

# Report

	ERR1795072.contigs	ERR1795073.contigs
# contigs (>= 1000 bp)	36	34
# contigs (>= 5000 bp)	32	29
# contigs (>= 10000 bp)	30	27
# contigs (>= 25000 bp)	25	23
# contigs (>= 50000 bp)	22	21
Total length (>= 1000 bp)	4356838	3354489
Total length (>= 5000 bp)	4345500	3341211
Total length (>= 10000 bp)	4333897	3329866
Total length (>= 25000 bp)	4237898	3254001
Total length (>= 50000 bp)	4144138	3186086
# contigs	38	40
Largest contig	429580	319952
Total length	4357961	3358027
Reference length	5505304	5505304
GC (%)	57.53	57.86
Reference GC (%)	57.31	57.31
N50	203826	165976
NG50	157716	98269
N75	131726	123245
NG75	65279	-
L50	7	8
LG50	10	16
L75	14	14
LG75	22	-
# misassemblies	49	31
# misassembled contigs	12	10
Misassembled contigs length	2273449	1387654
# local misassemblies	140	99
# scaffold gap ext. mis.	0	0
# scaffold gap loc. mis.	0	0
# unaligned mis. contigs	10	12
# unaligned contigs	1 + 31 part	0 + 30 part
Unaligned length	1918029	1313399
Genome fraction (%)	44.296	37.092
Duplication ratio	1.001	1.001
# N's per 100 kbp	0.00	0.00
# mismatches per 100 kbp	3935.12	3925.27
# indels per 100 kbp	44.61	46.96
Largest alignment	179997	172590
Total aligned length	2438234	2043459
NA50	6221	9819
NGA50	-	-
LA50	74	47

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

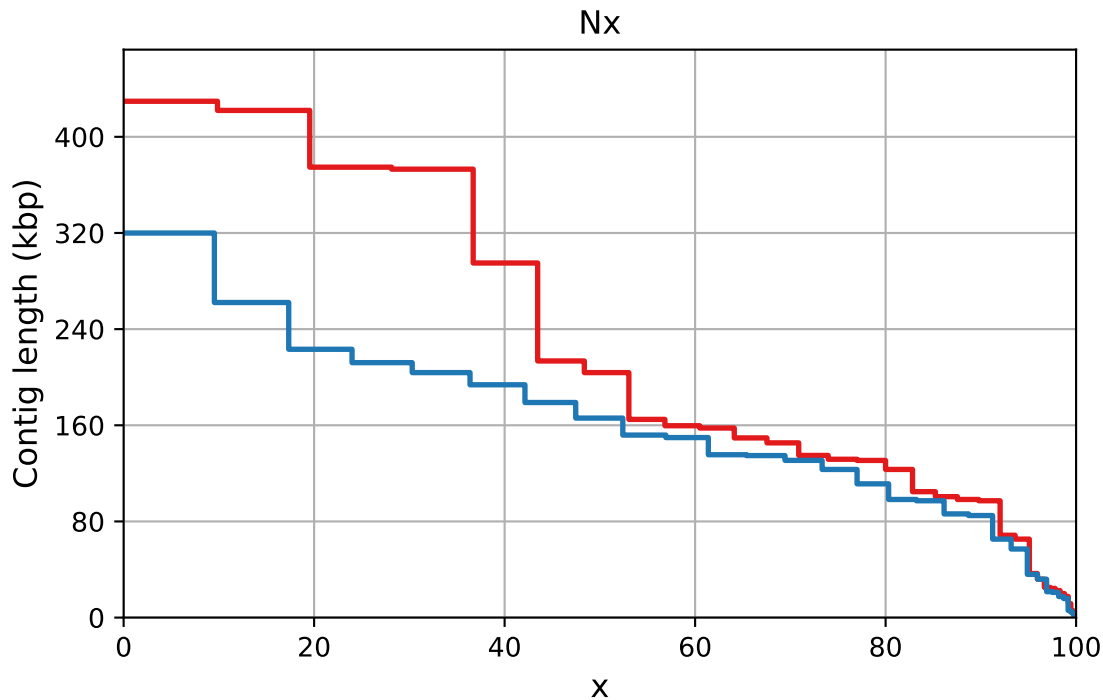
	ERR1795072.contigs	ERR1795073.contigs
# misassemblies	49	31
# contig misassemblies	49	31
# c. relocations	49	31
# c. translocations	0	0
# c. inversions	0	0
# scaffold misassemblies	0	0
# s. relocations	0	0
# s. translocations	0	0
# s. inversions	0	0
# misassembled contigs	12	10
Misassembled contigs length	2273449	1387654
# possibly misassembled contigs	4	4
# possible misassemblies	5	5
# local misassemblies	140	99
# scaffold gap ext. mis.	0	0
# scaffold gap loc. mis.	0	0
# unaligned mis. contigs	10	12
# mismatches	95964	80156
# indels	1088	959
# indels (<= 5 bp)	1014	894
# indels (> 5 bp)	74	65
Indels length	3040	2606

