

Report

	ERR1795072.contigs	ERR1795073.contigs
# contigs (>= 1000 bp)	77	91
# contigs (>= 5000 bp)	59	66
# contigs (>= 10000 bp)	54	61
# contigs (>= 25000 bp)	39	43
# contigs (>= 50000 bp)	30	33
Total length (>= 1000 bp)	5384094	5416851
Total length (>= 5000 bp)	5343732	5356006
Total length (>= 10000 bp)	5309864	5317186
Total length (>= 25000 bp)	5043416	5019497
Total length (>= 50000 bp)	4739448	4661625
# contigs	90	109
Largest contig	429580	329050
Total length	5392261	5429057
Reference length	5447116	5447116
GC (%)	57.29	57.28
Reference GC (%)	57.33	57.33
N50	157716	149771
NG50	157716	135497
N75	98280	97206
NG75	98280	97206
L50	10	13
LG50	10	14
L75	21	25
LG75	21	25
# misassemblies	45	43
# misassembled contigs	29	28
Misassembled contigs length	3664684	3246702
# local misassemblies	48	53
# scaffold gap ext. mis.	0	0
# scaffold gap loc. mis.	0	0
# unaligned mis. contigs	10	7
# unaligned contigs	0 + 46 part	1 + 50 part
Unaligned length	537532	494256
Genome fraction (%)	89.087	90.488
Duplication ratio	1.003	1.004
# N's per 100 kbp	0.00	0.00
# mismatches per 100 kbp	648.33	641.24
# indels per 100 kbp	11.94	11.33
Largest alignment	257370	257239
Total aligned length	4849032	4927747
NA50	94046	77715
NGA50	91510	77715
NA75	35310	35310
NGA75	34646	35310
LA50	18	21
LGA50	19	21
LA75	41	45
LGA75	43	45

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

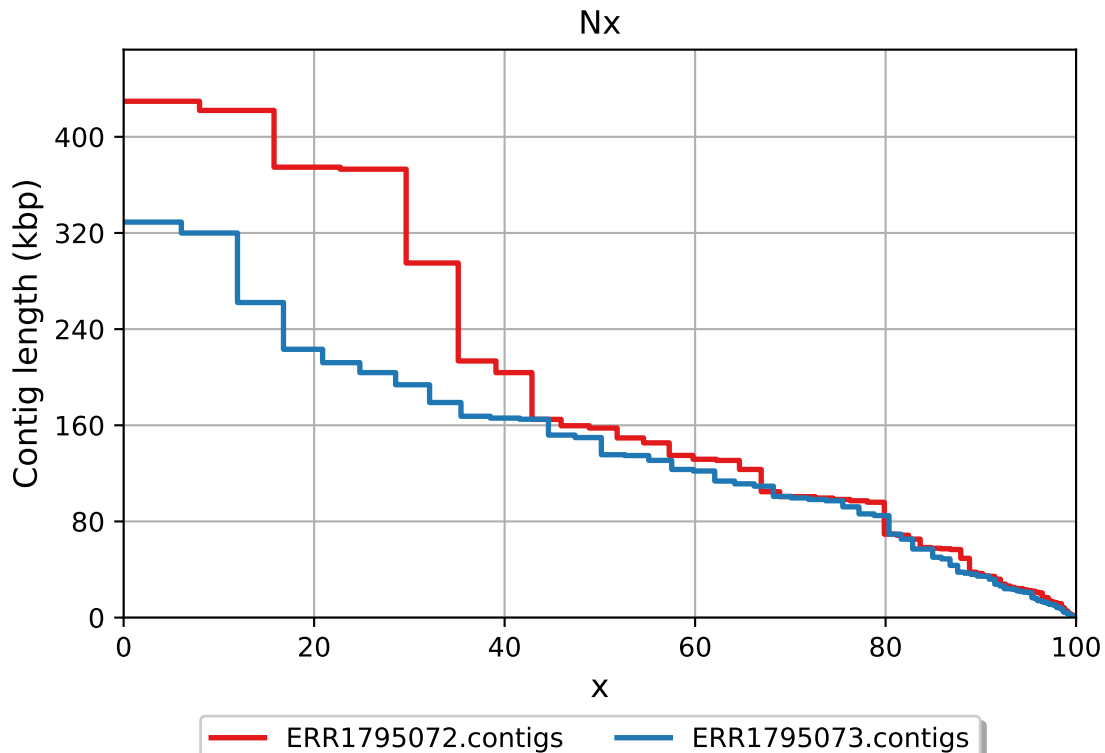
	ERR1795072.contigs	ERR1795073.contigs
# misassemblies	45	43
# contig misassemblies	45	43
# c. relocations	42	42
# c. translocations	0	0
# c. inversions	3	1
# scaffold misassemblies	0	0
# s. relocations	0	0
# s. translocations	0	0
# s. inversions	0	0
# misassembled contigs	29	28
Misassembled contigs length	3664684	3246702
# possibly misassembled contigs	26	29
# possible misassemblies	32	39
# local misassemblies	48	53
# scaffold gap ext. mis.	0	0
# scaffold gap loc. mis.	0	0
# unaligned mis. contigs	10	7
# mismatches	31376	31521
# indels	578	557
# indels (<= 5 bp)	508	484
# indels (> 5 bp)	70	73
Indels length	2363	2162

