

# Report

	IDBA_UD	Ray	SOAPdenovo2	SPAdes
# contigs (>= 1000 bp)	4	3	1	3
# contigs (>= 5000 bp)	3	0	0	1
# contigs (>= 10000 bp)	1	0	0	0
# contigs (>= 25000 bp)	1	0	0	0
# contigs (>= 50000 bp)	1	0	0	0
Total length (>= 1000 bp)	157137	7531	2685	17272
Total length (>= 5000 bp)	154190	0	0	9625
Total length (>= 10000 bp)	135115	0	0	0
Total length (>= 25000 bp)	135115	0	0	0
Total length (>= 50000 bp)	135115	0	0	0
# contigs	6	5	3	3
Largest contig	135115	3573	2685	9625
Total length	158804	8906	3801	17272
Reference length	3156478	3156478	3156478	3156478
GC (%)	42.05	37.97	32.29	34.39
Reference GC (%)	37.27	37.27	37.27	37.27
N50	135115	2504	2685	9625
N75	135115	1454	613	4802
L50	1	2	1	1
L75	1	3	2	2
# 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 + 4 part	0 + 4 part	0 + 3 part	0 + 3 part
Unaligned length	155216	4942	2730	15325
Genome fraction (%)	0.104	0.125	0.034	0.062
Duplication ratio	1.093	1.002	0.998	0.994
# N's per 100 kbp	0.00	3312.37	605.10	0.00
# mismatches per 100 kbp	913.80	3463.09	1491.15	0.00
# indels per 100 kbp	0.00	25.28	0.00	51.05
Largest alignment	921	2423	391	776
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

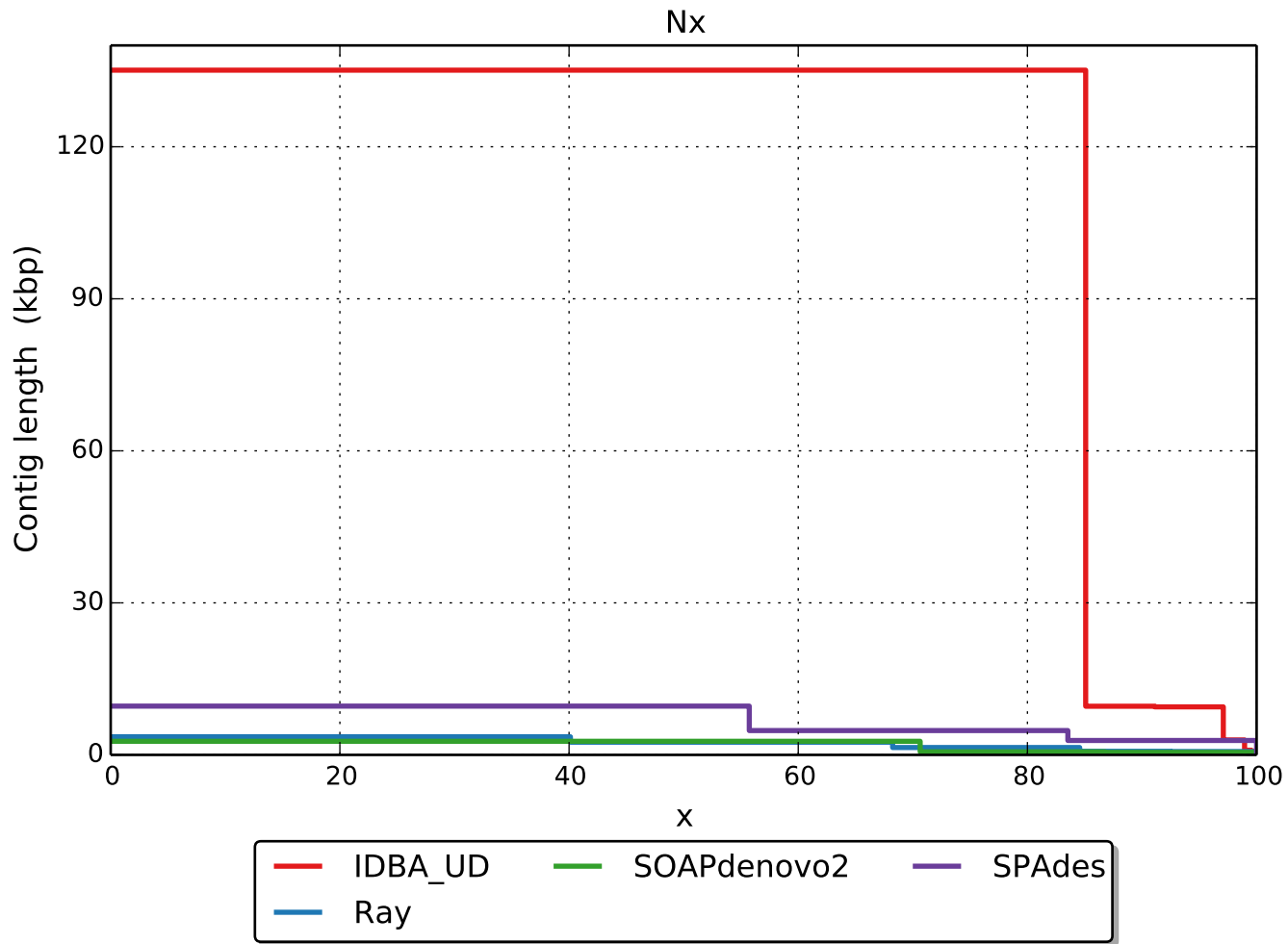
	IDBA_UD	Ray	SOAPdenovo2	SPAdes
# misassemblies	0	0	0	0
# relocations	0	0	0	0
# translocations	0	0	0	0
# inversions	0	0	0	0
# possibly misassembled contigs	2	1	1	1
# misassembled contigs	0	0	0	0
Misassembled contigs length	0	0	0	0
# local misassemblies	0	0	0	0
# structural variations	0	0	0	0
# mismatches	30	137	16	0
# indels	0	1	0	1
# short indels	0	1	0	0
# long indels	0	0	0	1
Indels length	0	1	0	19