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

## Unaligned report

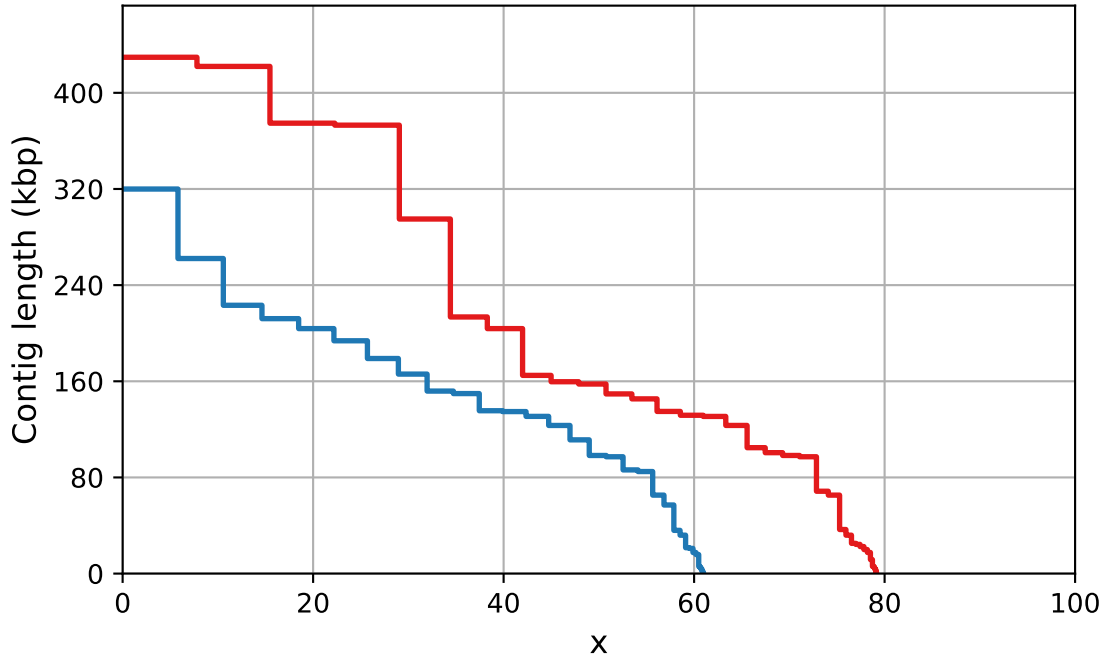
	ERR1795072.contigs	ERR1795073.contigs
# fully unaligned contigs	1	0
Fully unaligned length	545	0
# partially unaligned contigs	31	30
Partially unaligned length	1917484	1313399
# N's	0	0

