

# Report

	IDBA_UD	Ray	SOAPdenovo2	SPAdes
# contigs (>= 1000 bp)	3	1	0	4
# contigs (>= 5000 bp)	3	1	0	3
# contigs (>= 10000 bp)	3	1	0	3
# contigs (>= 25000 bp)	2	1	0	2
# contigs (>= 50000 bp)	2	1	0	1
Total length (>= 1000 bp)	380696	68607	0	239240
Total length (>= 5000 bp)	380696	68607	0	238149
Total length (>= 10000 bp)	380696	68607	0	238149
Total length (>= 25000 bp)	366546	68607	0	222294
Total length (>= 50000 bp)	366546	68607	0	189063
# contigs	3	1	2	4
Largest contig	246677	68607	859	189063
Total length	380696	68607	1485	239240
Reference length	4605106	4605106	4605106	4605106
GC (%)	46.68	47.25	40.82	47.56
Reference GC (%)	43.54	43.54	43.54	43.54
N50	246677	68607	859	189063
N75	119869	68607	626	189063
L50	1	1	1	1
L75	2	1	2	1
# misassemblies	0	0	0	0
# misassembled contigs	0	0	0	0
Misassembled contigs length	0	0	0	0
# local misassemblies	0	0	0	0
# structural variations	0	0	0	0
# unaligned contigs	0 + 3 part	0 + 1 part	0 + 2 part	0 + 3 part
Unaligned length	380371	68509	1153	237888
Genome fraction (%)	0.007	0.002	0.007	0.029
Duplication ratio	1.000	1.010	1.000	1.007
# N's per 100 kbp	6.30	413.95	7946.13	5.43
# mismatches per 100 kbp	3076.92	3092.78	903.61	2086.44
# indels per 100 kbp	615.38	1030.93	0.00	298.06
Largest alignment	129	98	207	1091
NGA50	-	-	-	-

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

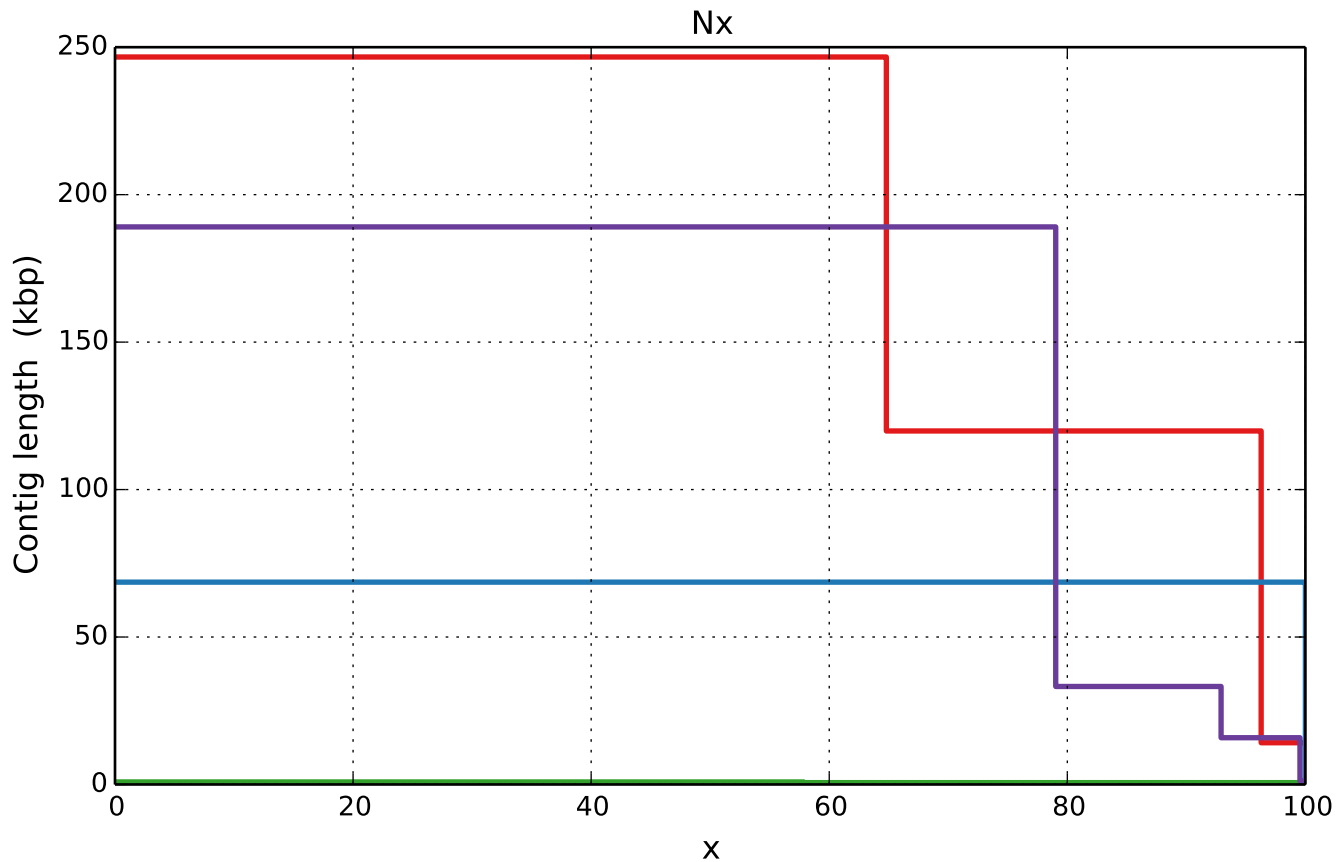
	IDBA_UD	Ray	SOAPdenovo2	SPAdes
# misassemblies	0	0	0	0
# relocations	0	0	0	0
# translocations	0	0	0	0
# inversions	0	0	0	0
# possibly misassembled contigs	0	0	0	0
# misassembled contigs	0	0	0	0
Misassembled contigs length	0	0	0	0
# local misassemblies	0	0	0	0
# structural variations	0	0	0	0
# mismatches	10	3	3	28
# indels	2	1	0	4
# short indels	2	1	0	3
# long indels	0	0	0	1
Indels length	2	1	0	12

