

Report

	contigs_1	contigs_2
# contigs (>= 0 bp)	3	4
# contigs (>= 1000 bp)	3	2
# contigs (>= 5000 bp)	0	0
# contigs (>= 10000 bp)	0	0
# contigs (>= 25000 bp)	0	0
# contigs (>= 50000 bp)	0	0
Total length (>= 0 bp)	6710	5870
Total length (>= 1000 bp)	6710	5460
Total length (>= 5000 bp)	0	0
Total length (>= 10000 bp)	0	0
Total length (>= 25000 bp)	0	0
Total length (>= 50000 bp)	0	0
# contigs	3	2
Largest contig	3980	3360
Total length	6710	5460
Reference length	10000	10000
GC (%)	51.28	52.44
Reference GC (%)	52.07	52.07
N50	3980	3360
NG50	1610	2100
N75	1610	2100
L50	1	1
LG50	2	2
L75	2	2
# misassemblies	1	2
# misassembled contigs	1	1
Misassembled contigs length	3980	3360
# local misassemblies	0	0
# unaligned contigs	0 + 0 part	0 + 0 part
Unaligned length	0	0
Genome fraction (%)	67.100	54.600
Duplication ratio	1.000	1.000
# N's per 100 kbp	0.00	0.00
# mismatches per 100 kbp	0.00	0.00
# indels per 100 kbp	0.00	0.00
# genes	5 + 4 part	1 + 6 part
# operons	1 + 1 part	0 + 2 part
# predicted genes (unique)	7	6
# predicted genes (>= 0 bp)	7	6
# predicted genes (>= 300 bp)	6	5
# predicted genes (>= 1500 bp)	1	1
# predicted genes (>= 3000 bp)	0	0
Largest alignment	2030	2100
Total aligned length	6710	5460
NA50	1950	1471
NGA50	1610	700
NA75	1610	1189
LA50	2	2
LGA50	3	4
LA75	3	3

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).

Gage report

	contigs_1	contigs_2
Contigs #	3	2
Min contig	1120	2100
Max contig	3980	3360
N50	1610 COUNT: 2	2100 COUNT: 2
Genome size	10000	10000
Assembly size	6710	5460
Chaff bases	0	0
Missing reference bases	3288(32.88%)	4539(45.39%)
Missing assembly bases	0(0.00%)	0(0.00%)
Missing assembly contigs	0(0.00%)	0(0.00%)
Duplicated reference bases	0	0
Compressed reference bases	0	0
Bad trim	0	0
Avg idy	100.00	100.00
SNPs	0	0
Indels < 5bp	0	0
Indels >= 5	1	2
Inversions	0	0
Relocation	0	0
Translocation	0	0
Corrected contig #	4	4
Corrected assembly size	6712	5461
Min correct contig	1120	700
Max correct contig	2030	2100
Corrected N50	1610 COUNT: 3	700 COUNT: 4