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).

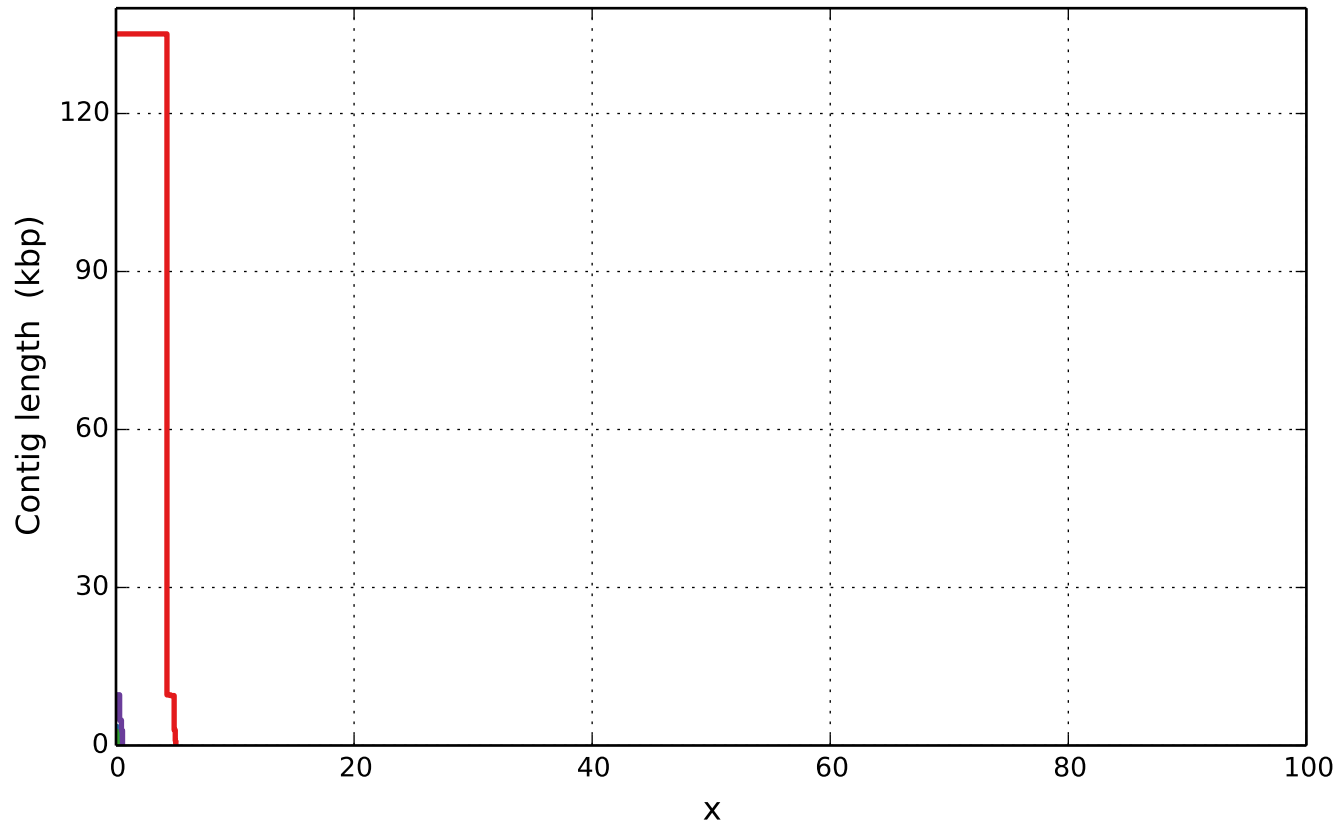
## Unaligned report

	IDBA_UD	Ray	SOAPdenovo2	SPAdes
# fully unaligned contigs	0	0	0	0
Fully unaligned length	0	0	0	0
# partially unaligned contigs	4	4	3	3
# with misassembly	3	1	1	3
# both parts are significant	2	1	1	1
Partially unaligned length	155216	4942	2730	15325
# N's	0	295	23	0