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



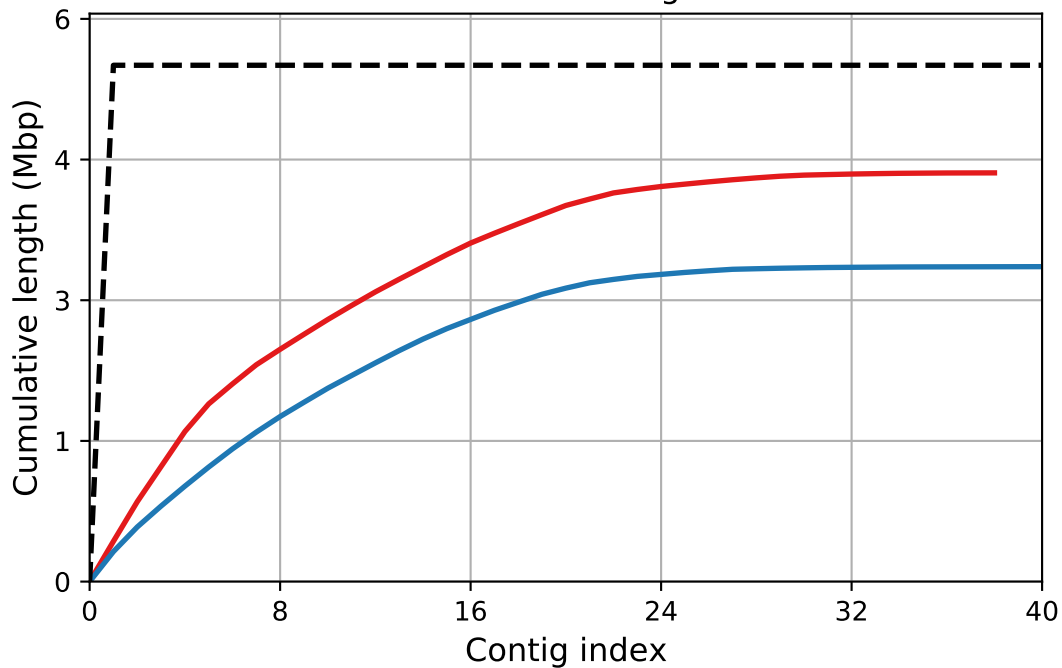
ERR1795072.contigs      ERR1795073.contigs