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

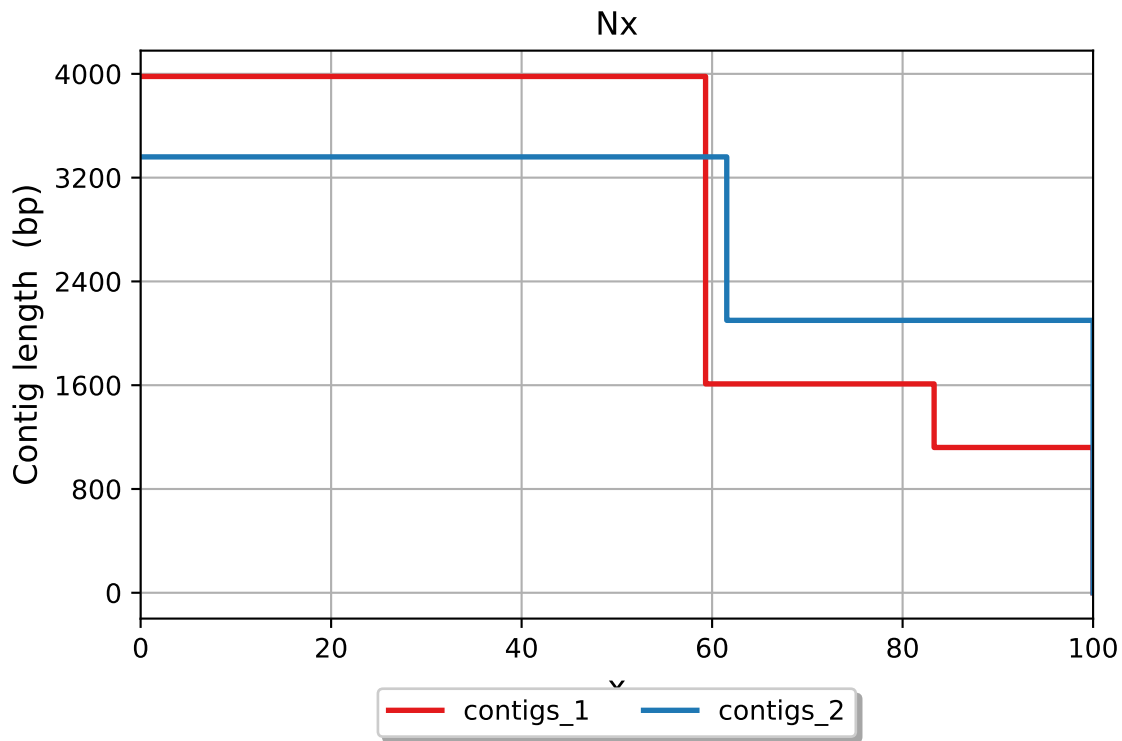
	contigs_1	contigs_2
# misassemblies	1	2
# relocations	1	2
# translocations	0	0
# inversions	0	0
# misassembled contigs	1	1
Misassembled contigs length	3980	3360
# local misassemblies	0	0
# mismatches	0	0
# indels	0	0
# short indels	0	0
# long indels	0	0
Indels length	0	0

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).

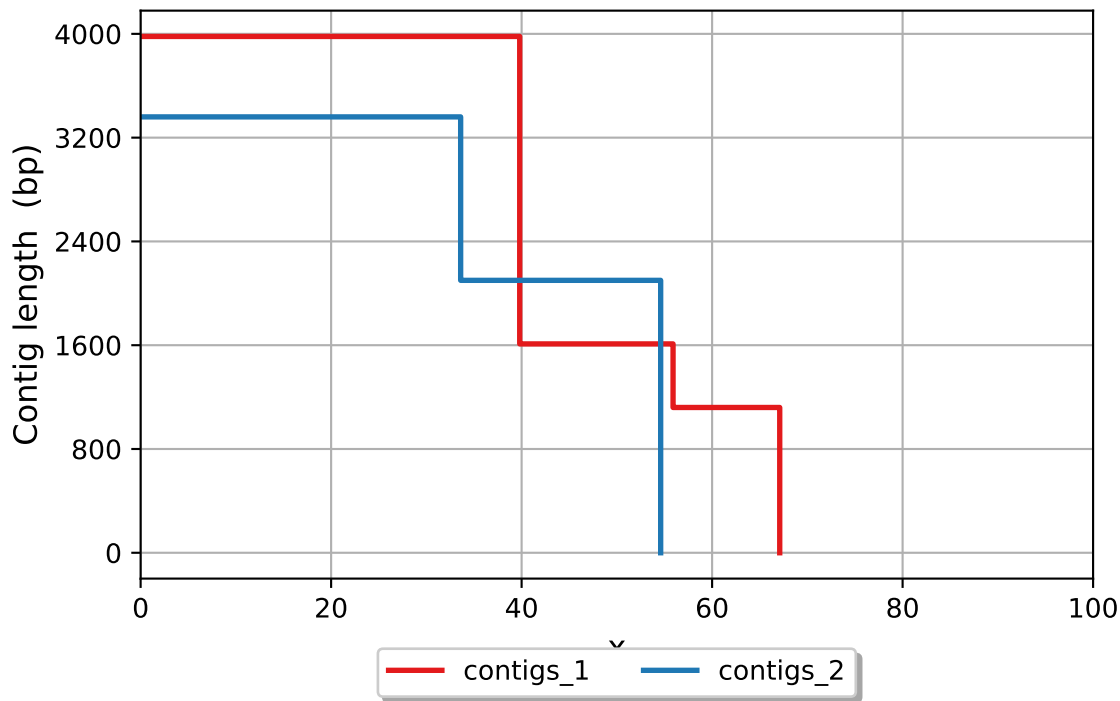
Unaligned report

	contigs_1	contigs_2
# fully unaligned contigs	0	0
Fully unaligned length	0	0
# partially unaligned contigs	0	0
# with misassembly	0	0
# both parts are significant	0	0
Partially unaligned length	0	0
# N's	0	0

