

Report

	ERR1795072.contigs	ERR1795073.contigs
# contigs (>= 1000 bp)	55	65
# contigs (>= 5000 bp)	49	56
# contigs (>= 10000 bp)	46	53
# contigs (>= 25000 bp)	36	39
# contigs (>= 50000 bp)	28	31
Total length (>= 1000 bp)	5064744	4949139
Total length (>= 5000 bp)	5050787	4928766
Total length (>= 10000 bp)	5031276	4907715
Total length (>= 25000 bp)	4848388	4674117
Total length (>= 50000 bp)	4572273	4395775
# contigs	62	75
Largest contig	429580	329050
Total length	5068765	4955435
Reference length	5606998	5606998
GC (%)	57.41	57.49
Reference GC (%)	57.23	57.23
N50	159621	149771
NG50	149488	134791
N75	100600	98269
NG75	69397	65279
L50	9	12
LG50	11	14
L75	18	22
LG75	23	28
# misassemblies	53	49
# misassembled contigs	23	25
Misassembled contigs length	3774367	3525145
# local misassemblies	37	37
# scaffold gap ext. mis.	0	0
# scaffold gap loc. mis.	0	0
# unaligned mis. contigs	2	5
# unaligned contigs	0 + 35 part	1 + 41 part
Unaligned length	507751	457581
Genome fraction (%)	81.244	80.085
Duplication ratio	1.001	1.002
# N's per 100 kbp	0.00	0.00
# mismatches per 100 kbp	689.06	683.04
# indels per 100 kbp	12.05	11.96
Largest alignment	251977	251981
Total aligned length	4556862	4493666
NA50	81632	74965
NGA50	65177	58526
NA75	33557	30838
NGA75	19424	18235
LA50	19	20
LGA50	23	25
LA75	44	46
LGA75	60	67

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

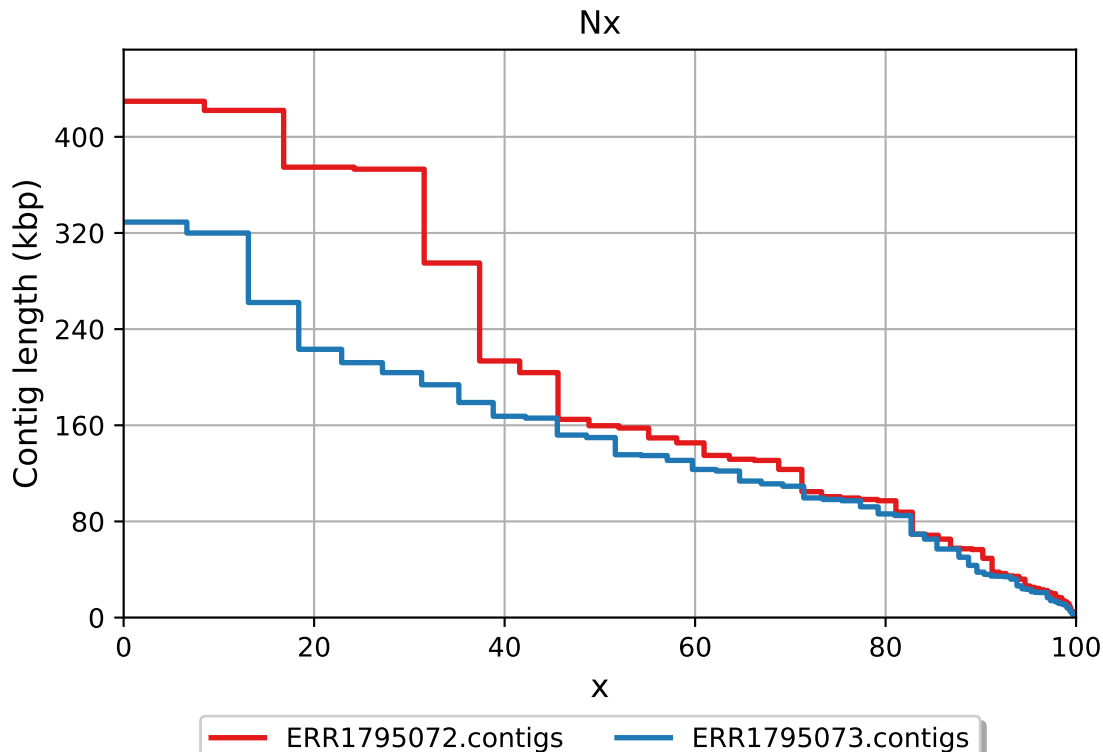
	ERR1795072.contigs	ERR1795073.contigs
# misassemblies	53	49
# contig misassemblies	53	49
# c. relocations	51	48
# c. translocations	0	0
# c. inversions	2	1
# scaffold misassemblies	0	0
# s. relocations	0	0
# s. translocations	0	0
# s. inversions	0	0
# misassembled contigs	23	25
Misassembled contigs length	3774367	3525145
# possibly misassembled contigs	15	14
# possible misassemblies	23	16
# local misassemblies	37	37
# scaffold gap ext. mis.	0	0
# scaffold gap loc. mis.	0	0
# unaligned mis. contigs	2	5
# mismatches	31389	30671
# indels	549	537
# indels (<= 5 bp)	475	462
# indels (> 5 bp)	74	75
Indels length	2397	2346