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

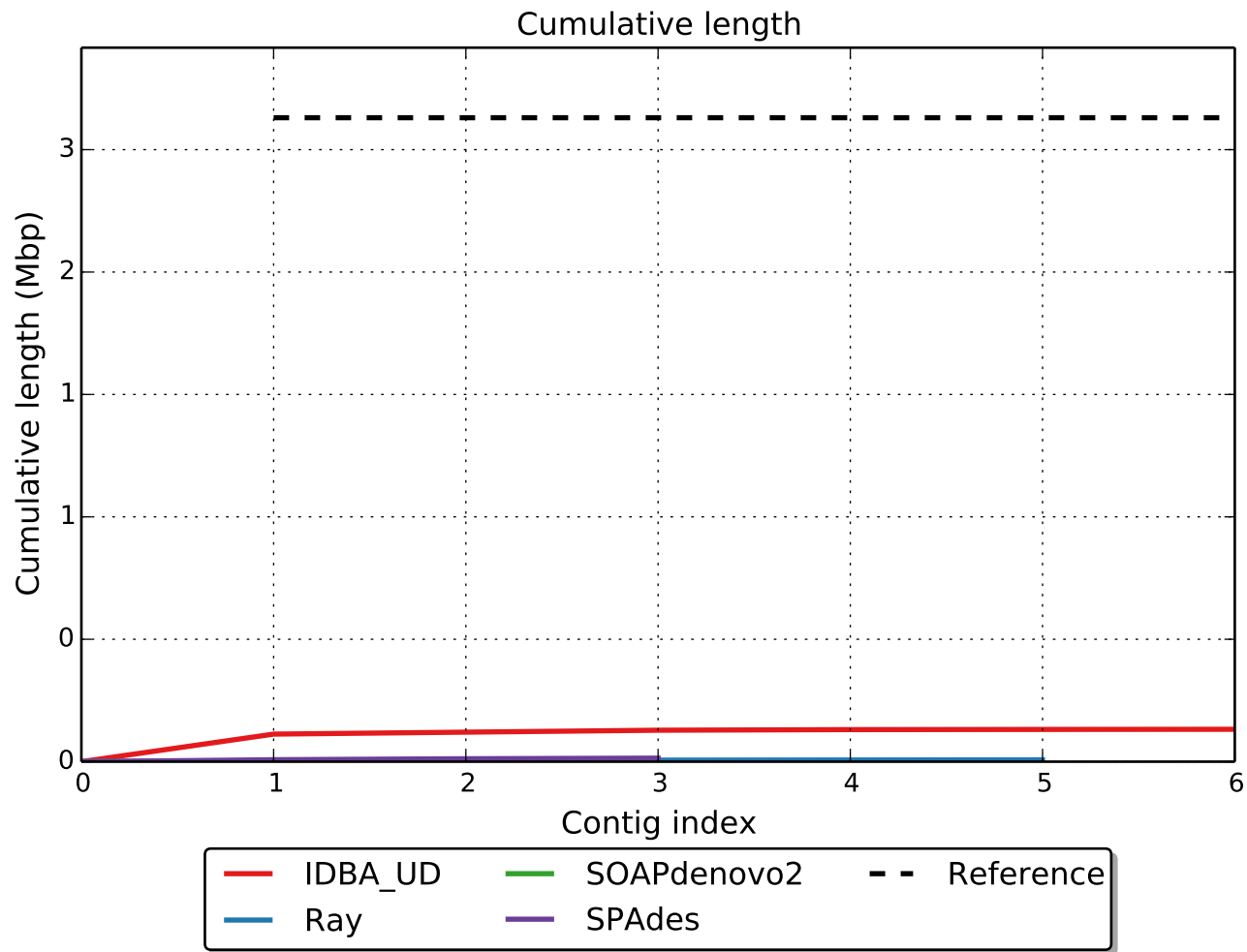