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).

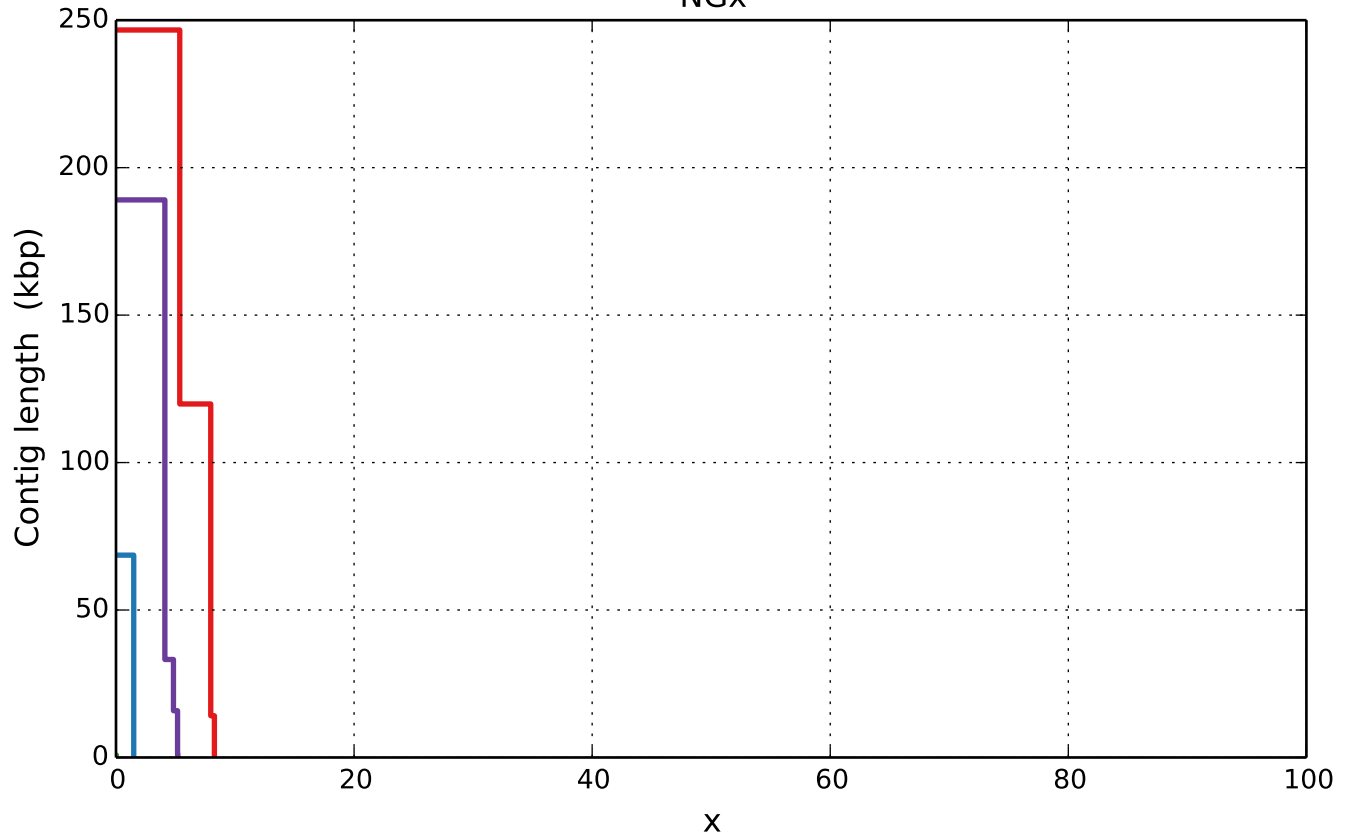
## Unaligned report

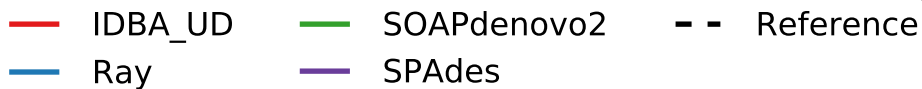
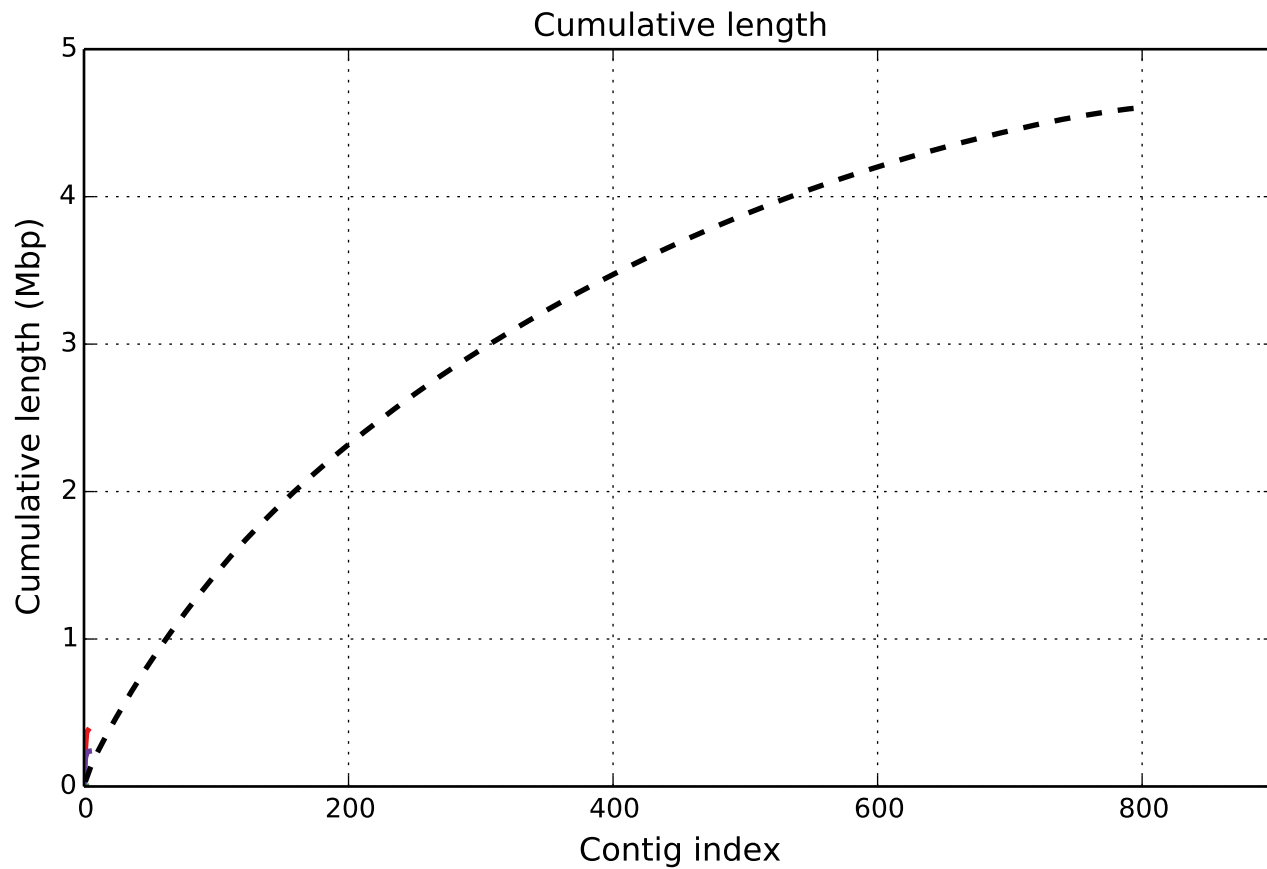
	IDBA_UD	Ray	SOAPdenovo2	SPAdes
# fully unaligned contigs	0	0	0	0
Fully unaligned length	0	0	0	0
# partially unaligned contigs	3	1	2	3
# with misassembly	0	0	0	0
# both parts are significant	0	0	0	0
Partially unaligned length	380371	68509	1153	237888
# N's	24	284	118	13