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).

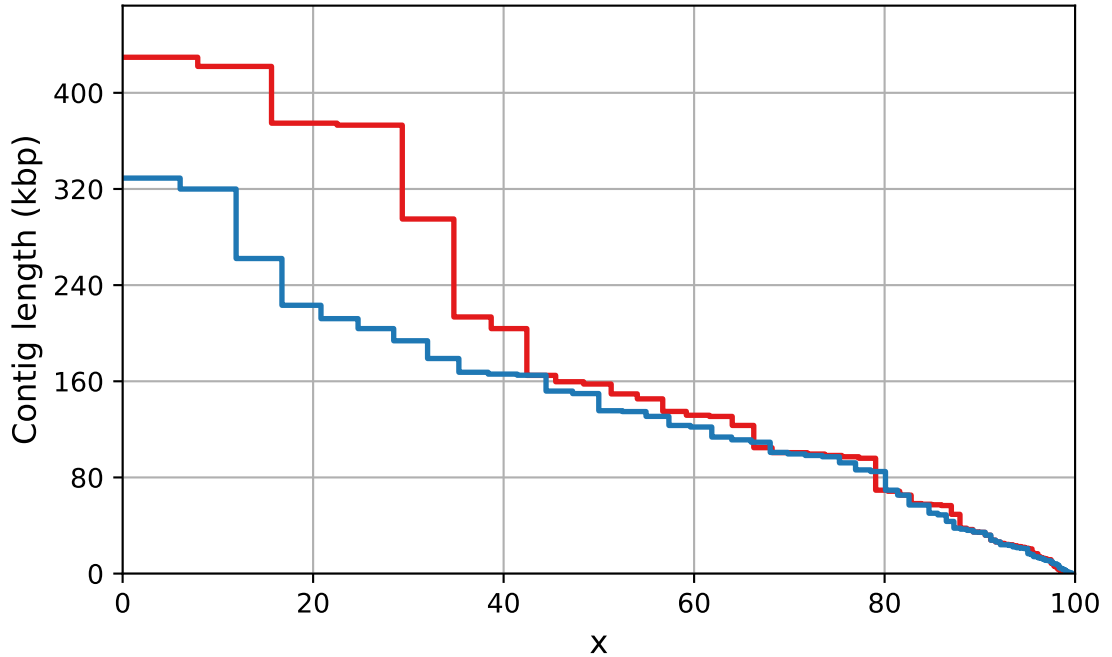
Unaligned report

	ERR1795072.contigs	ERR1795073.contigs
# fully unaligned contigs	0	1
Fully unaligned length	0	505
# partially unaligned contigs	46	50
Partially unaligned length	537532	493751
# 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).