— IDBA\_UD

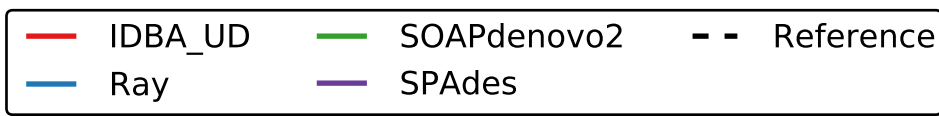
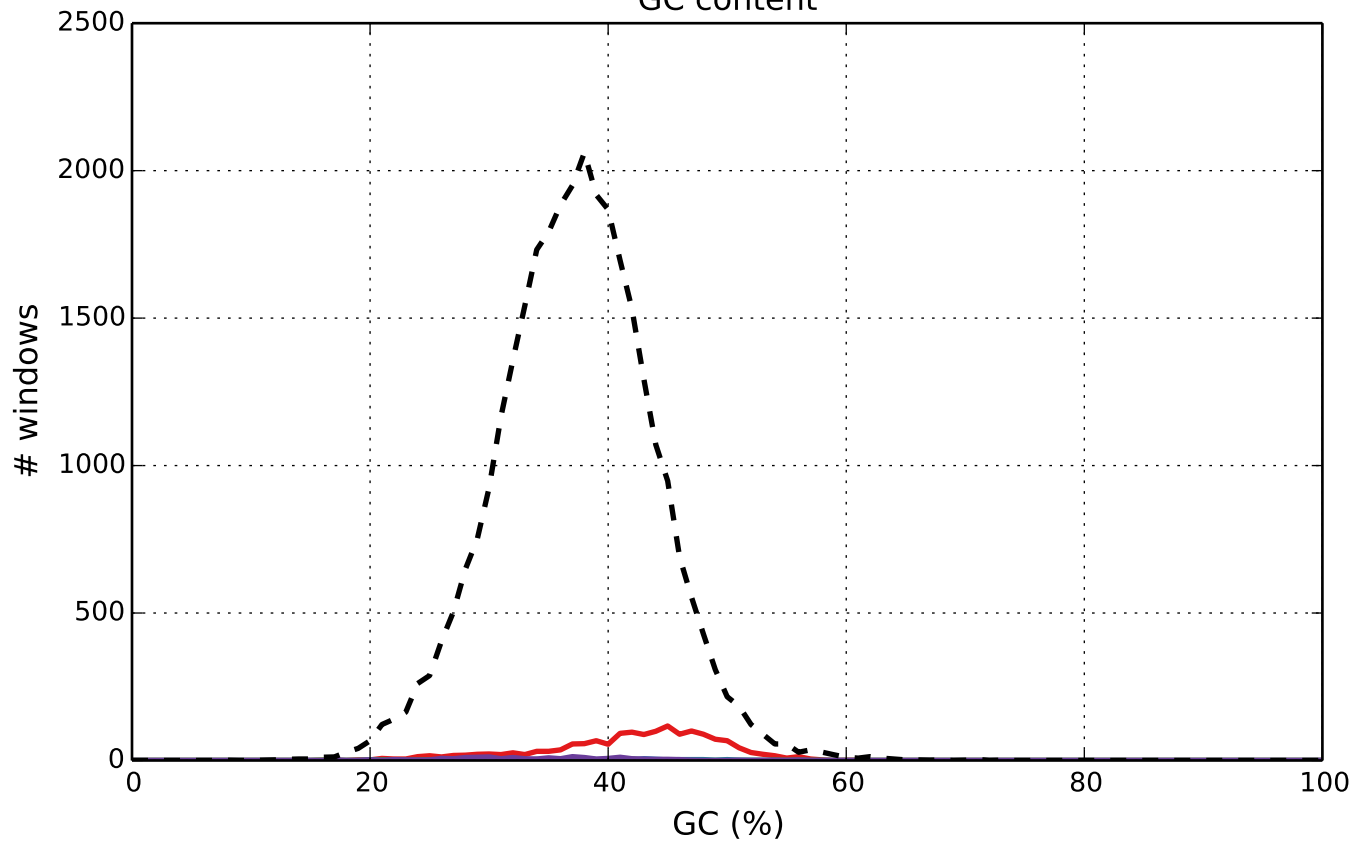
— SOAPdenovo2