# NGx



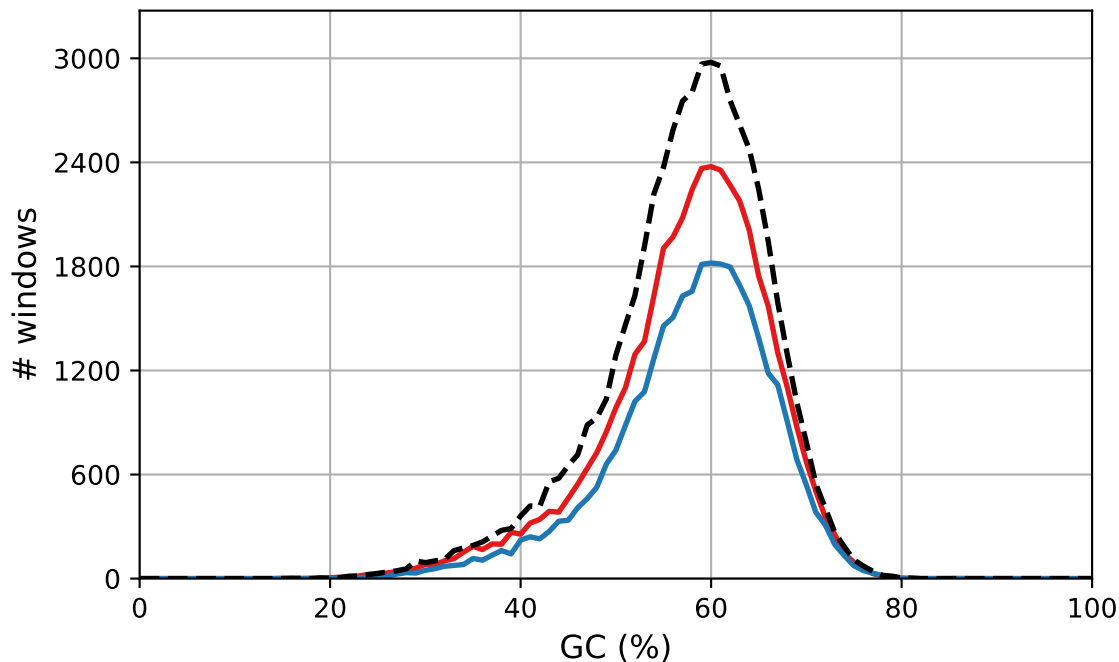
ERR1795072.contigs ERR1795073.contigs

Cumulative length



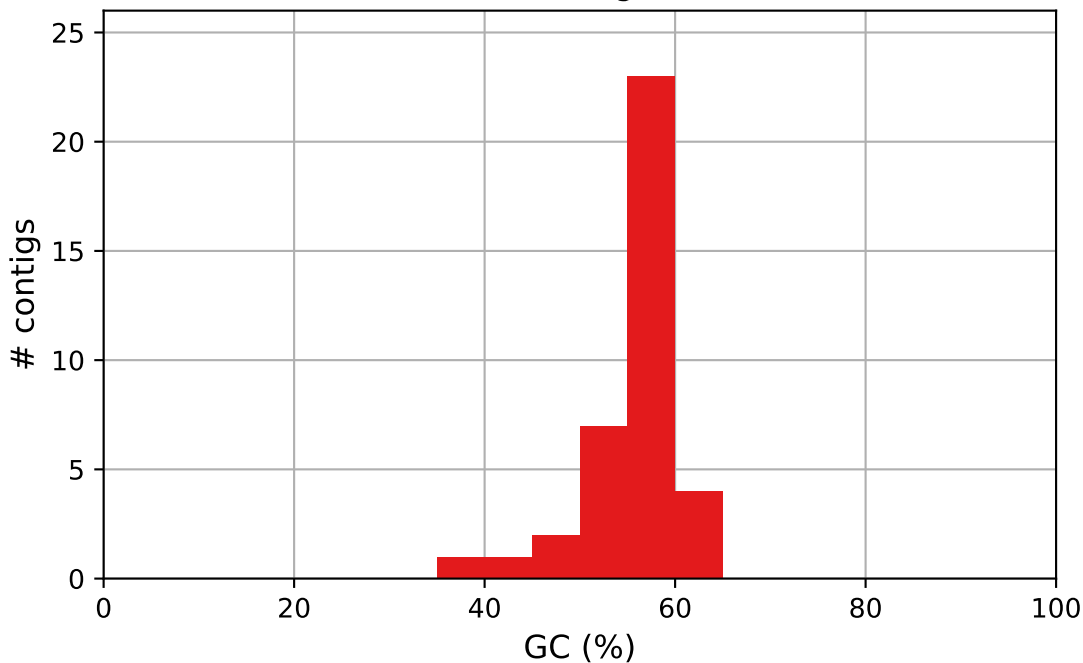
ERR1795072.contigs    ERR1795073.contigs    - - Reference