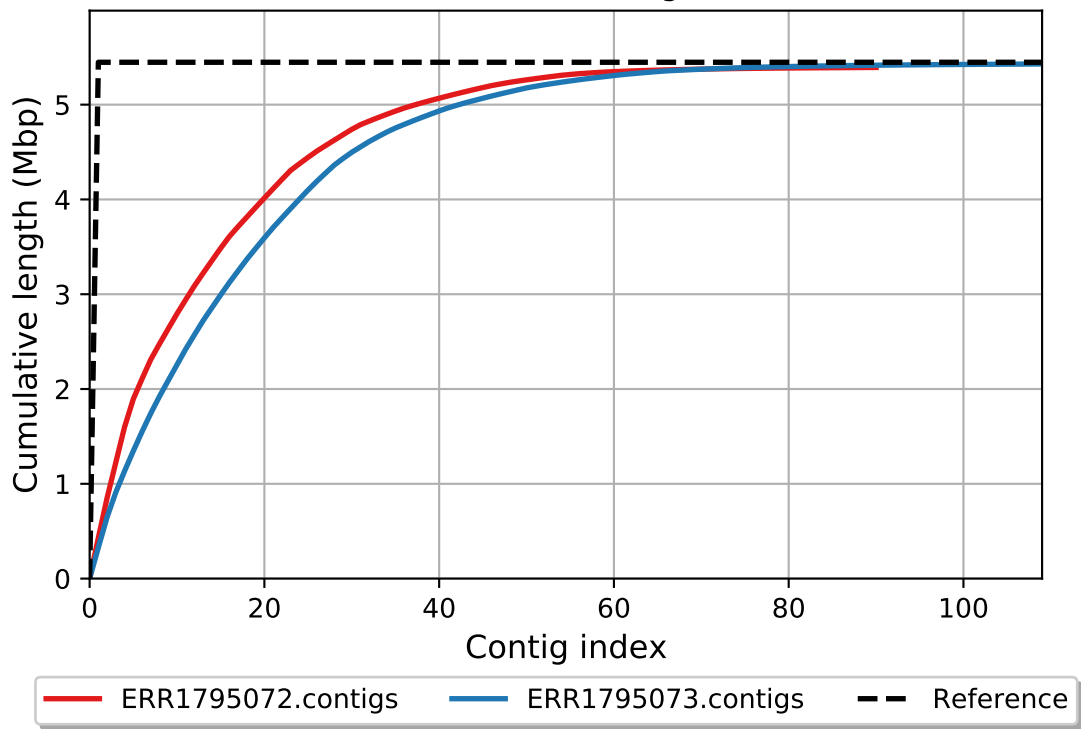


NGx

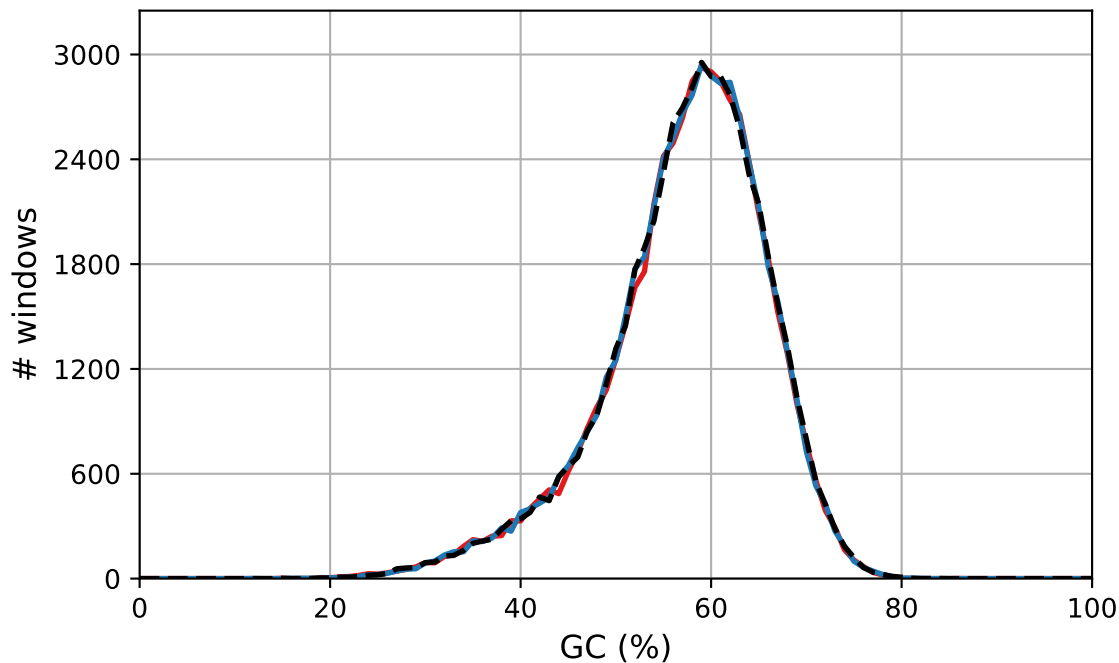


ERR1795072.contigs ERR1795073.contigs

Cumulative length

