

# Report

	IDBA_UD	Ray	SOAPdenovo2	SPAdes
# contigs (>= 1000 bp)	4	1	1	1
# contigs (>= 5000 bp)	1	1	0	1
# contigs (>= 10000 bp)	1	0	0	0
# contigs (>= 25000 bp)	0	0	0	0
# contigs (>= 50000 bp)	0	0	0	0
Total length (>= 1000 bp)	15829	7690	2354	6159
Total length (>= 5000 bp)	10709	7690	0	6159
Total length (>= 10000 bp)	10709	0	0	0
Total length (>= 25000 bp)	0	0	0	0
Total length (>= 50000 bp)	0	0	0	0
# contigs	4	1	1	1
Largest contig	10709	7690	2354	6159
Total length	15829	7690	2354	6159
Reference length	2671313	2671313	2671313	2671313
GC (%)	40.07	38.08	36.49	35.67
Reference GC (%)	36.82	36.82	36.82	36.82
N50	10709	7690	2354	6159
N75	2719	7690	2354	6159
L50	1	1	1	1
L75	2	1	1	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 + 4 part	0 + 1 part	0 + 1 part	0 + 1 part
Unaligned length	14458	6728	1392	5197
Genome fraction (%)	0.049	0.036	0.036	0.036
Duplication ratio	1.053	1.001	1.001	1.001
# N's per 100 kbp	1345.63	1755.53	0.00	0.00
# mismatches per 100 kbp	2457.76	2601.46	2601.46	2601.46
# indels per 100 kbp	153.61	104.06	104.06	104.06
Largest alignment	962	962	962	962
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

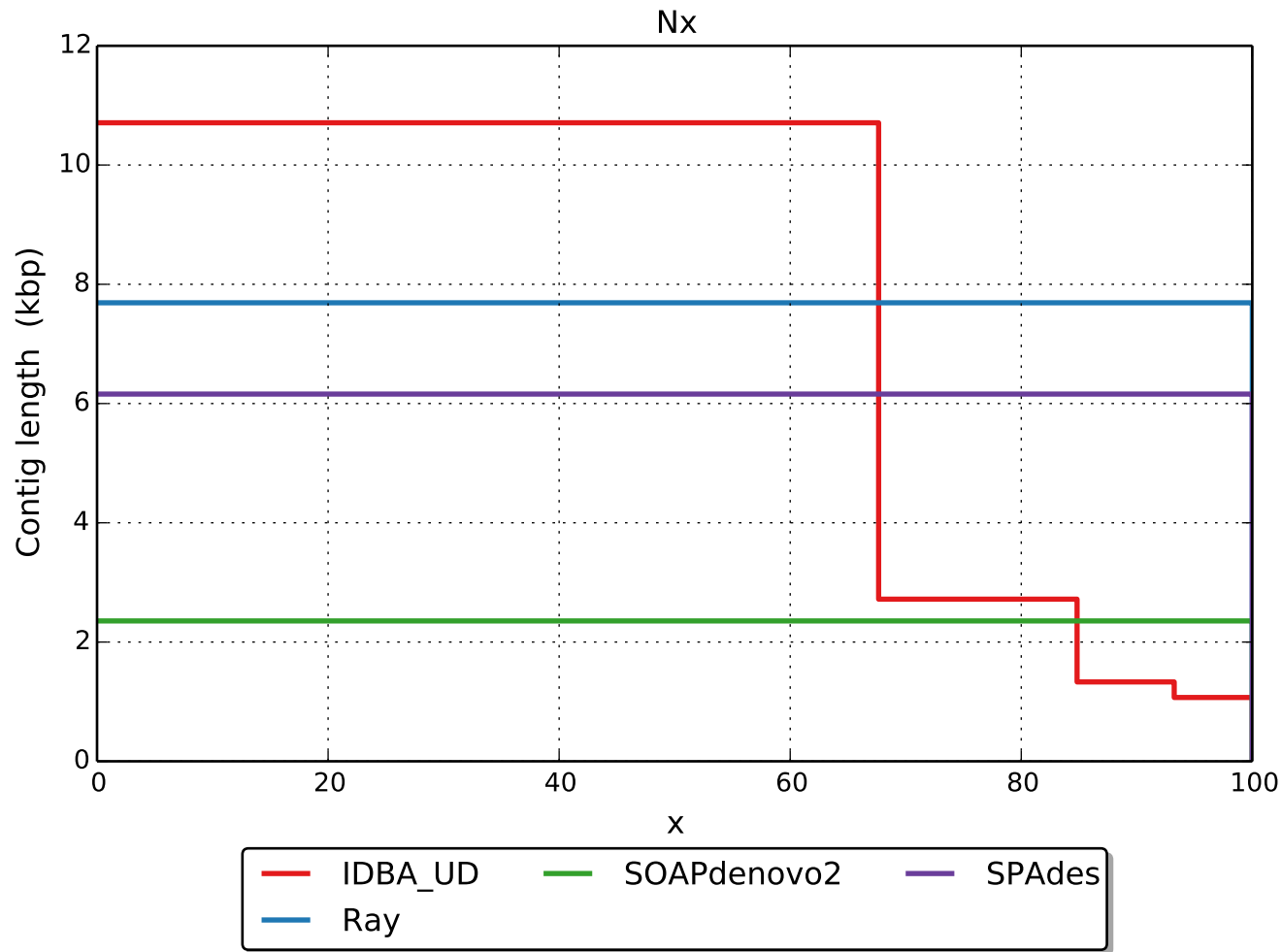
	IDBA_UD	Ray	SOAPdenovo2	SPAdes
# misassemblies	0	0	0	0
# relocations	0	0	0	0
# translocations	0	0	0	0
# inversions	0	0	0	0
# possibly misassembled contigs	1	1	1	1
# misassembled contigs	0	0	0	0
Misassembled contigs length	0	0	0	0
# local misassemblies	0	0	0	0
# structural variations	0	0	0	0
# mismatches	32	25	25	25
# indels	2	1	1	1
# short indels	2	1	1	1
# long indels	0	0	0	0
Indels length	2	1	1	1