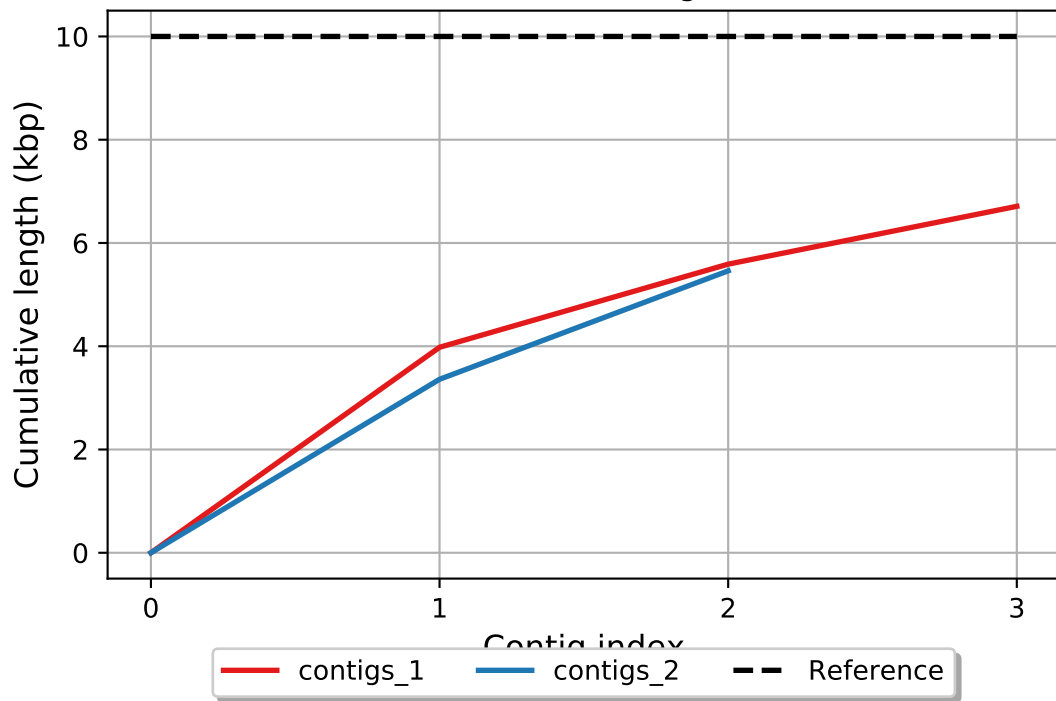
All statistics are based on contigs of size ≥ 500 bp, unless otherwise noted (e.g., "# contigs (≥ 0 bp)" and "Total length (≥ 0 bp)" include all contigs).