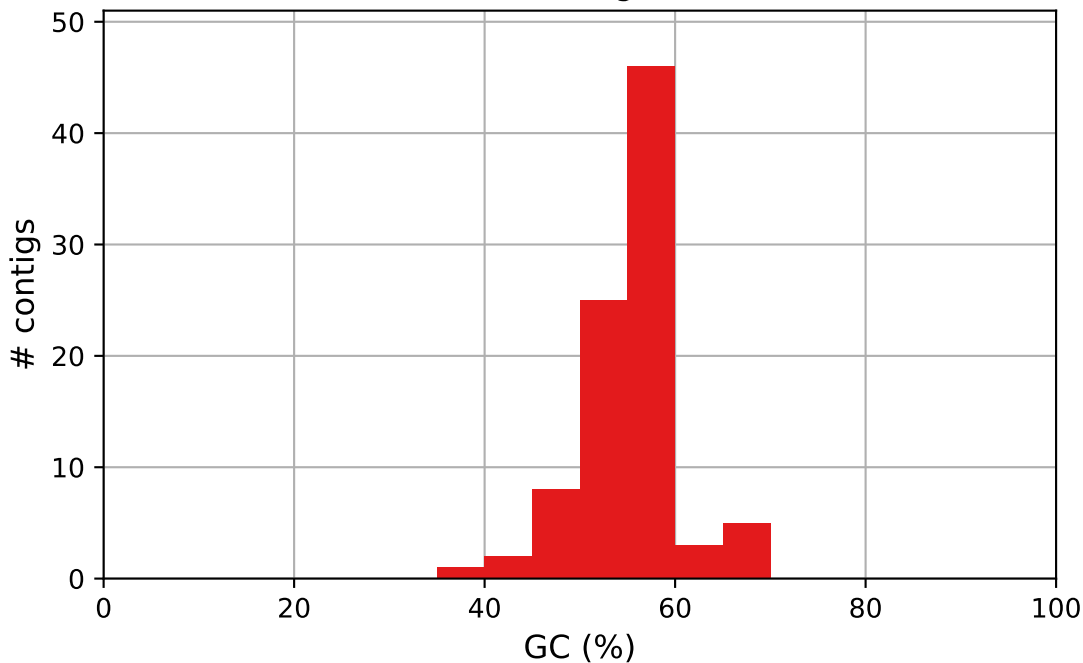


GC content



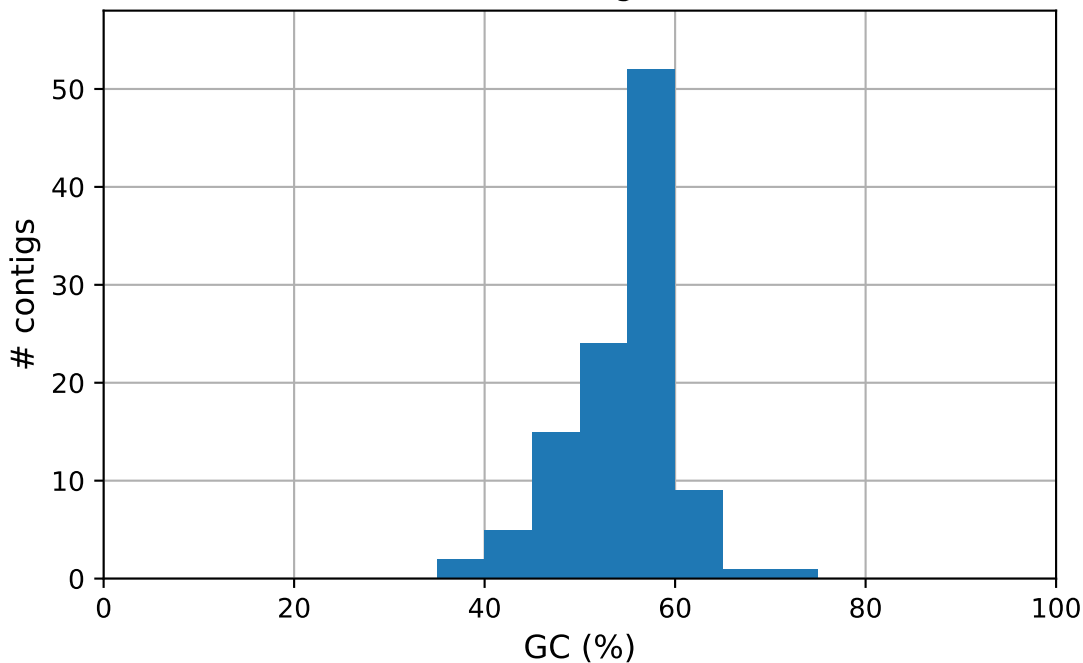
ERR1795072.contigs ERR1795073.contigs Reference