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).

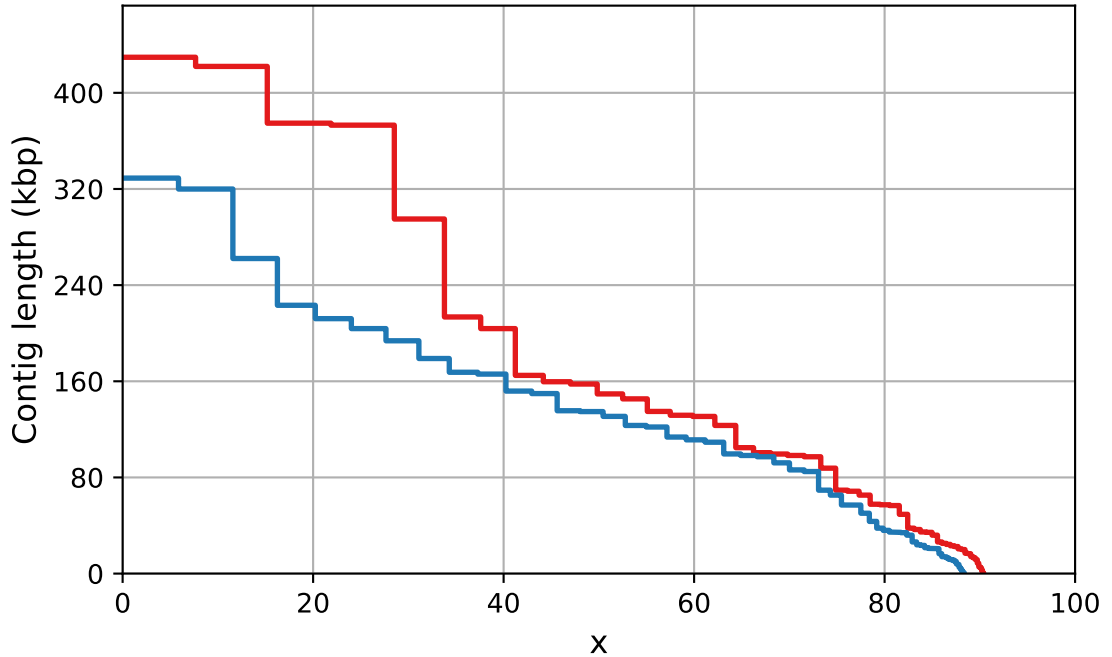
Unaligned report

	ERR1795072.contigs	ERR1795073.contigs
# fully unaligned contigs	0	1
Fully unaligned length	0	505
# partially unaligned contigs	35	41
Partially unaligned length	507751	457076
# 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).