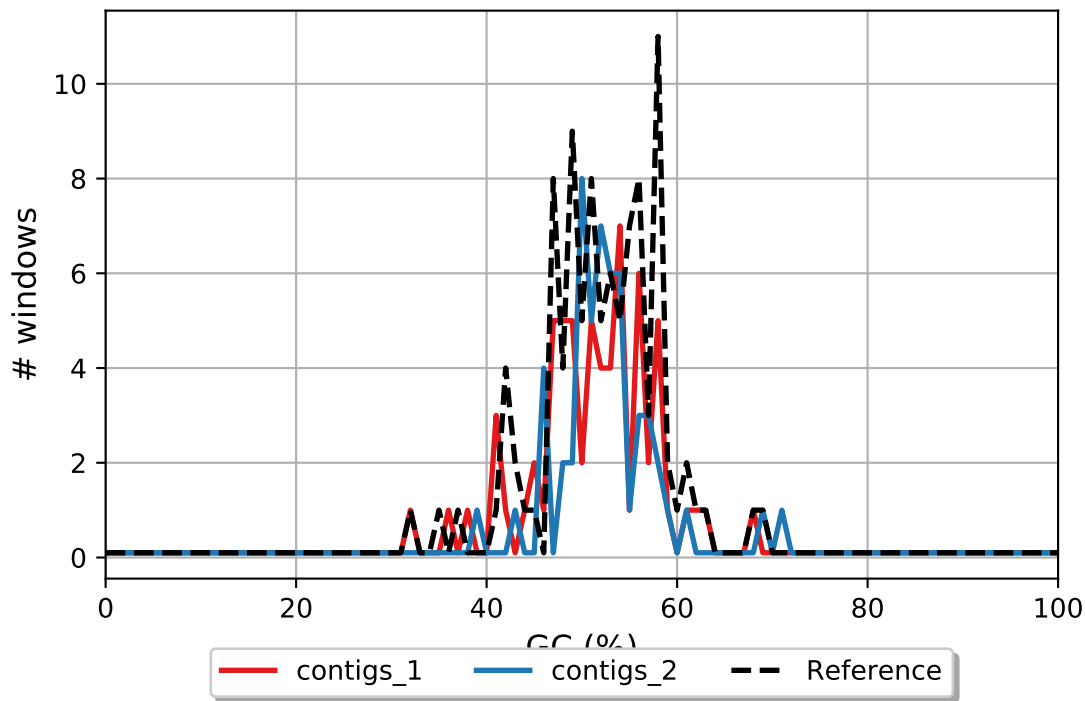
NGx



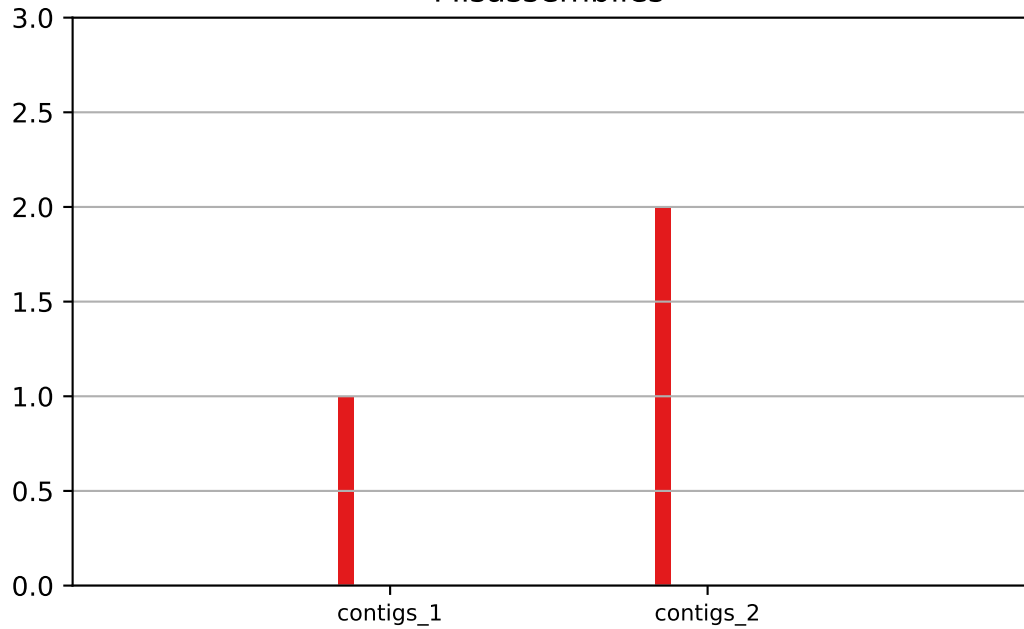
Cumulative length



