

Report

	spades_assembly
# contigs (>= 0 bp)	151
# contigs (>= 1000 bp)	78
# contigs (>= 5000 bp)	58
# contigs (>= 10000 bp)	53
# contigs (>= 25000 bp)	47
# contigs (>= 50000 bp)	30
Total length (>= 0 bp)	4572866
Total length (>= 1000 bp)	4556855
Total length (>= 5000 bp)	4513956
Total length (>= 10000 bp)	4476060
Total length (>= 25000 bp)	4375355
Total length (>= 50000 bp)	3734280
# contigs	85
Largest contig	299328
Total length	4561906
Reference length	4641652
GC (%)	50.75
Reference GC (%)	50.79
N50	126004
NG50	117615
N75	65942
NG75	60768
L50	12
LG50	13
L75	25
LG75	26
# misassemblies	3
# misassembled contigs	1
Misassembled contigs length	299328
# local misassemblies	12
# unaligned contigs	0 + 0 part
Unaligned length	0
Genome fraction (%)	98.225
Duplication ratio	1.001
# N's per 100 kbp	0.00
# mismatches per 100 kbp	3.22
# indels per 100 kbp	0.42
Largest alignment	282562
Total aligned length	4561689
NA50	112394
NGA50	112394
NA75	65891
NGA75	60768
LA50	14
LGA50	14
LA75	27
LGA75	28

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

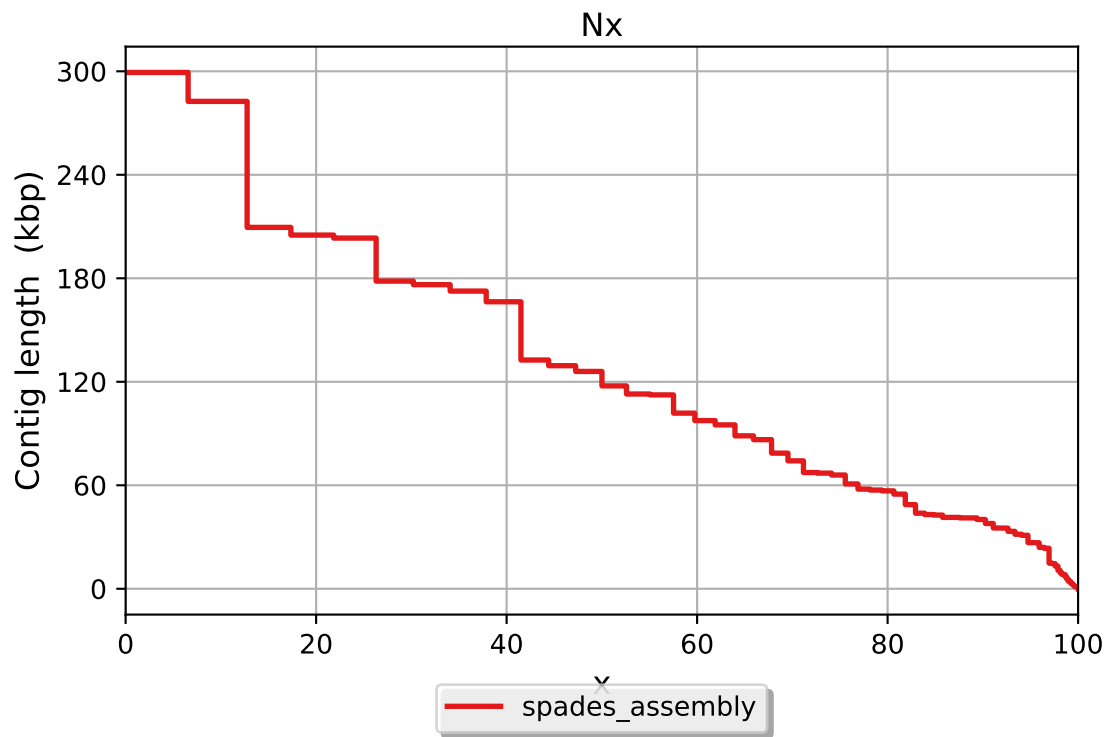
	spades_assembly
# misassemblies	3
# relocations	1
# translocations	0
# inversions	2
# misassembled contigs	1
Misassembled contigs length	299328
# local misassemblies	12
# mismatches	147
# indels	19
# indels (<= 5 bp)	18
# indels (> 5 bp)	1
Indels length	111

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).