ERR1795072.contigs GC content



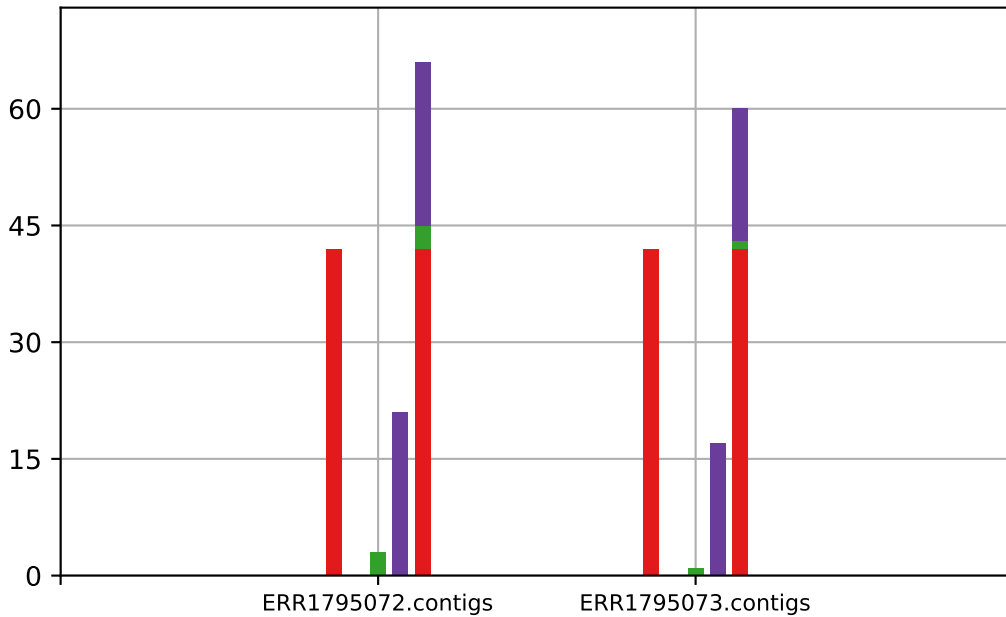
ERR1795072.contigs

ERR1795073.contigs GC content