GC content

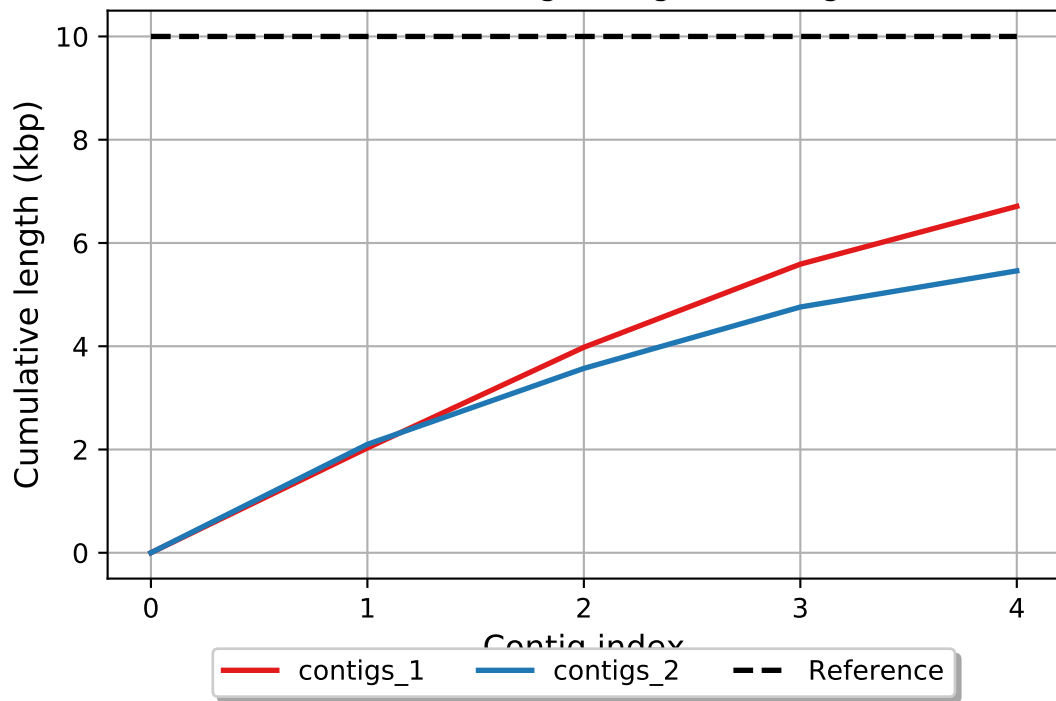


Misassemblies

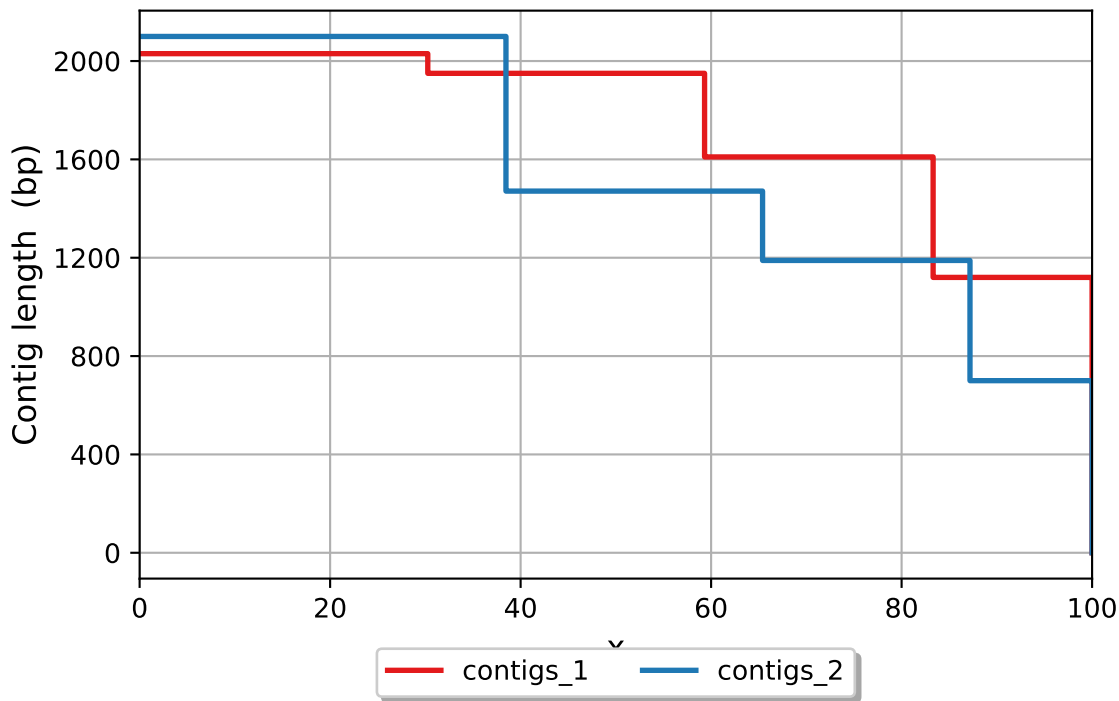


