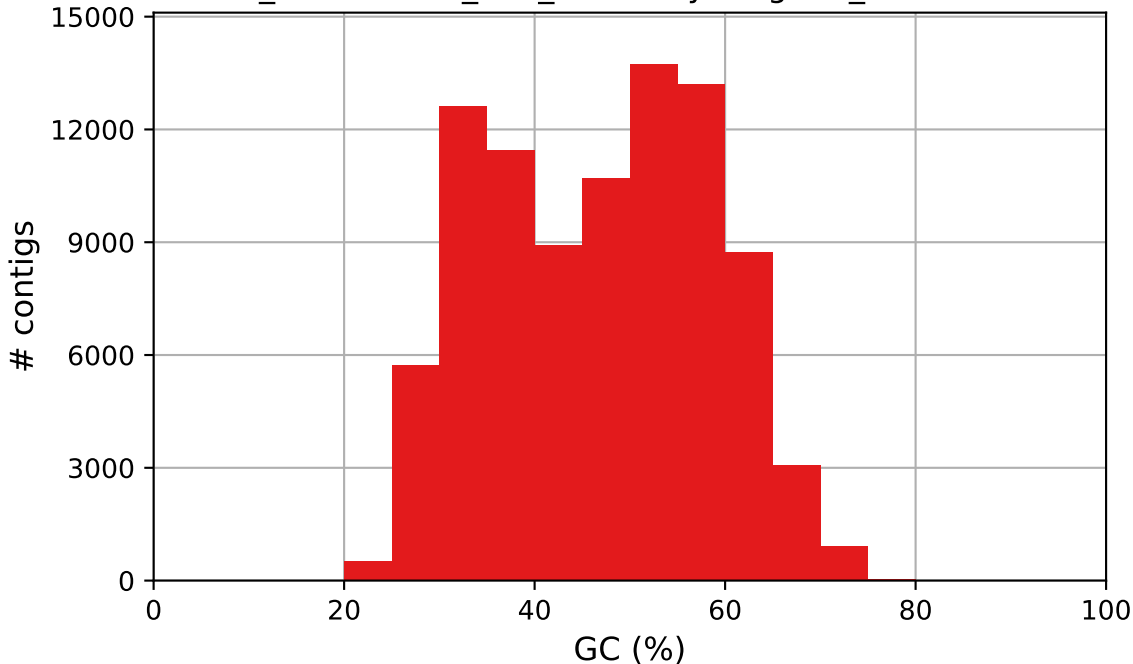
GC content



2129_dna_assembly.megahit_asm

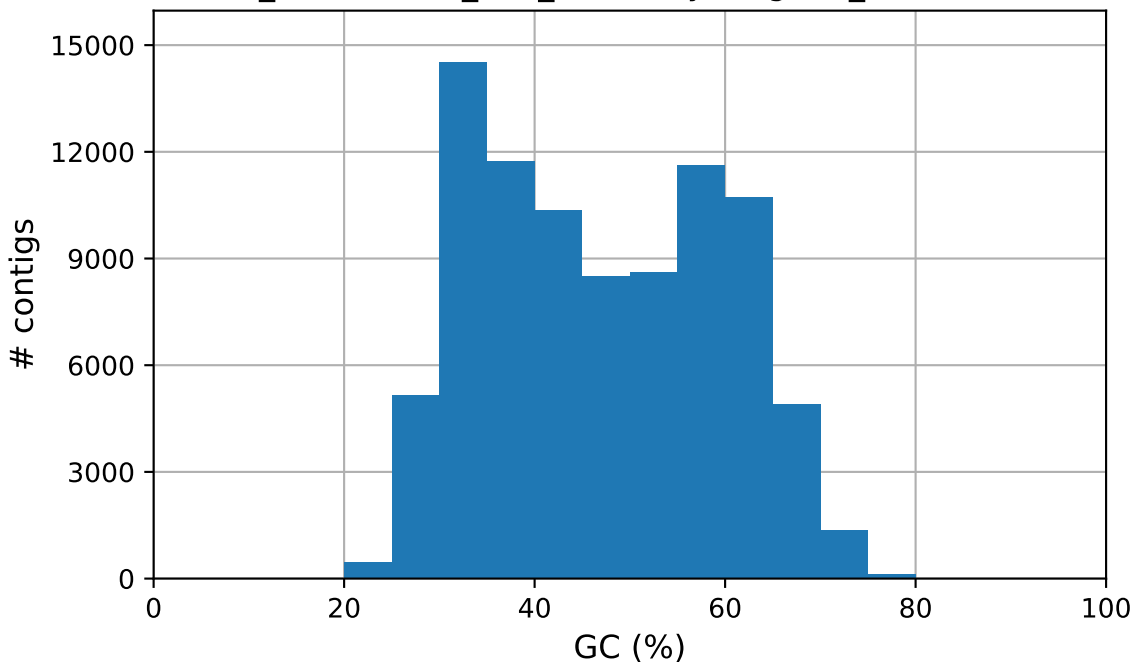
220410_RR4342133_dna_assembly.megahit_asm