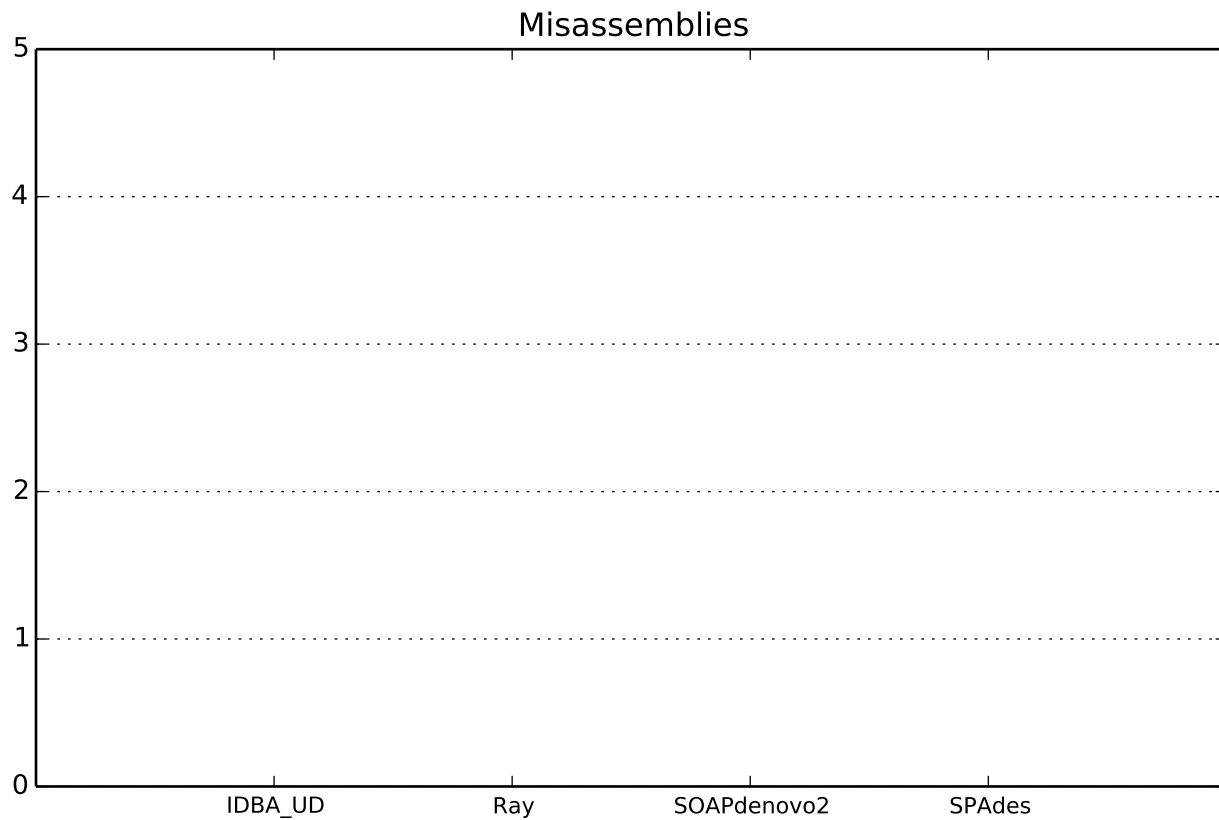
— SPAdes

— Ray