GC content



ERR1795072.contigs    ERR1795073.contigs    Reference

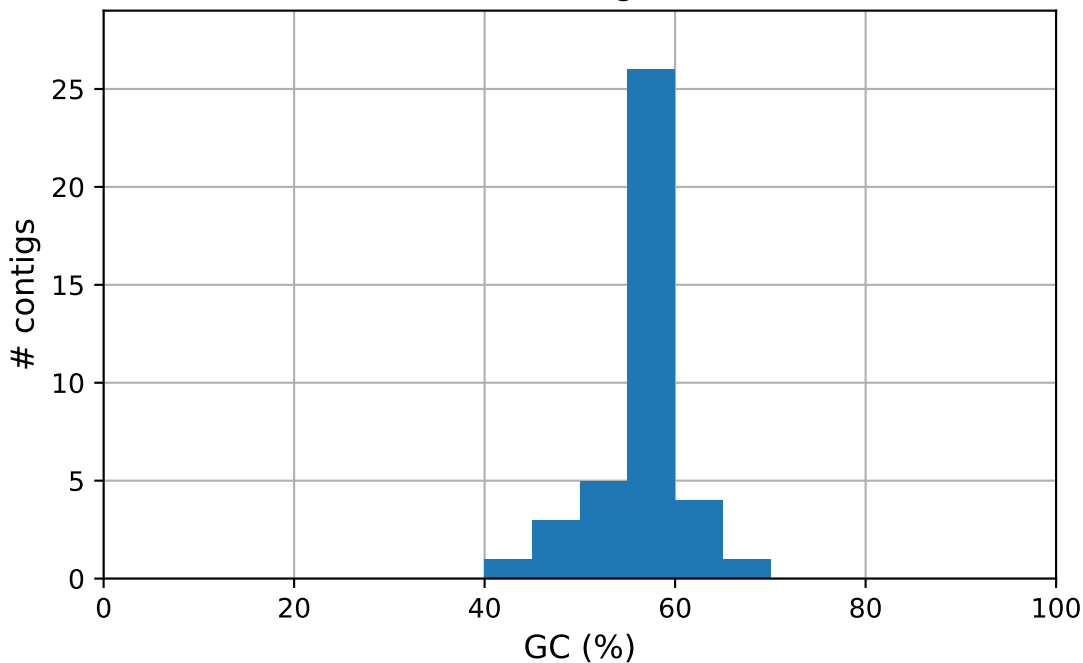
ERR1795072.contigs GC content



ERR1795072.contigs