 # relocations

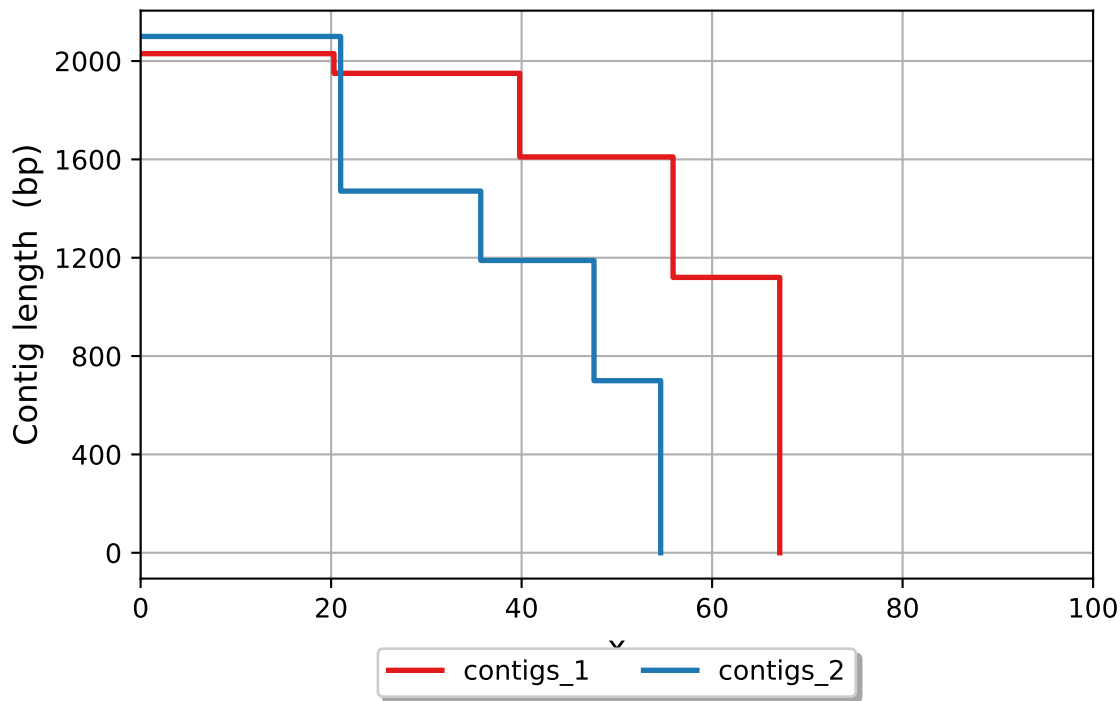
Cumulative length (aligned contigs)