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).

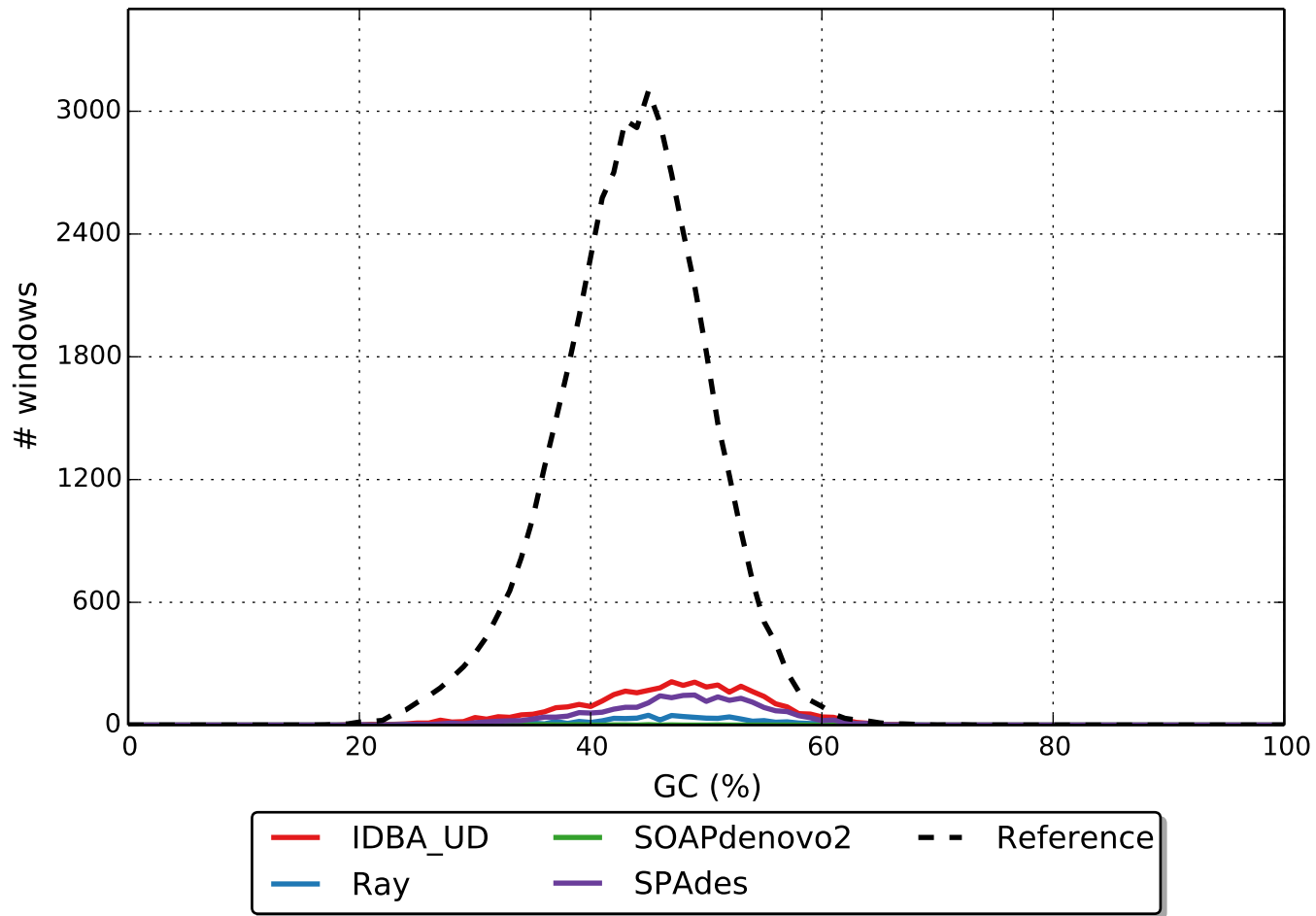


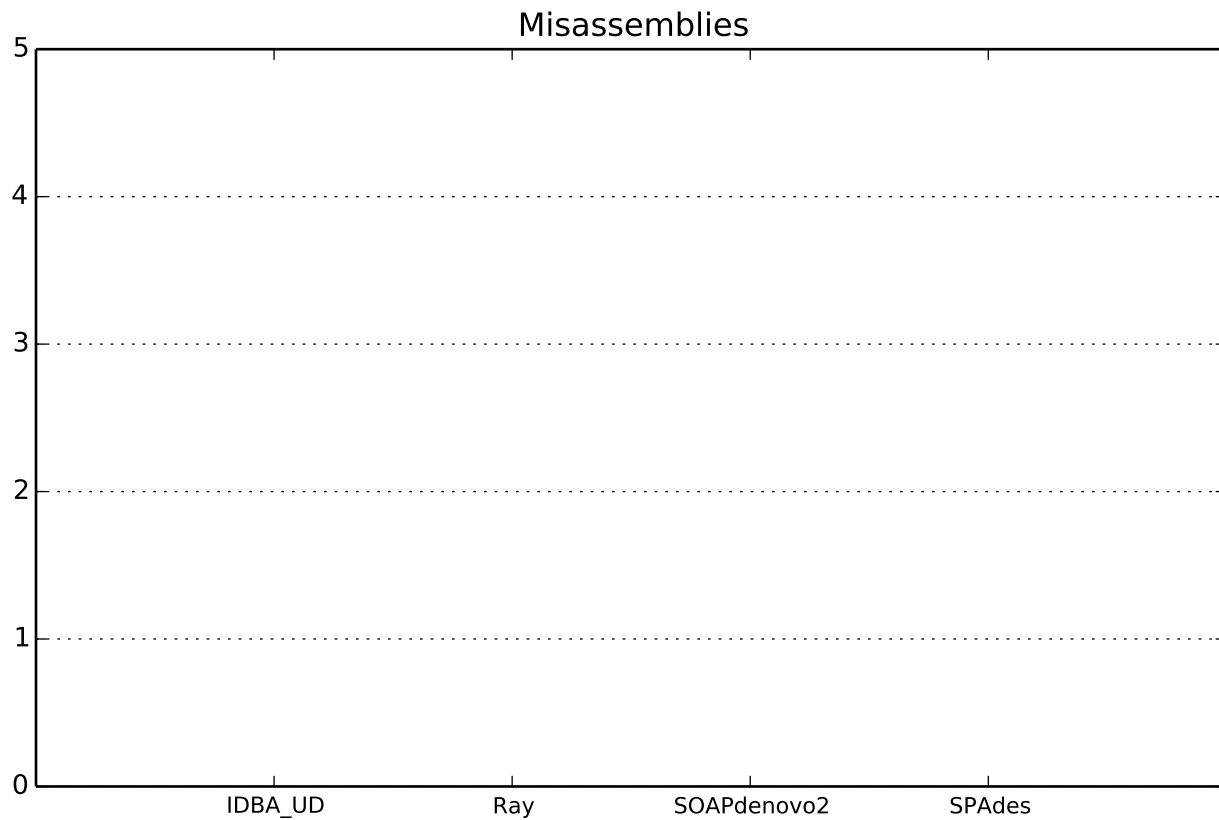
NGx