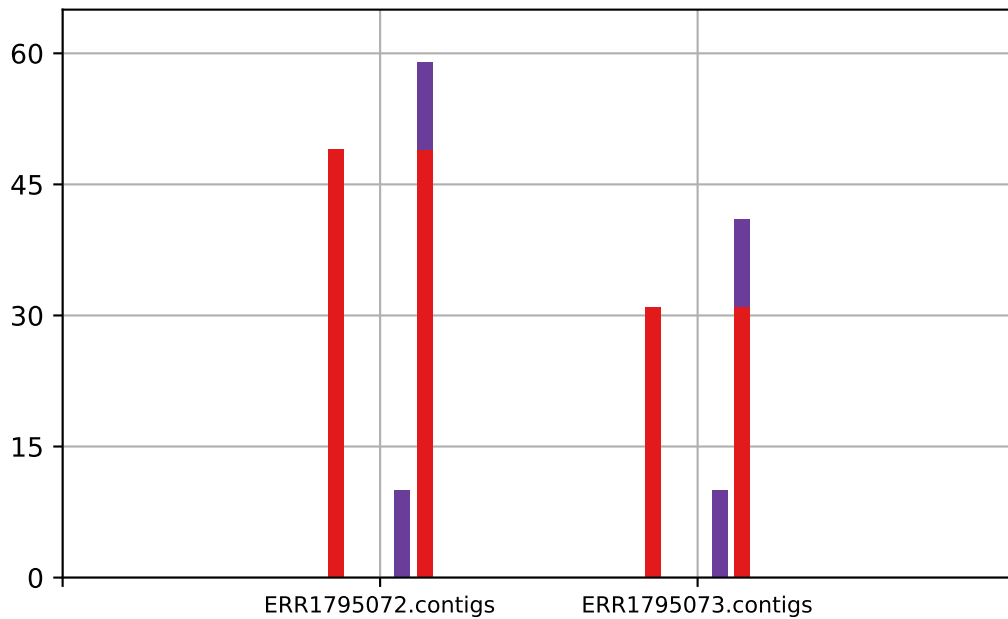


ERR1795073.contigs GC content



ERR1795073.contigs

## Misassemblies

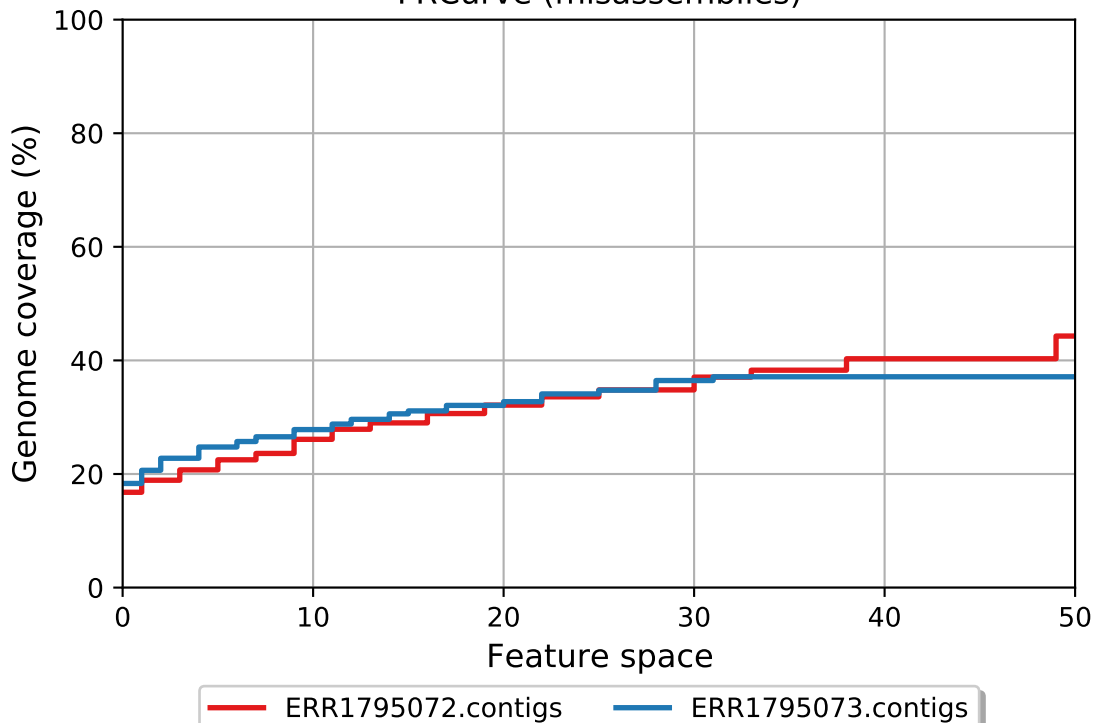