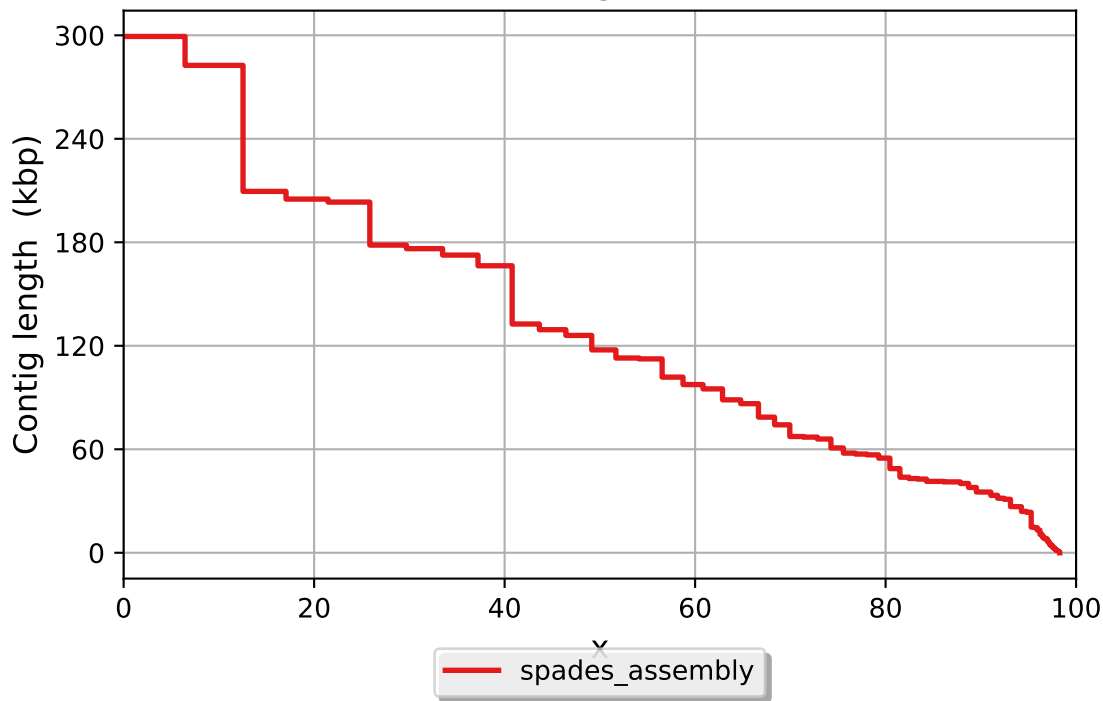
Unaligned report

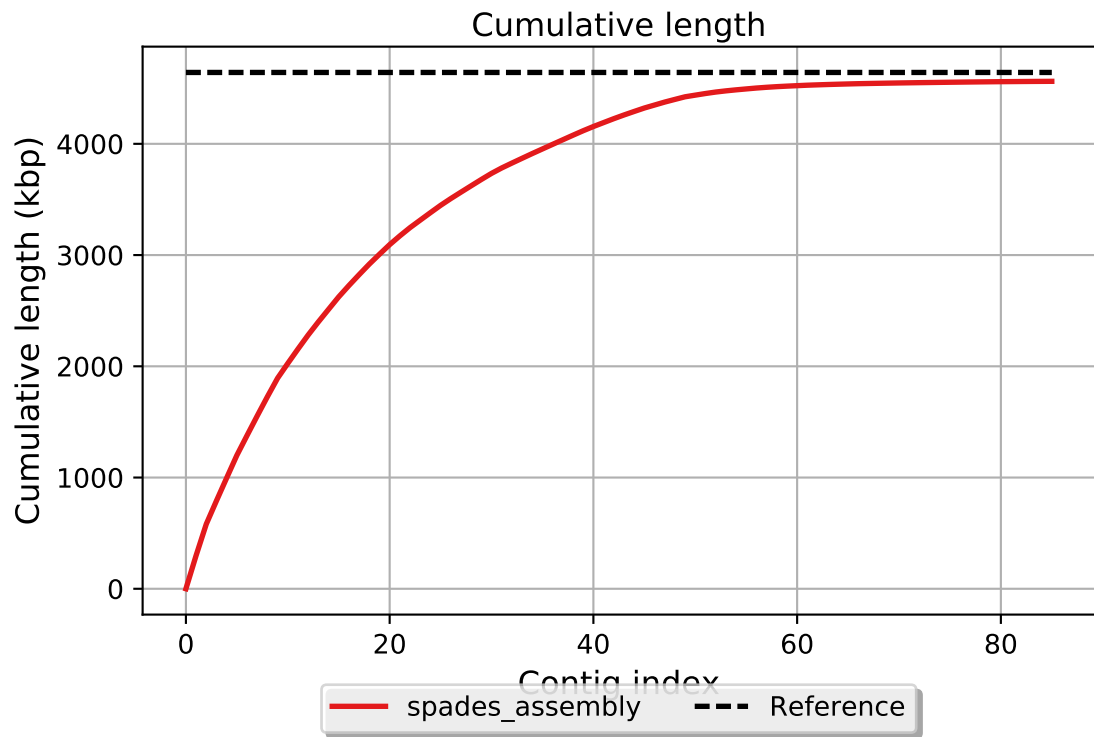
	spades_assembly
# fully unaligned contigs	0
Fully unaligned length	0
# partially unaligned contigs	0
# with misassembly	0
# both parts are