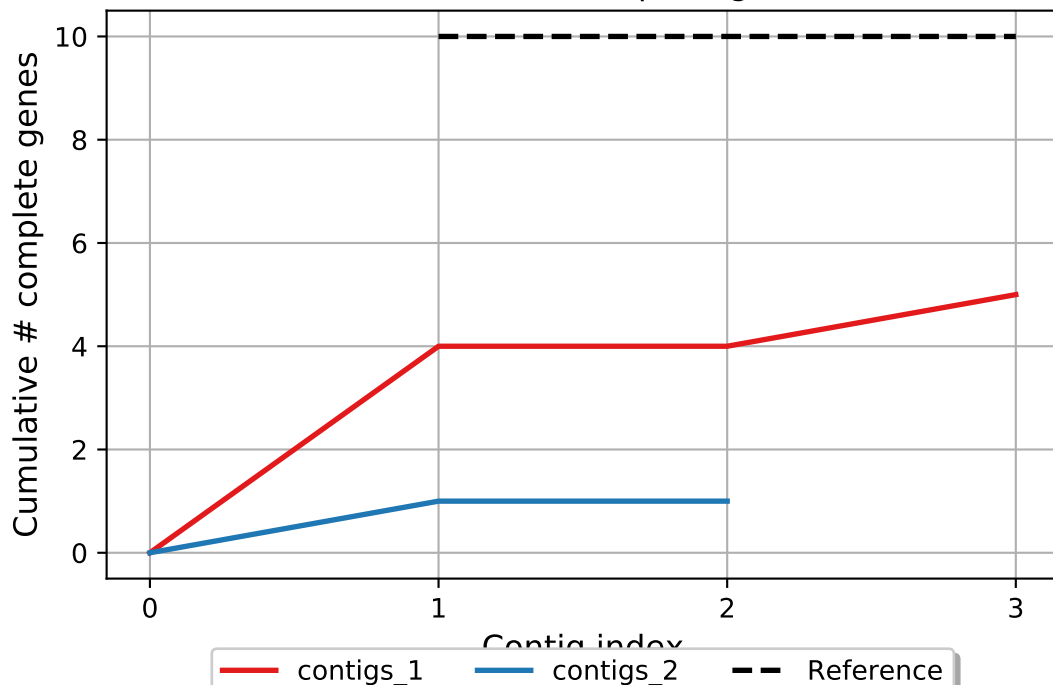
NAx



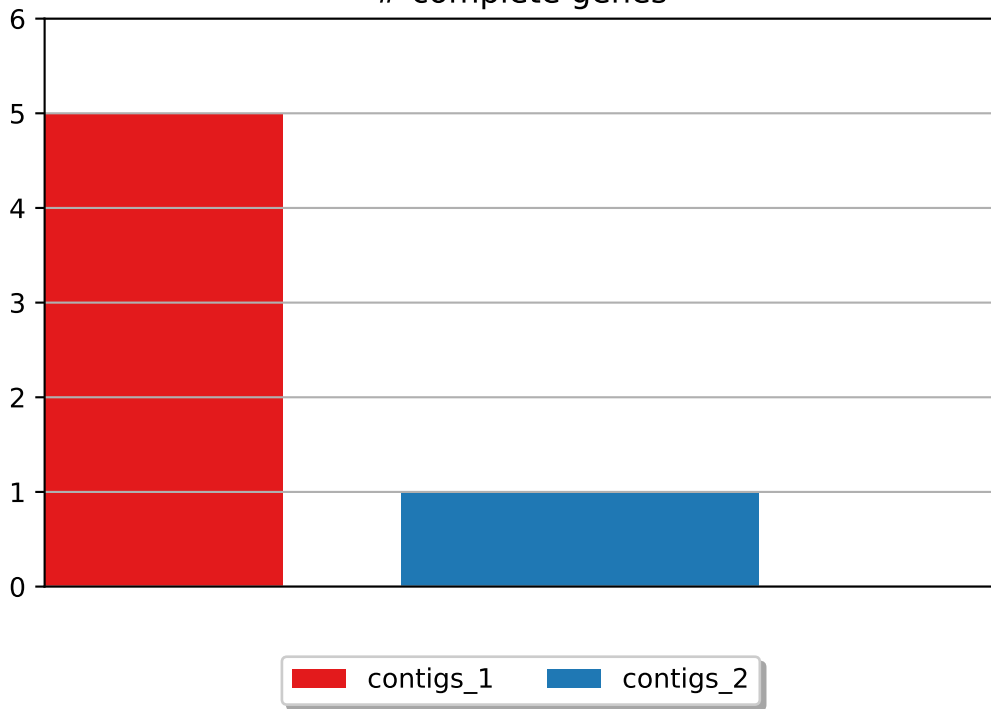
NGAx



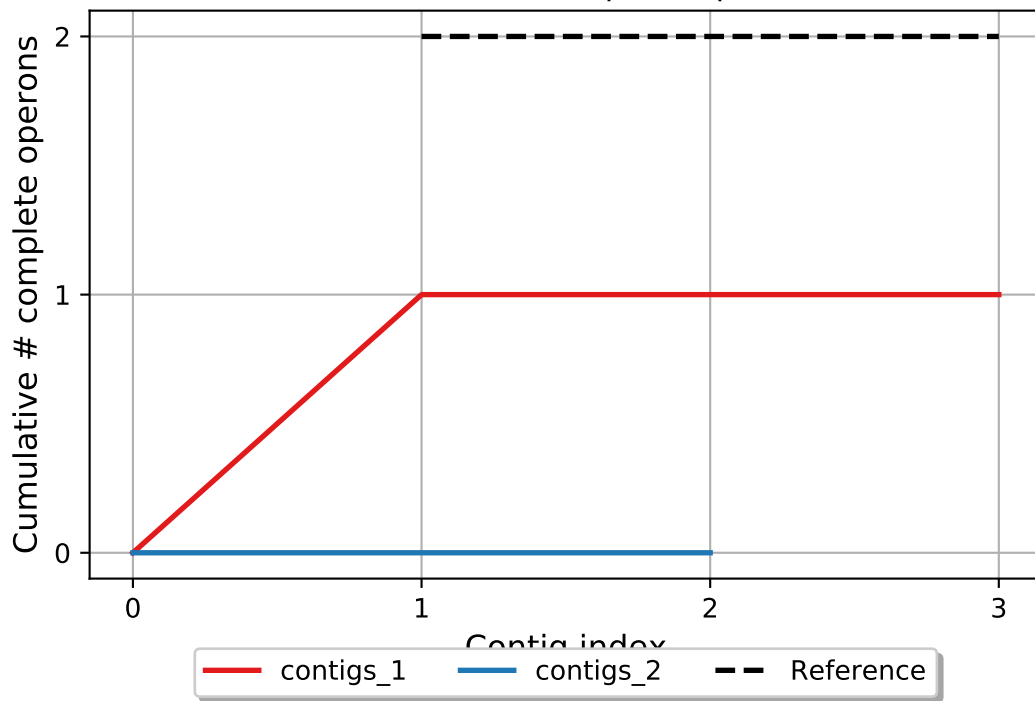