ERR1795073.contigs

Misassemblies



relocations

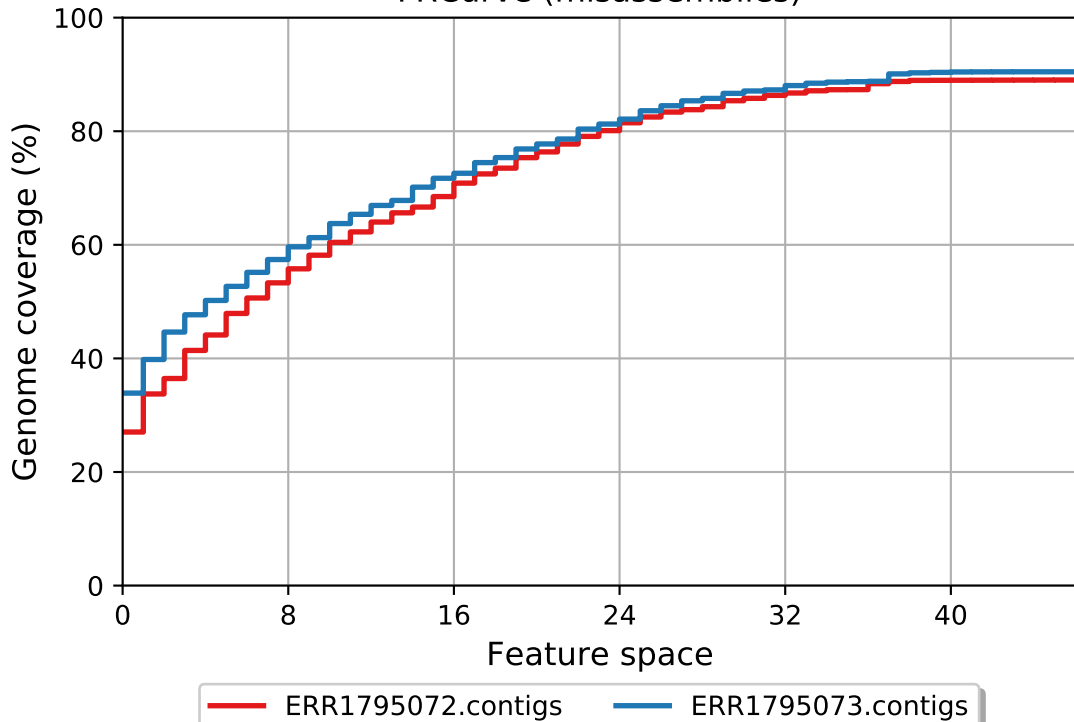


inversions