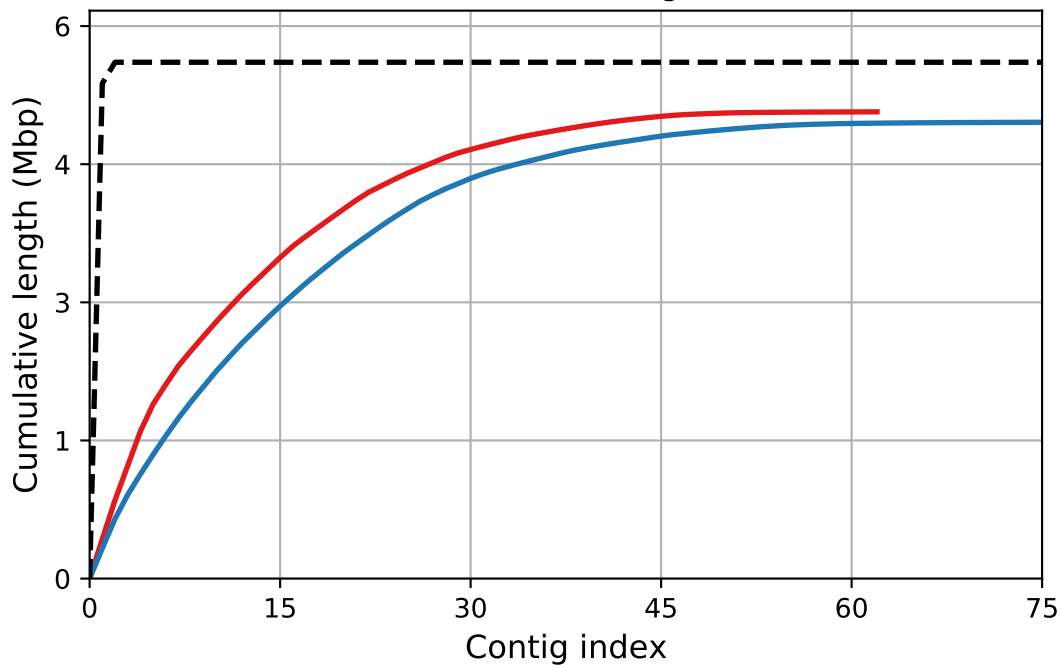


NGx



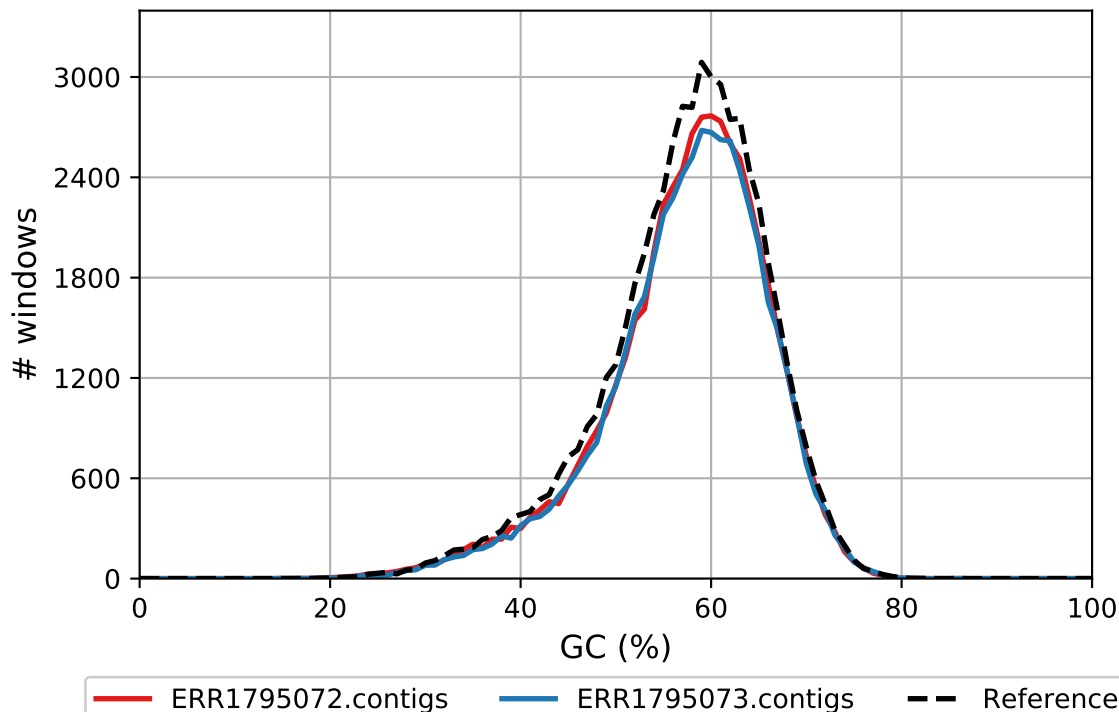
ERR1795072.contigs ERR1795073.contigs