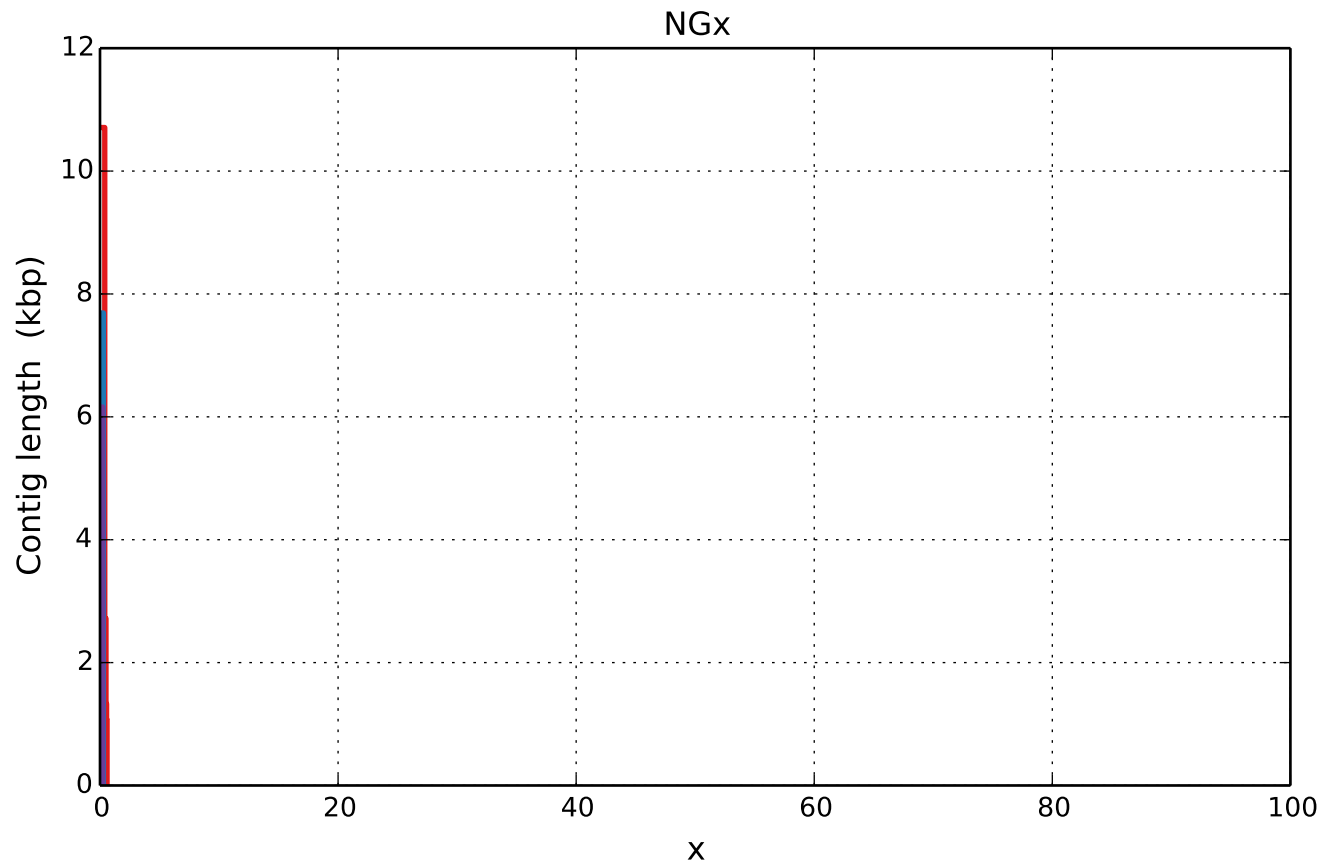
All statistics are based on contigs of size  $\geq 500$  bp, unless otherwise noted (e.g., "# contigs ( $\geq 0$  bp)" and "Total length ( $\geq 0$  bp)" include all contigs).