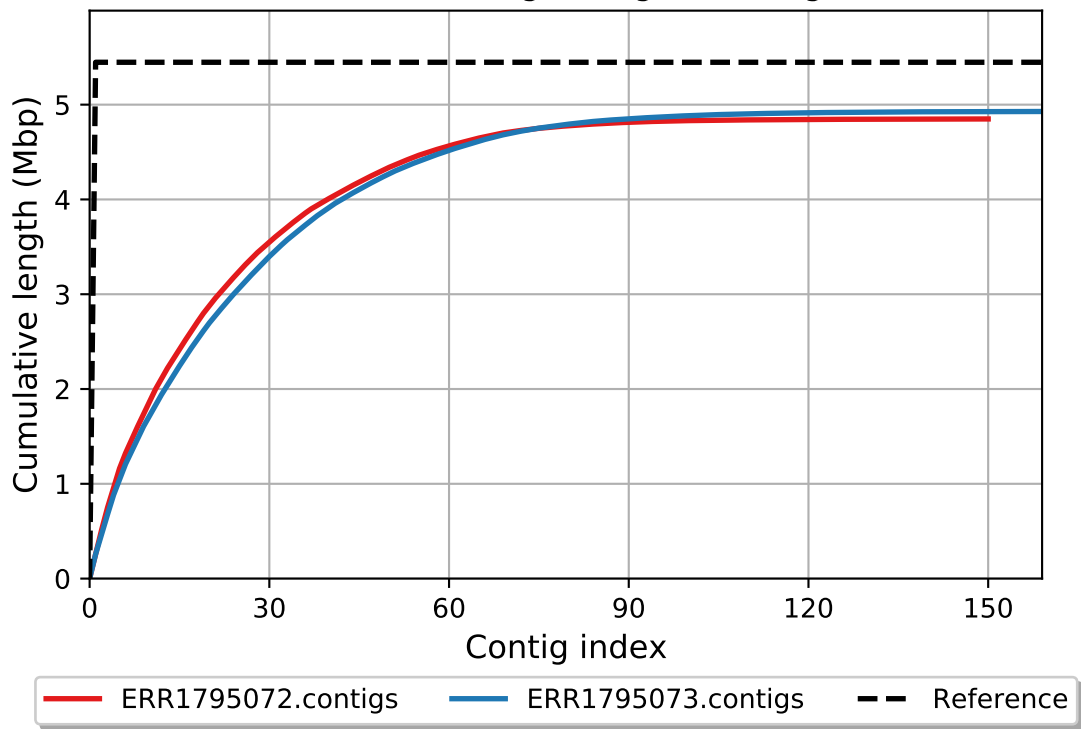


interspecies translocations

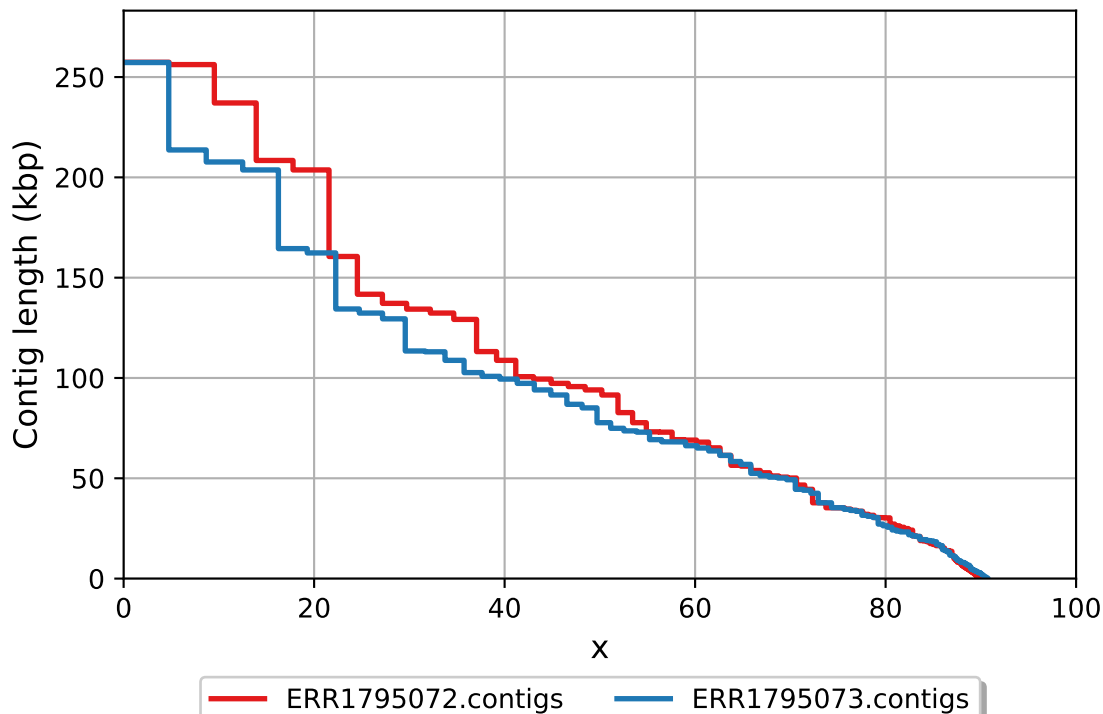
FRCurve (misassemblies)