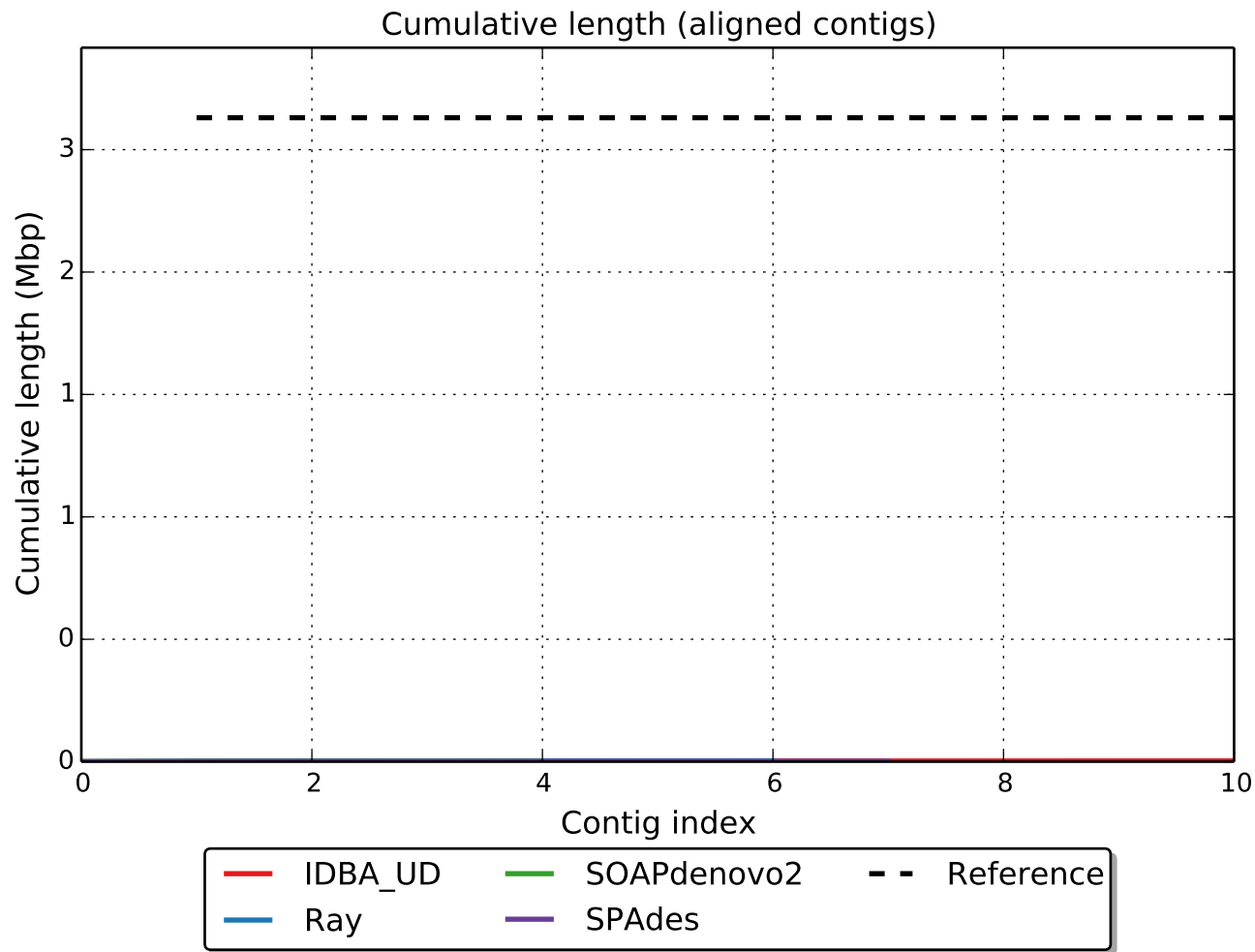


GC content

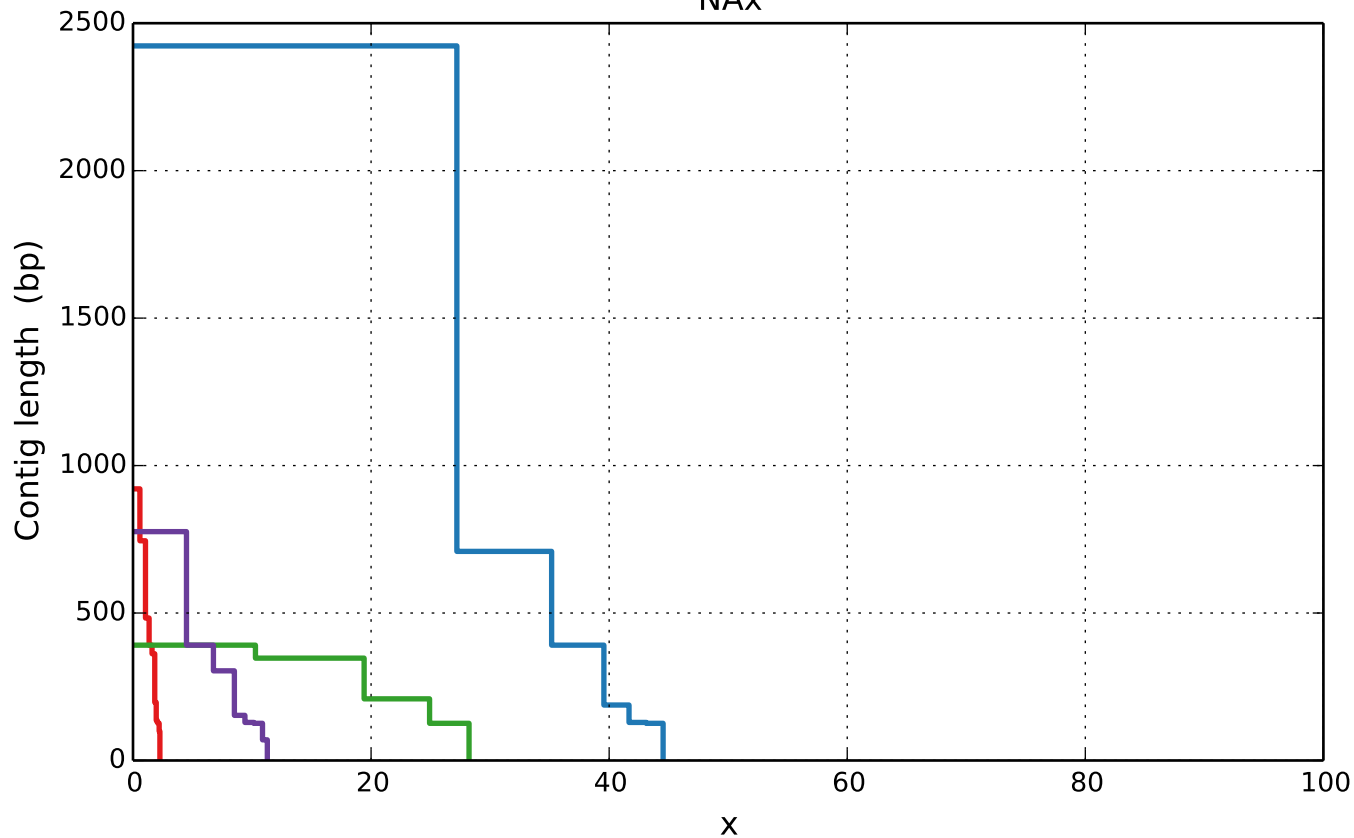








NAx



IDBA\_UD

SOAPdenovo2

SPAdes

Ray

NGAx