## Unaligned report

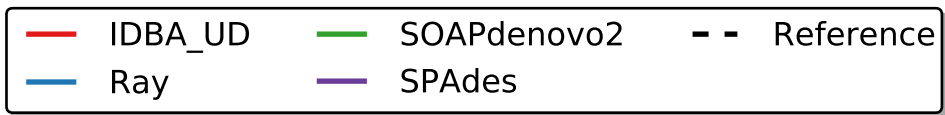
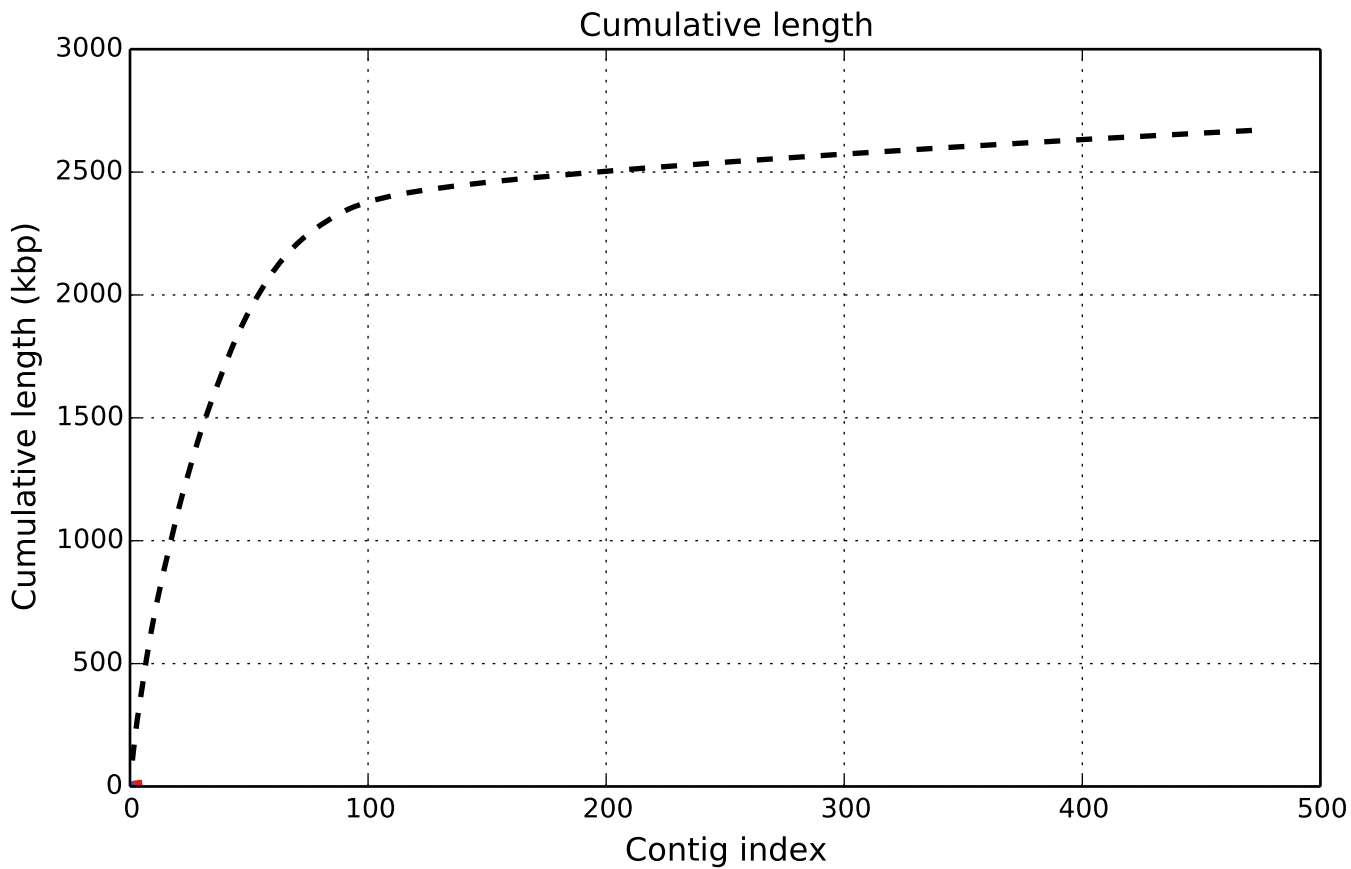
	IDBA_UD	Ray	SOAPdenovo2	SPAdes
# fully unaligned contigs	0	0	0	0
Fully unaligned length	0	0	0	0
# partially unaligned contigs	4	1	1	1
# with misassembly	0	0	0	0
# both parts are significant	1	1	1	1
Partially unaligned length	14458	6728	1392	5197
# N's	213	135	0	0