Cumulative length

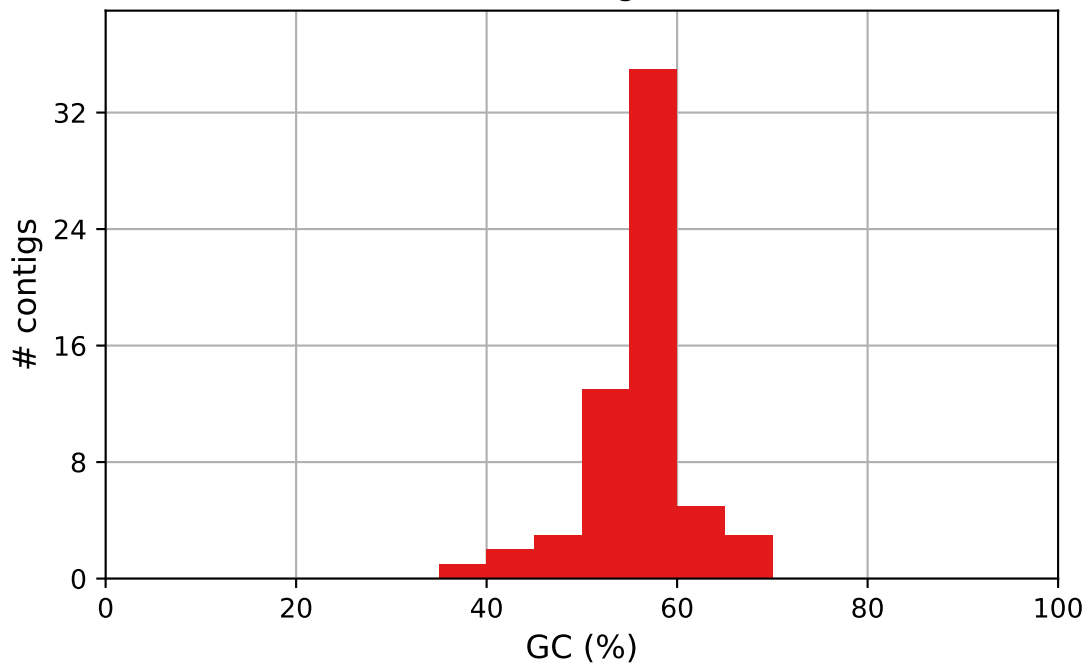


ERR1795072.contigs ERR1795073.contigs - - Reference

GC content