significant	0
Partially unaligned length	0
# N's	0

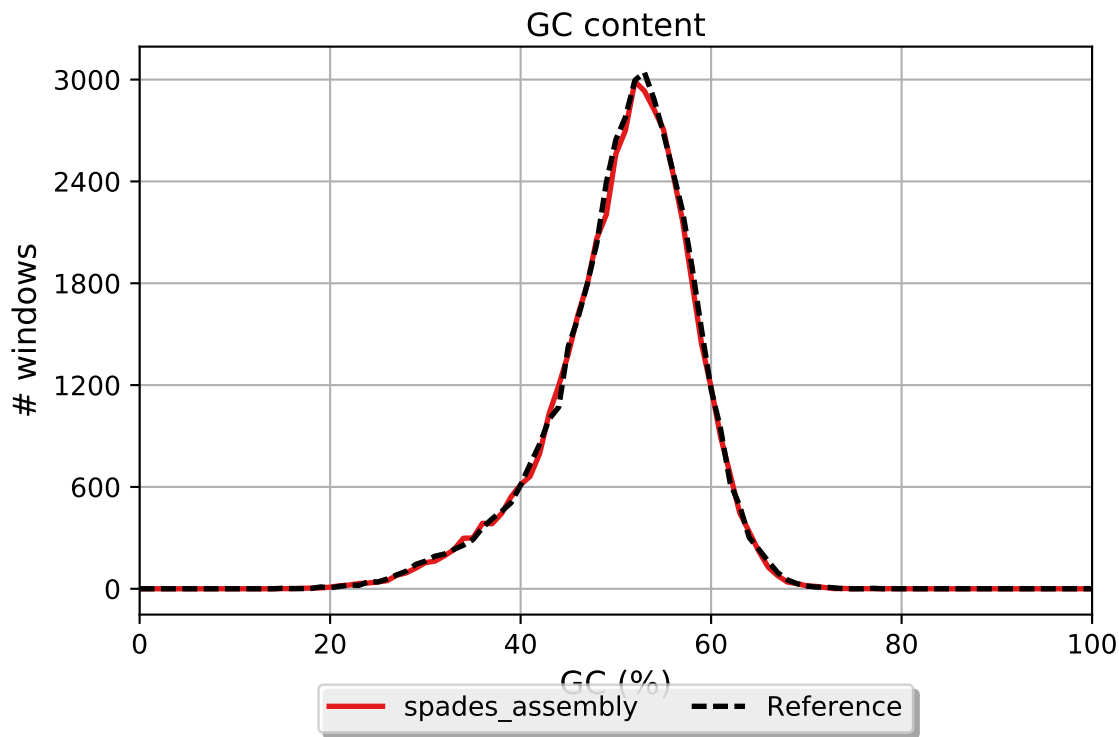
All statistics are based on contigs of size ≥ 500 bp, unless otherwise noted (e.g., "# contigs (≥ 0 bp)" and "Total length (≥ 0 bp)" include all contigs).