Cumulative # complete genes



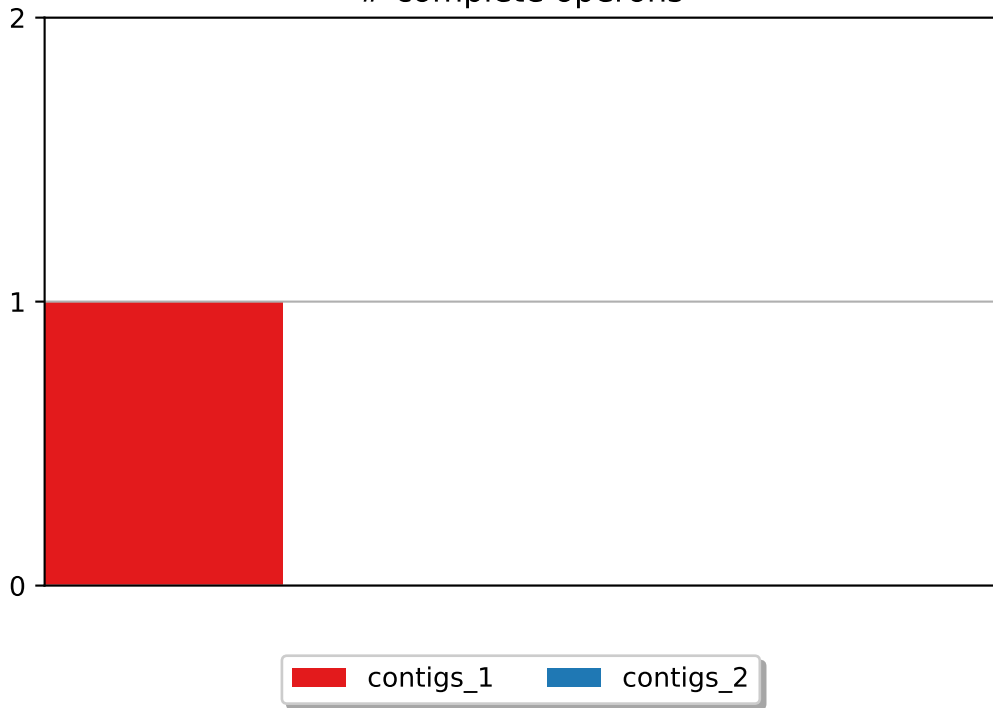
complete genes



Cumulative # complete operons



complete operons



Genome fraction, %