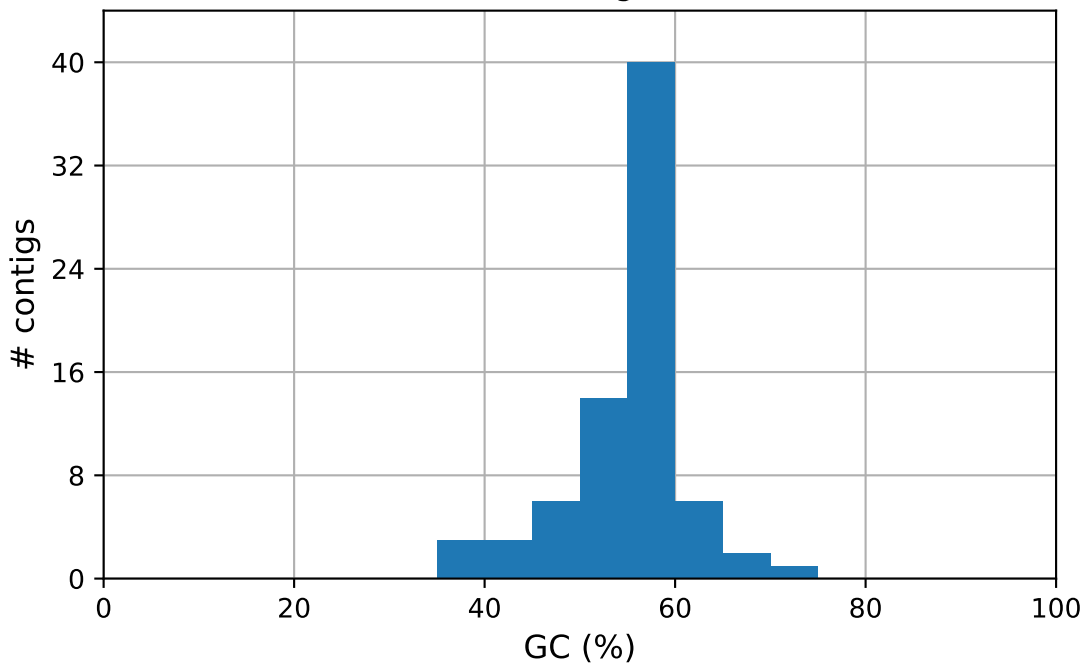


ERR1795072.contigs GC content



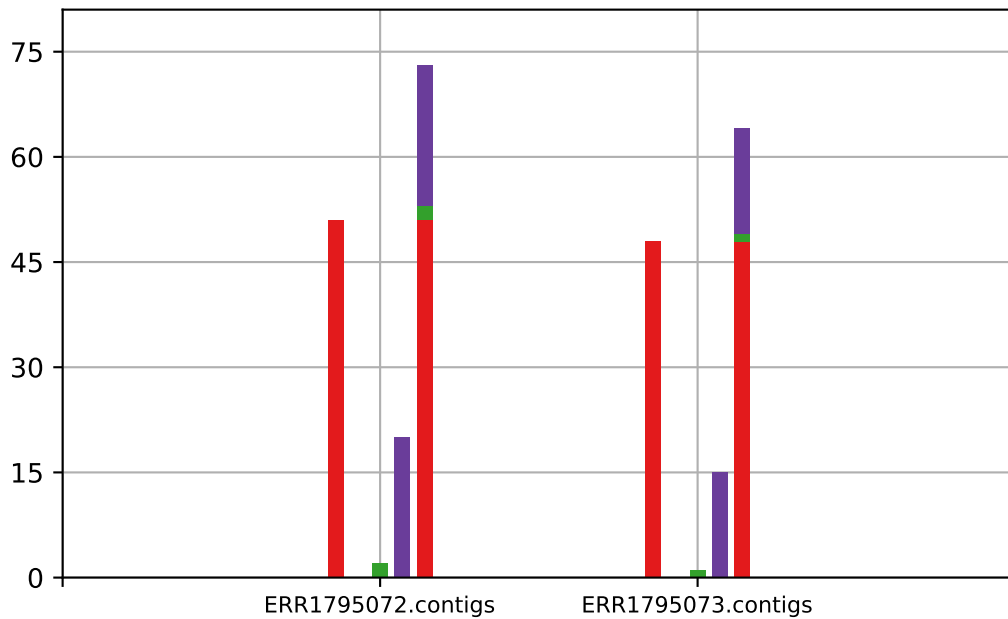
ERR1795072.contigs