220410_RR4342129_dna_assembly.megahit_asm GC content



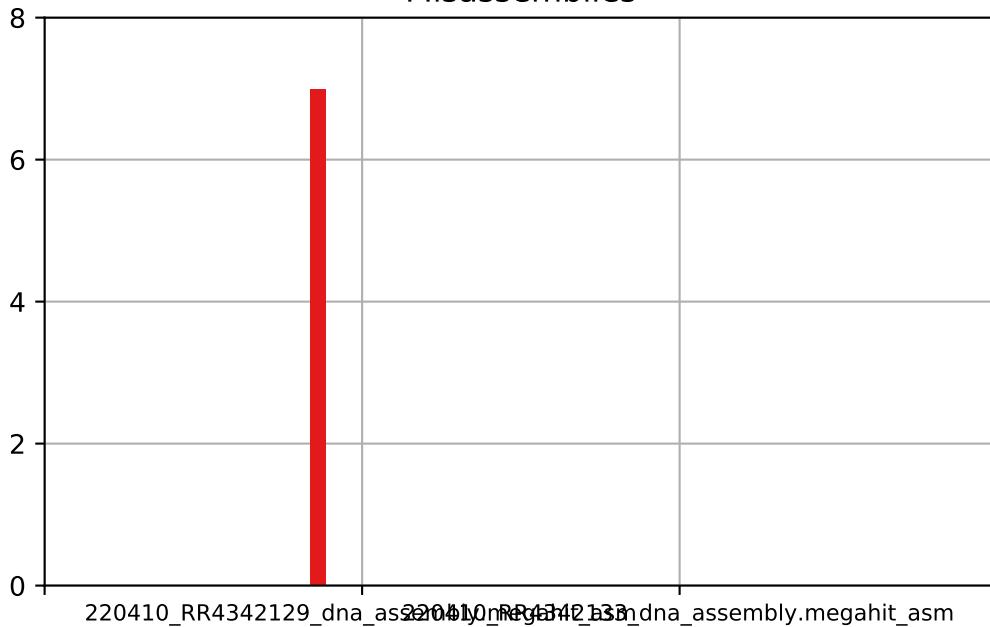
220410_RR4342129_dna_assembly.megahit_asm