# relocations

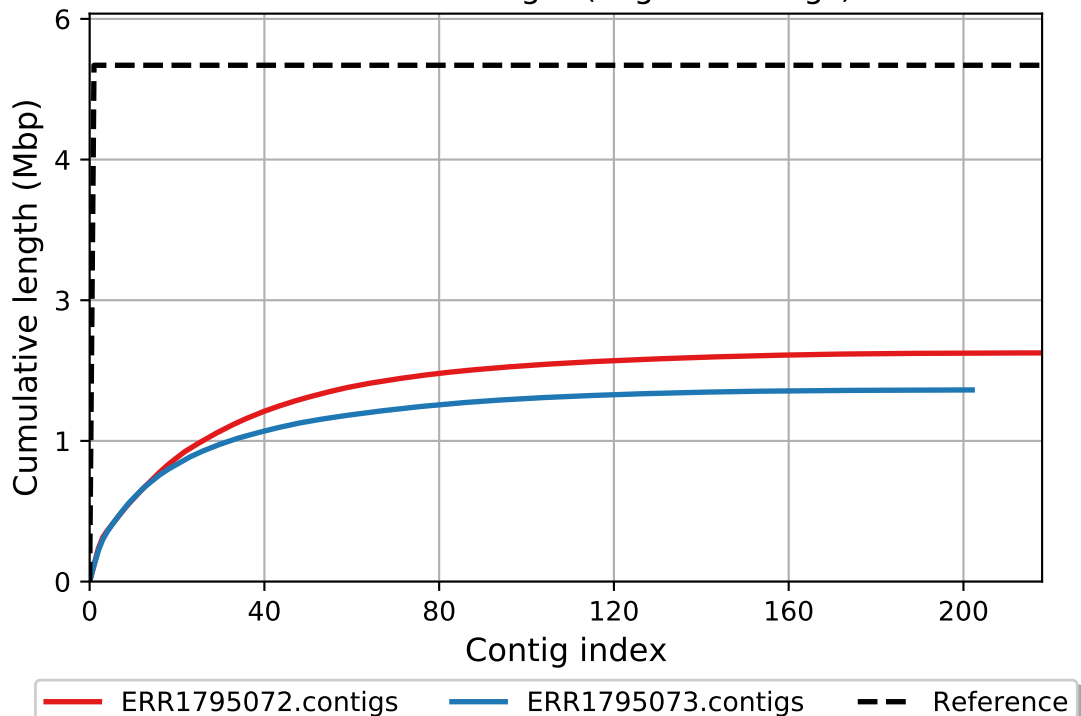


# interspecies translocations

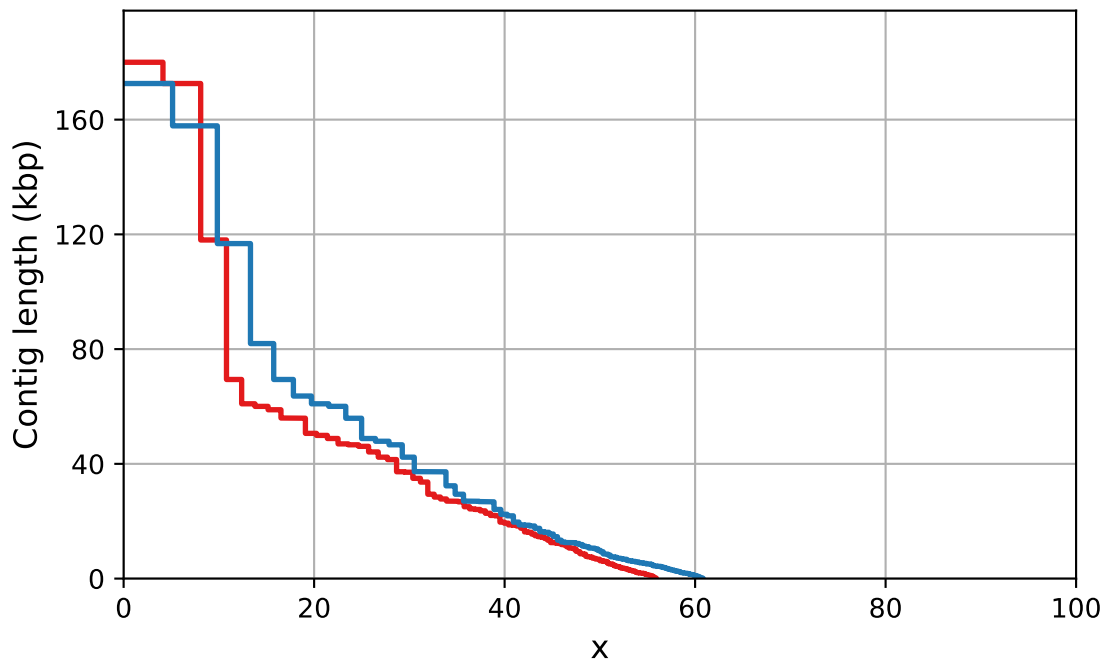
FRCurve (misassemblies)



Cumulative length (aligned contigs)