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).

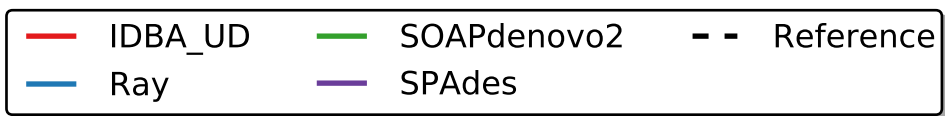
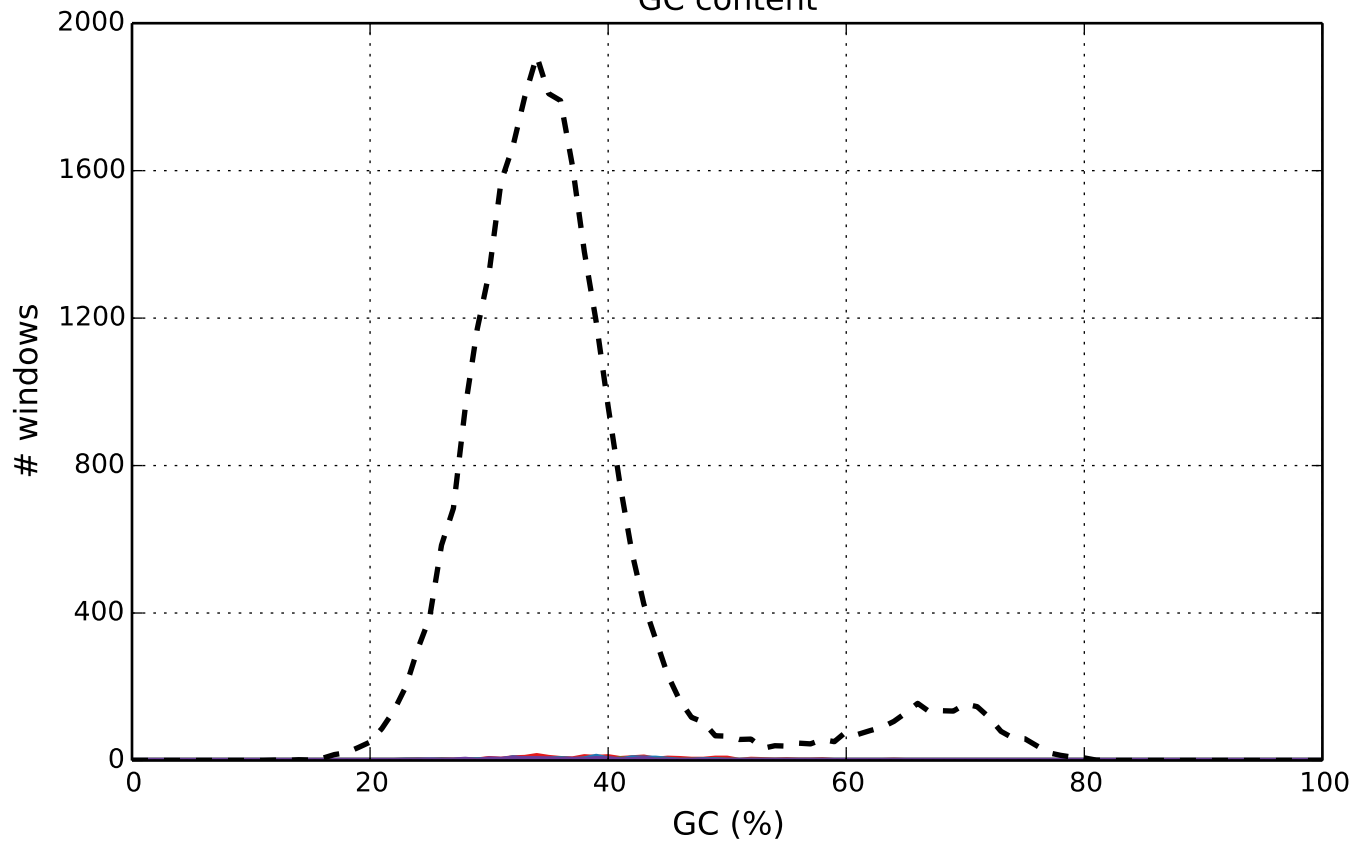