220410_RR4342133_dna_assembly.megahit_asm GC content



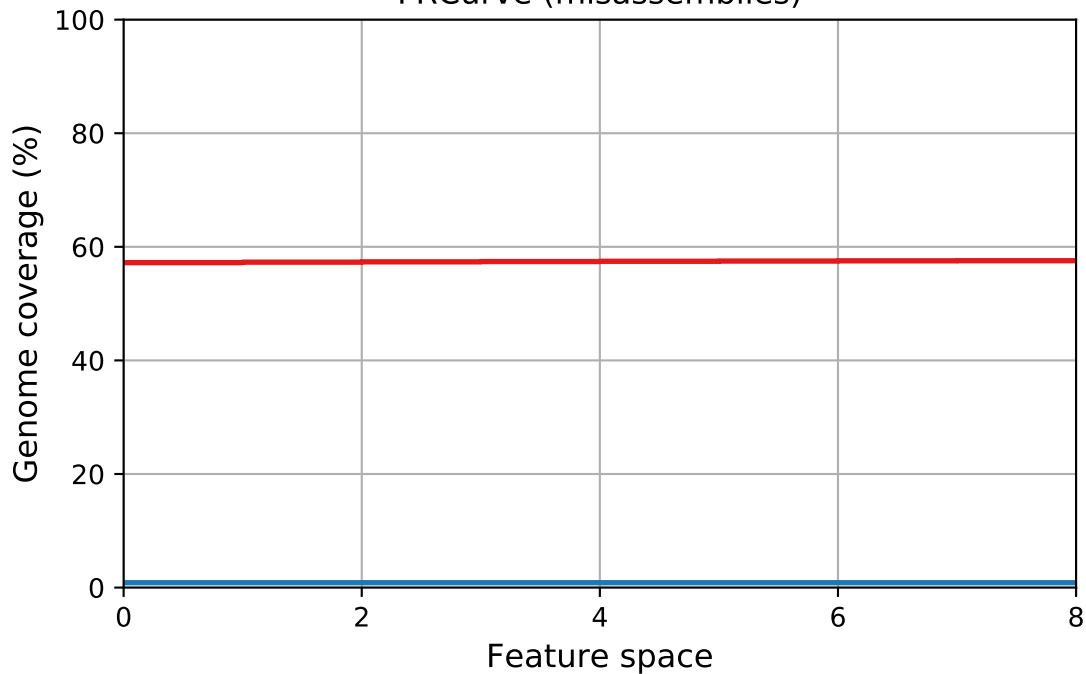
220410_RR4342133_dna_assembly.megahit_asm

Misassemblies



 # relocations

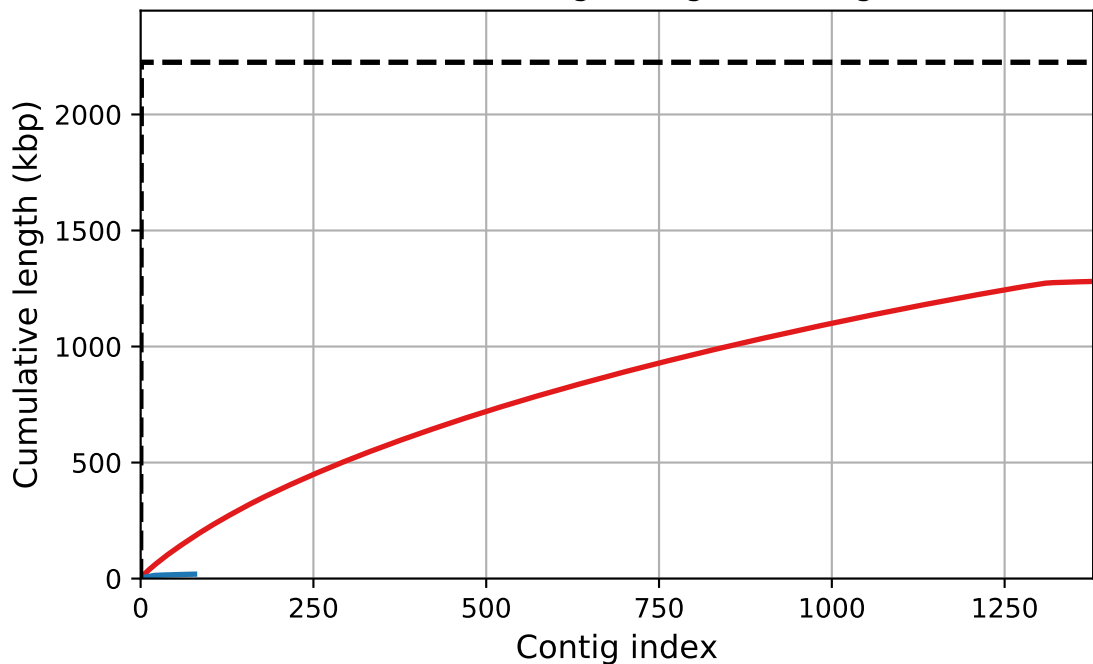
FRCurve (misassemblies)