ERR1795073.contigs GC content



ERR1795073.contigs

Misassemblies



relocations

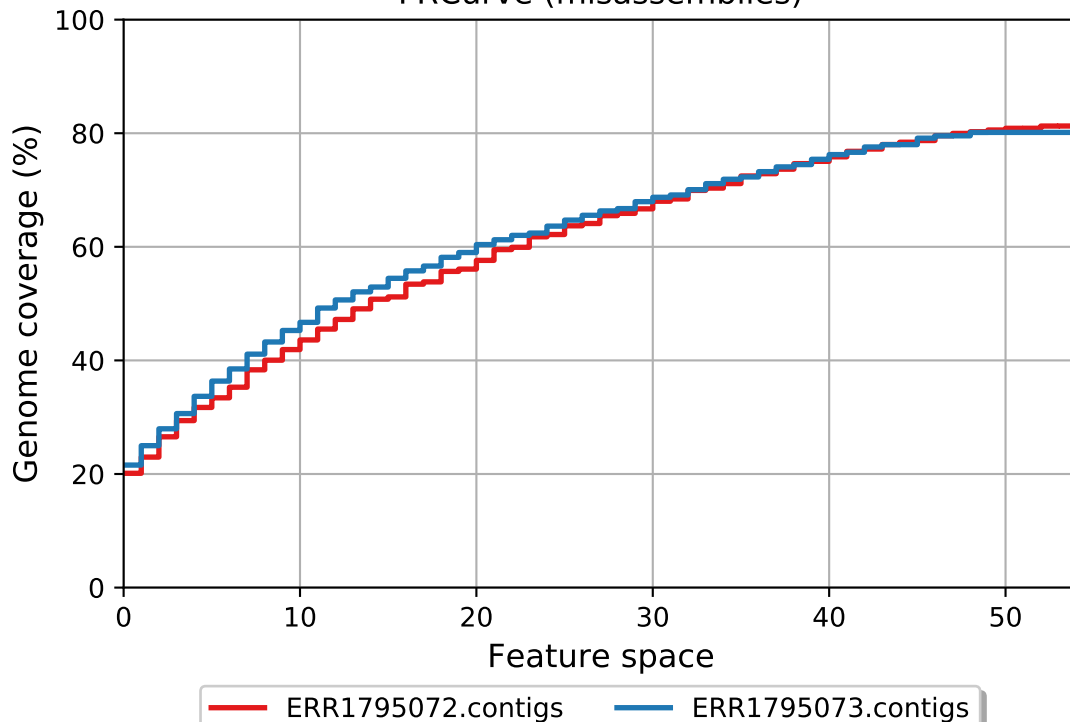


inversions