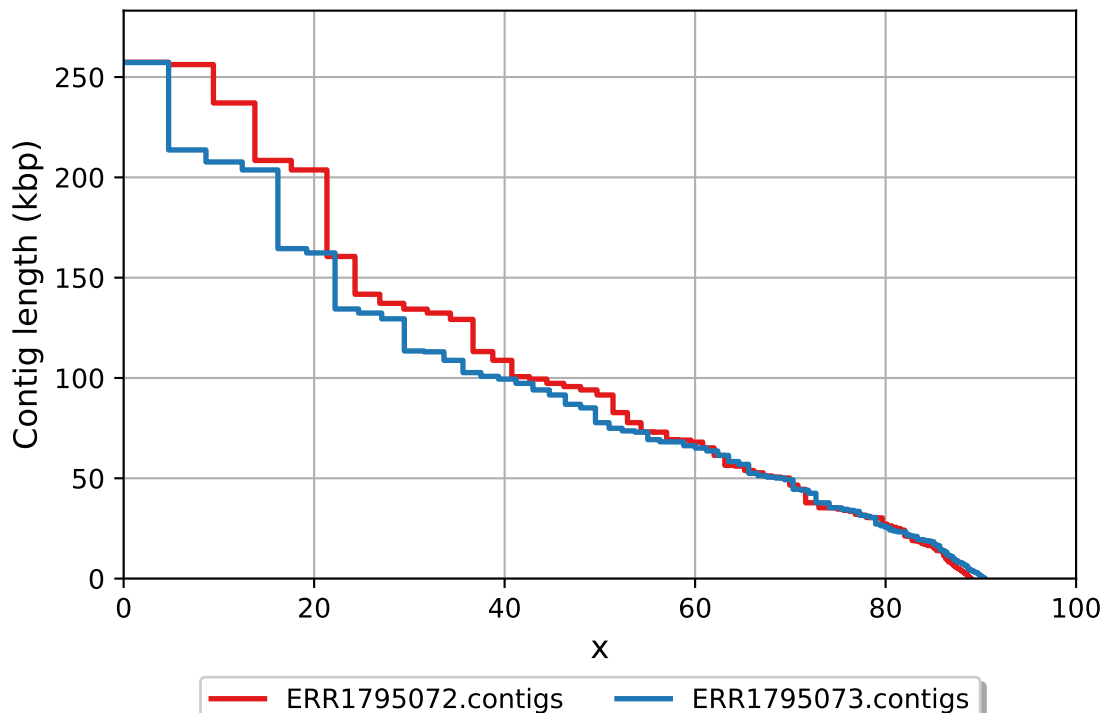
Cumulative length (aligned contigs)



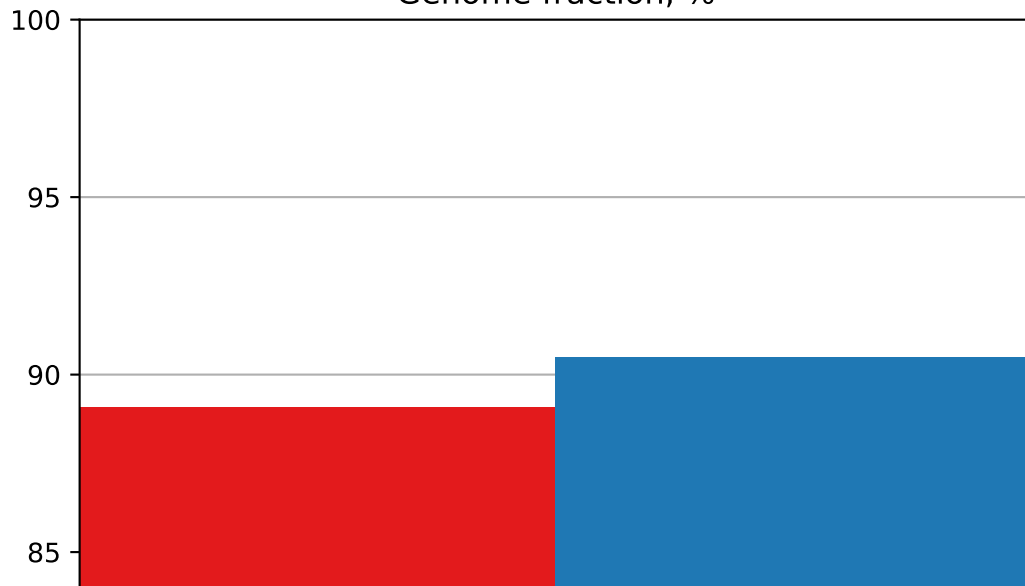
NAx



NGAx



Genome fraction, %



ERR1795072.contigs



ERR1795073.contigs