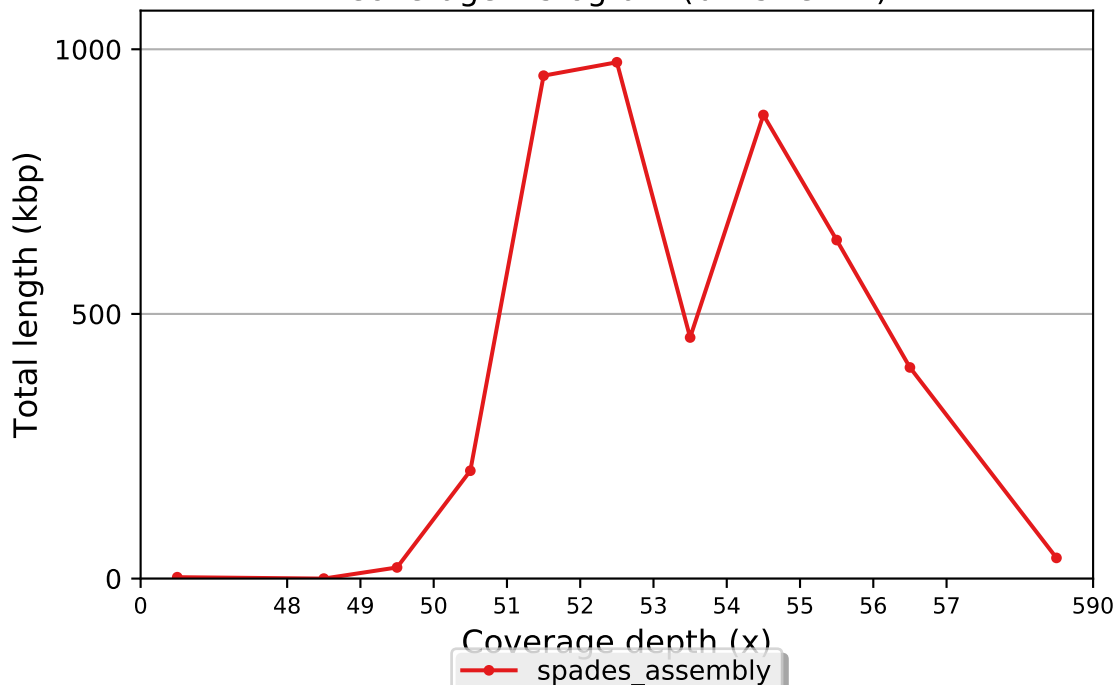
NGx



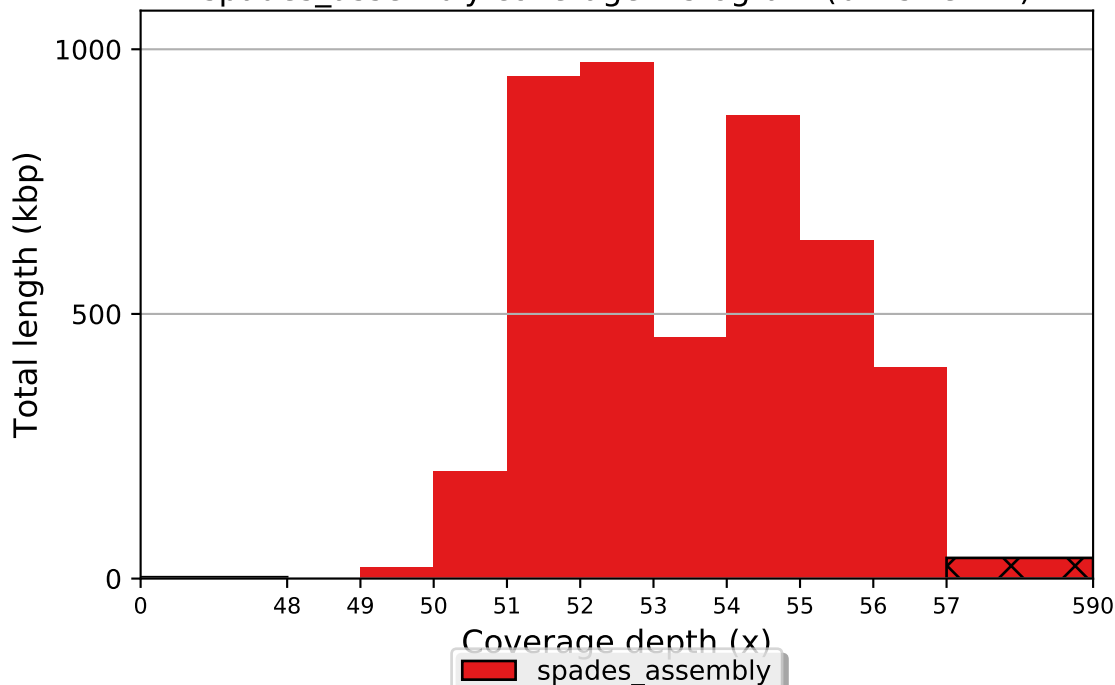