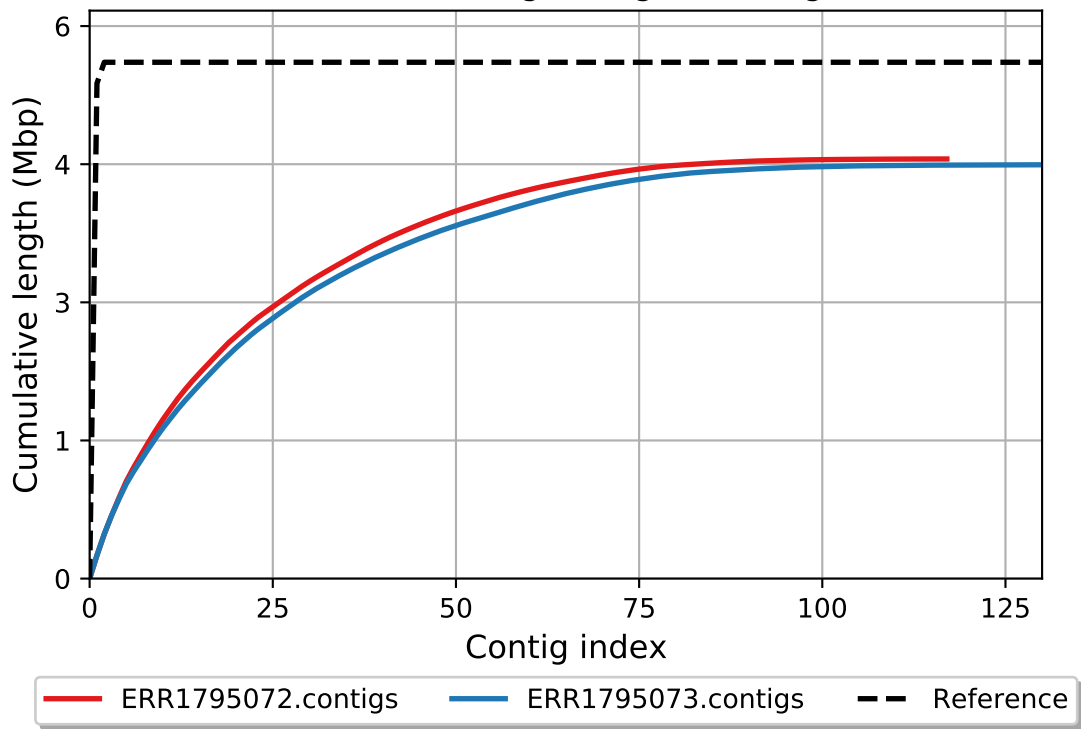


interspecies translocations

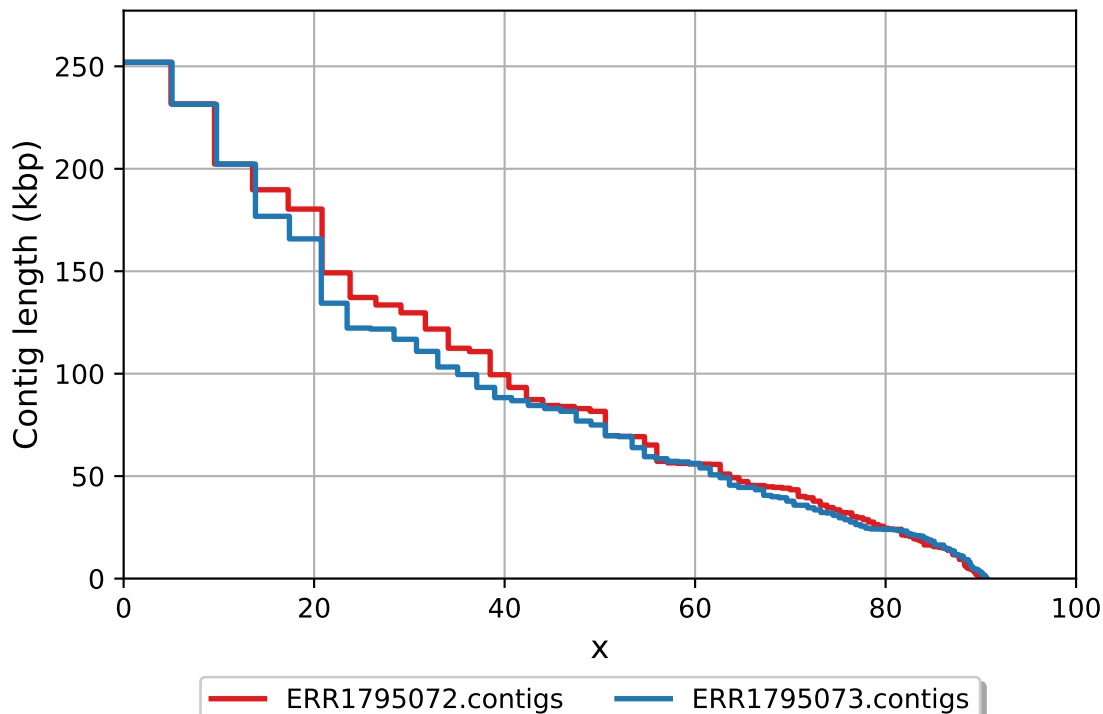
FRCurve (misassemblies)