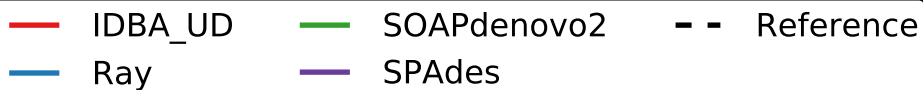
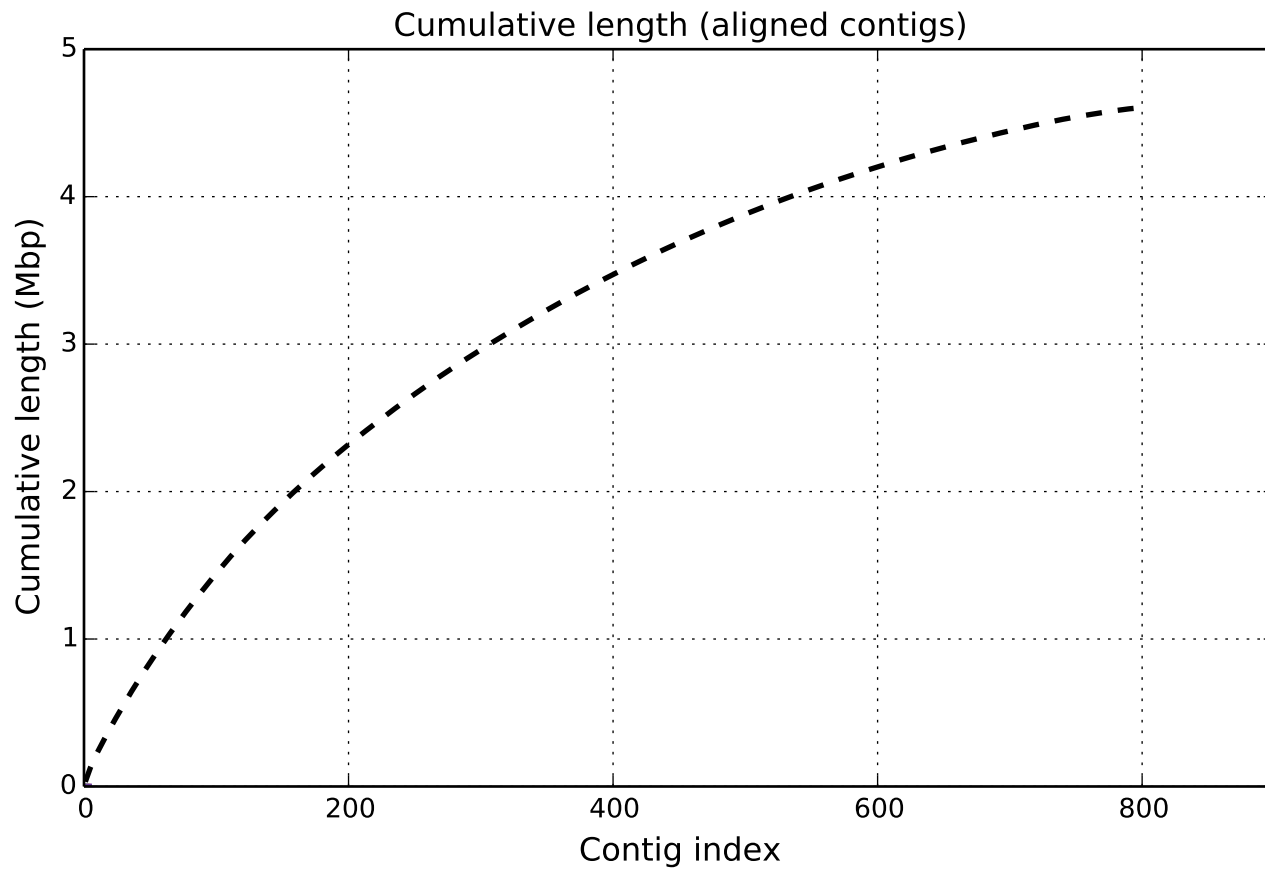