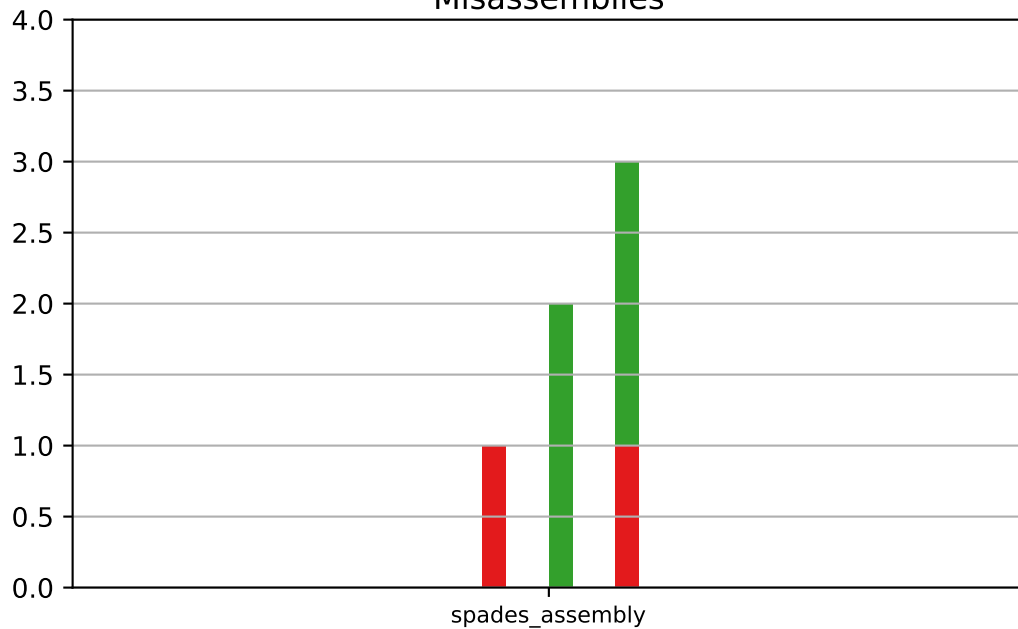
Coverage histogram (bin size: 1x)