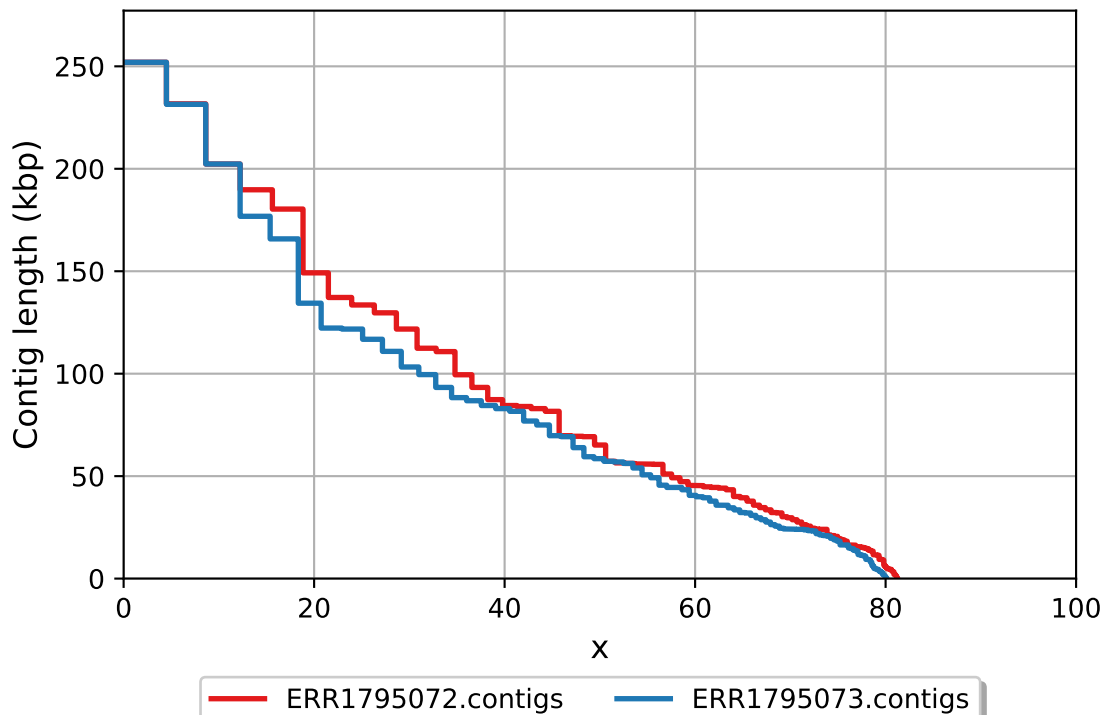
Cumulative length (aligned contigs)



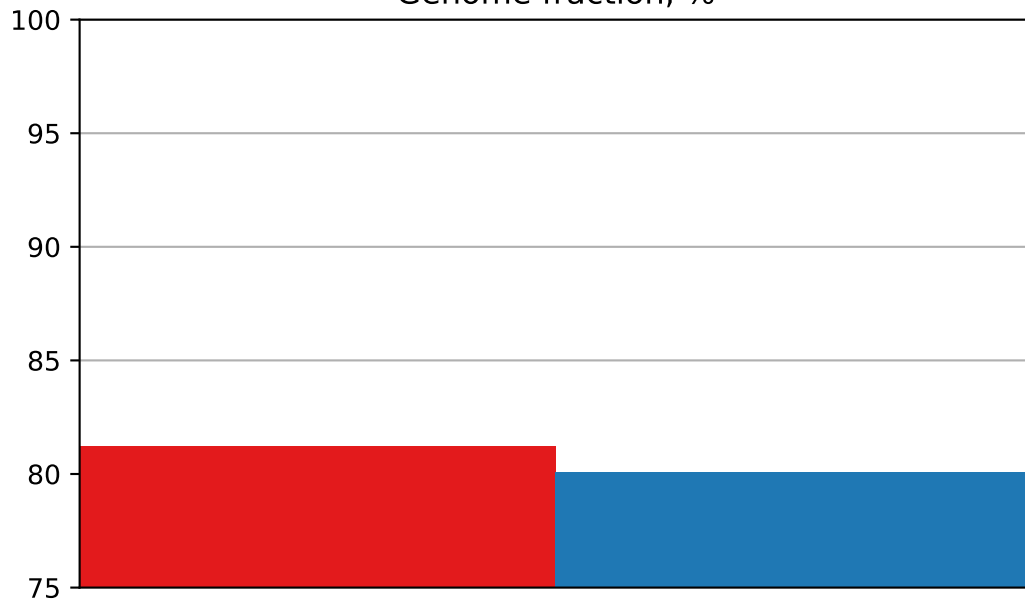
NAx



NGAx



Genome fraction, %



ERR1795072.contigs



ERR1795073.contigs