GC content

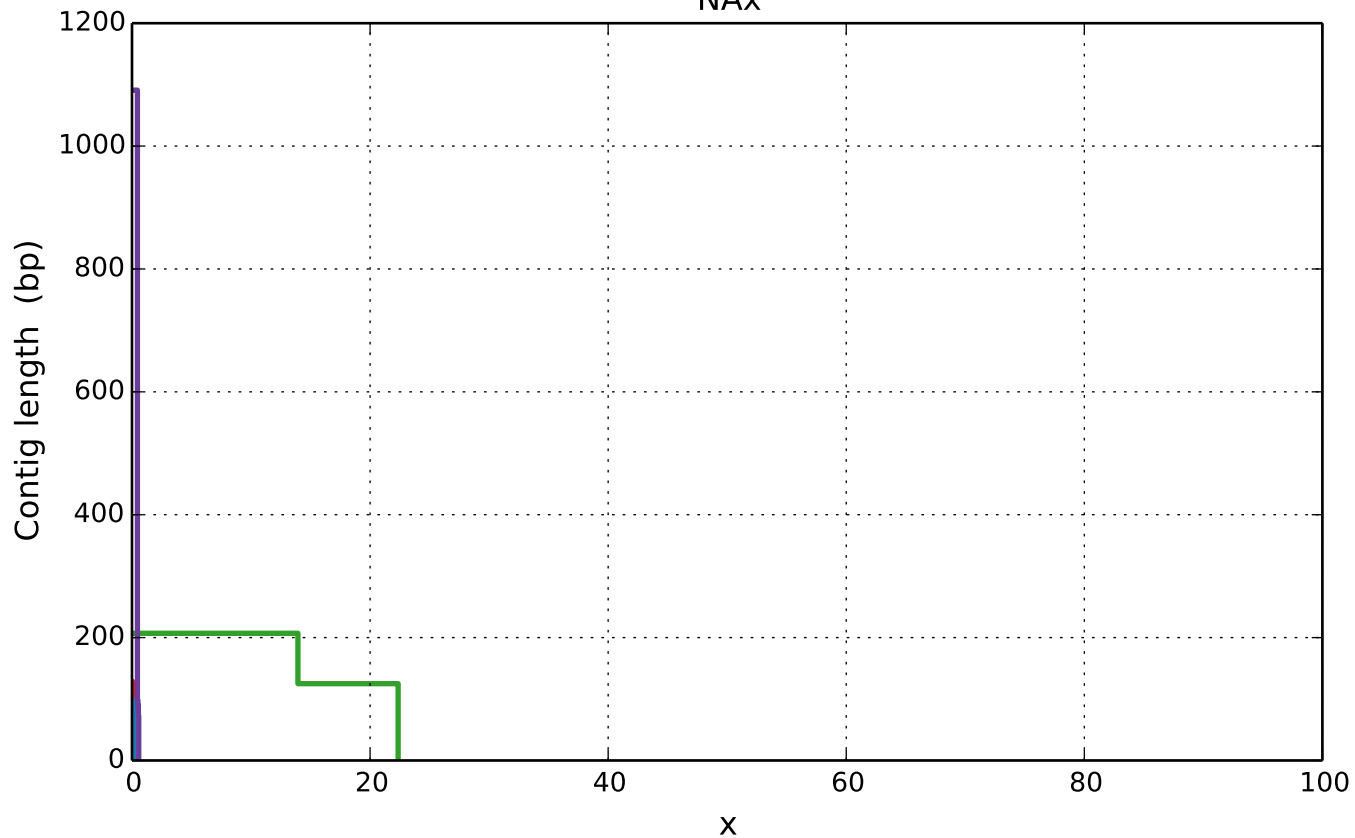








NAx



NGAx