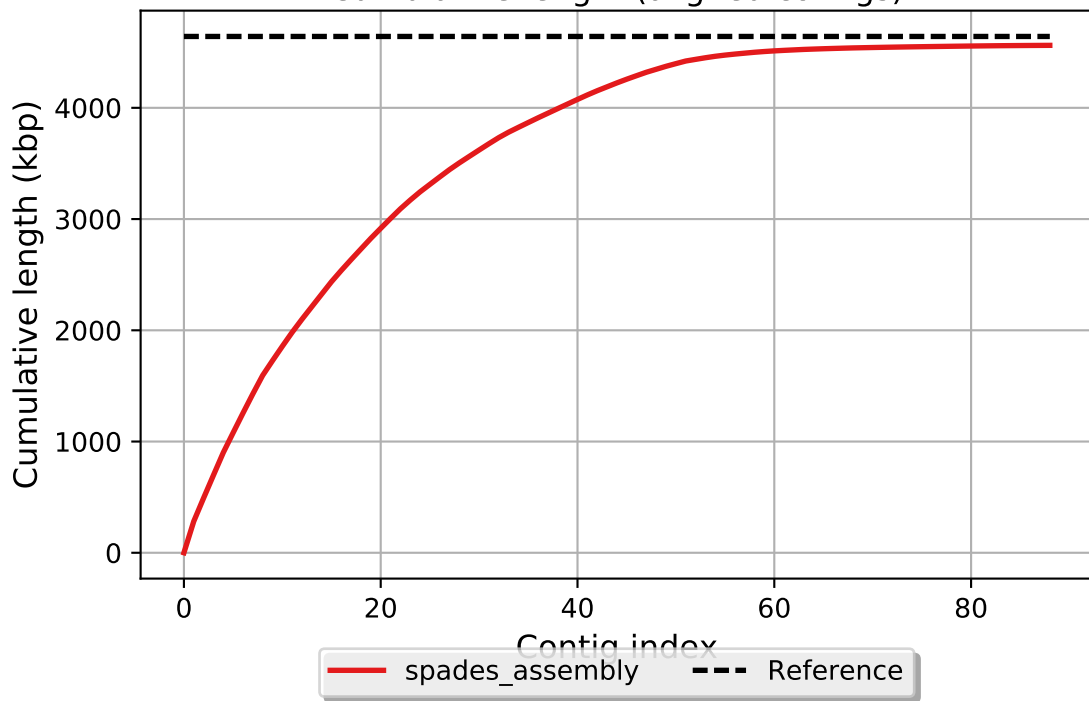
spades_assembly coverage histogram (bin size: 1x)



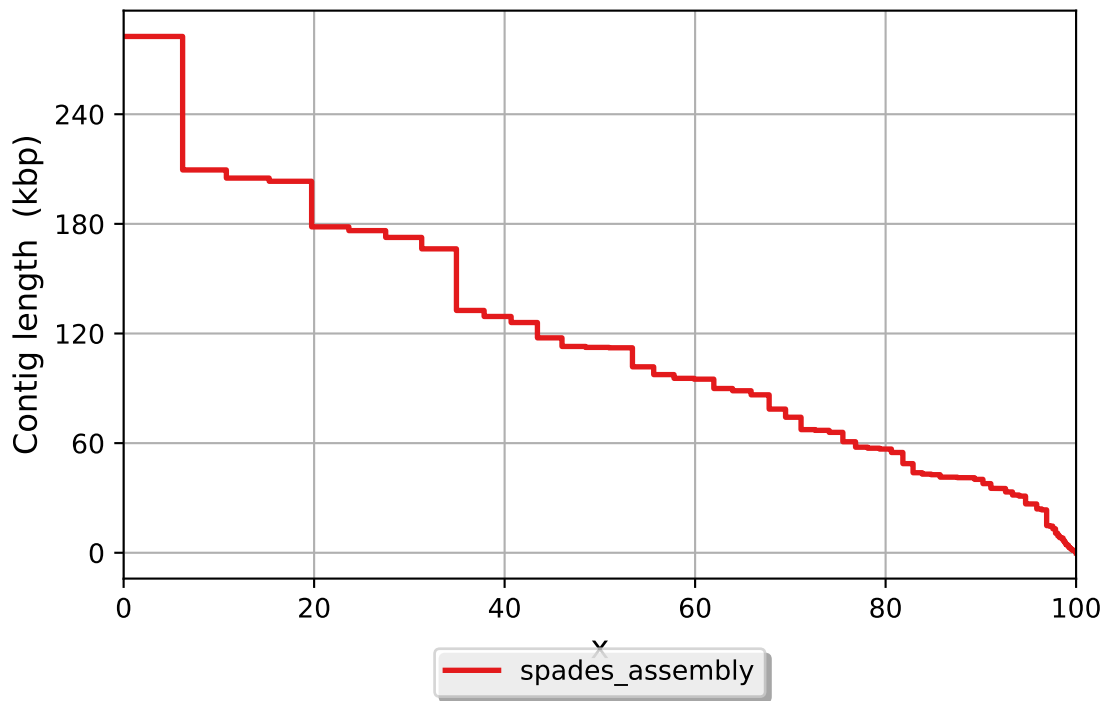
Misassemblies



Cumulative length (aligned contigs)



NAx



NGAx