10_RR4342129_dna_assembly.megahit_asm

220410_RR4342133_dna_assembly.m

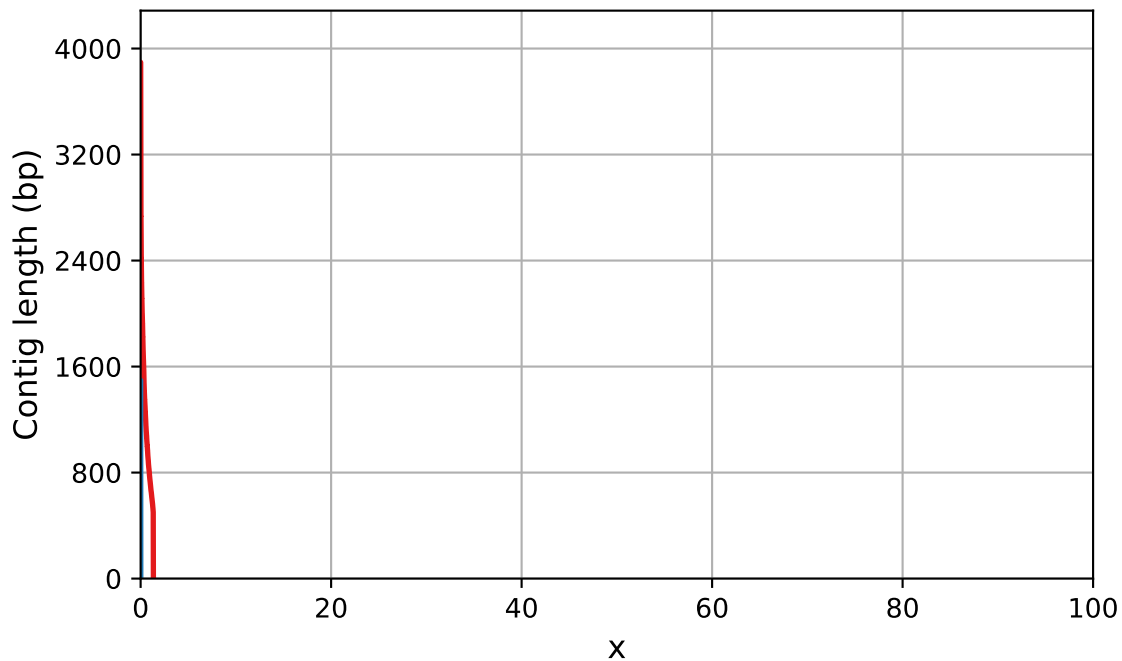
Cumulative length (aligned contigs)



2129_dna_assembly.megahit_asm

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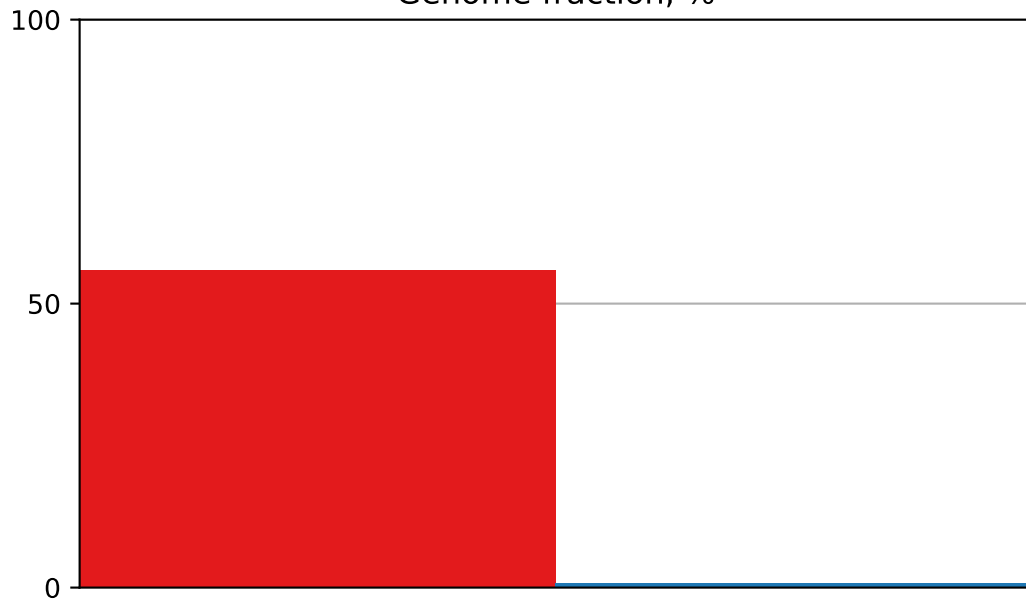
NAx



10_RR4342129_dna_assembly.megahit_asm

220410_RR4342133_dna_assembly.m

Genome fraction, %



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