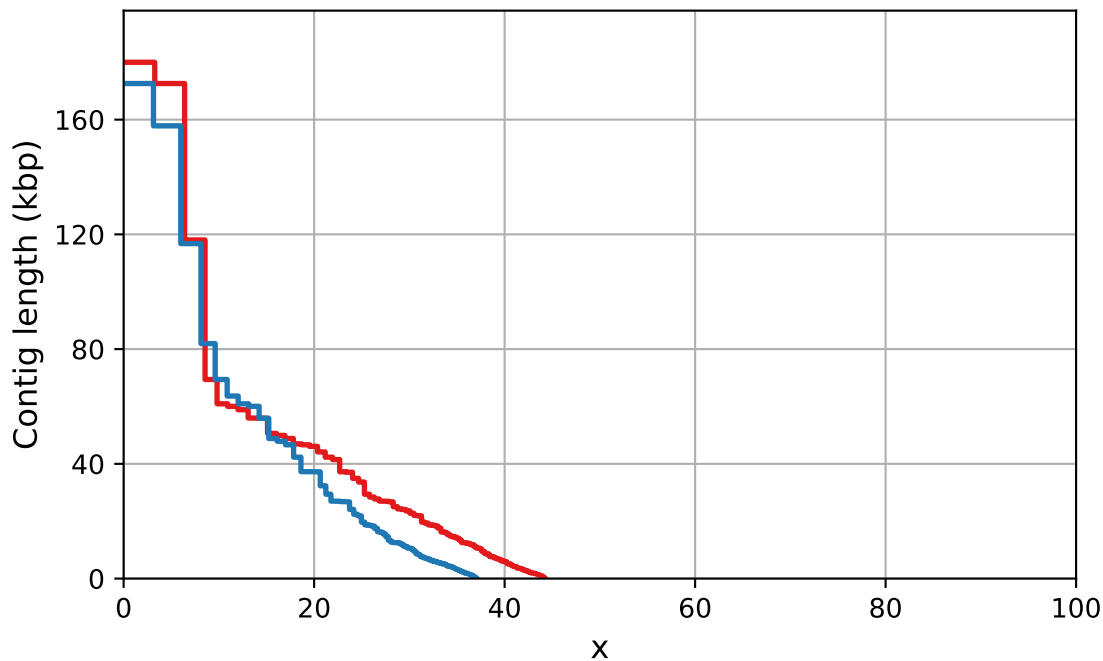


NAx



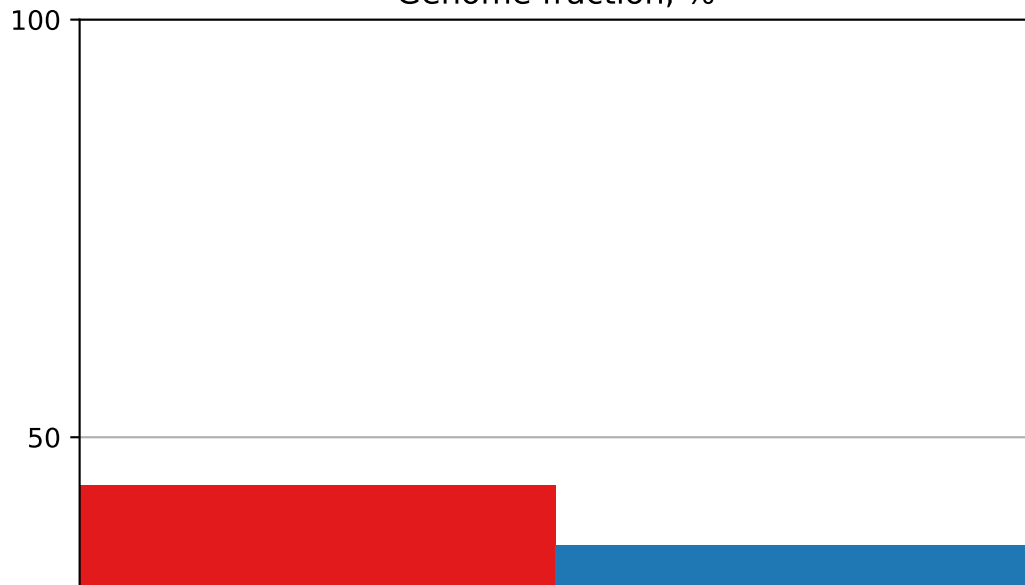
ERR1795072.contigs ERR1795073.contigs

# NGAx



ERR1795072.contigs ERR1795073.contigs

Genome fraction, %



ERR1795072.contigs



ERR1795073.contigs