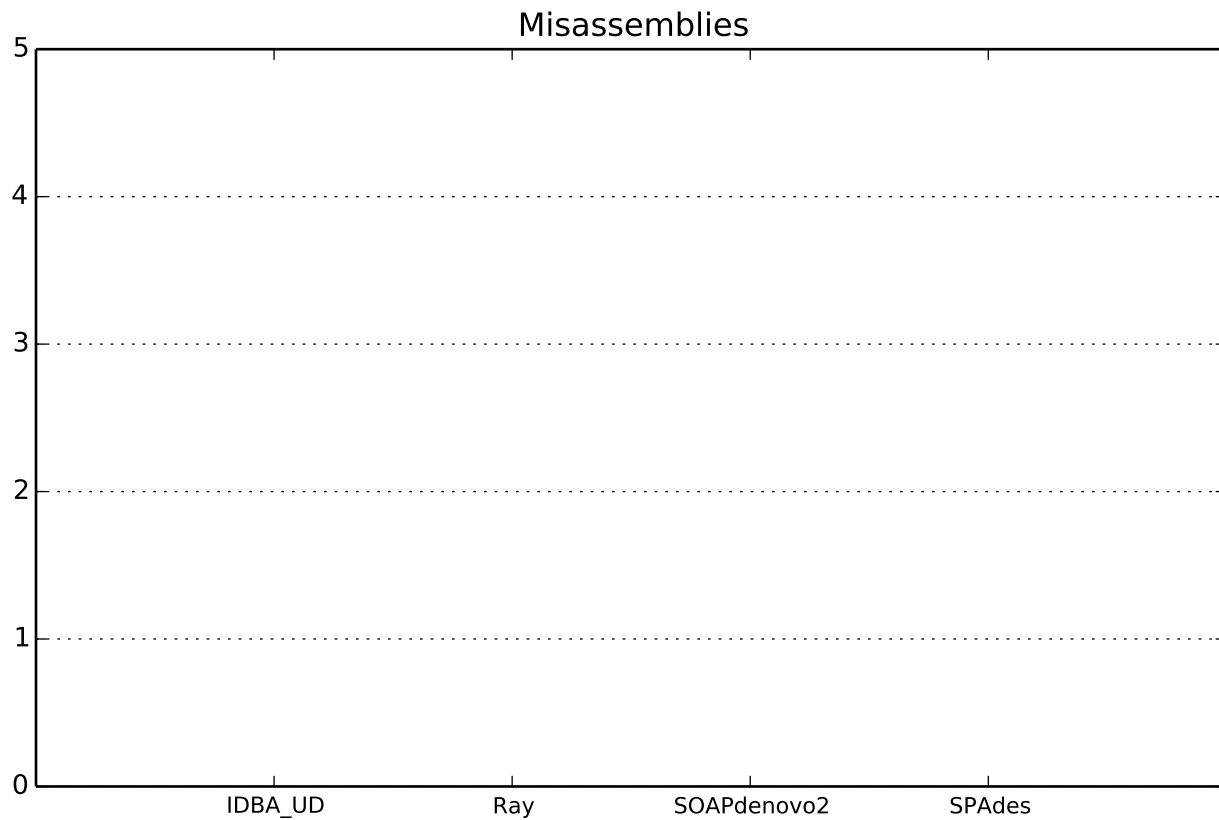


— IDBA\_UD    — SOAPdenovo2    — SPAdes  
— Ray



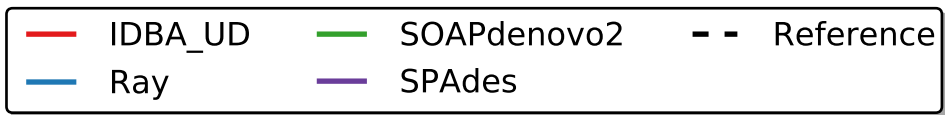
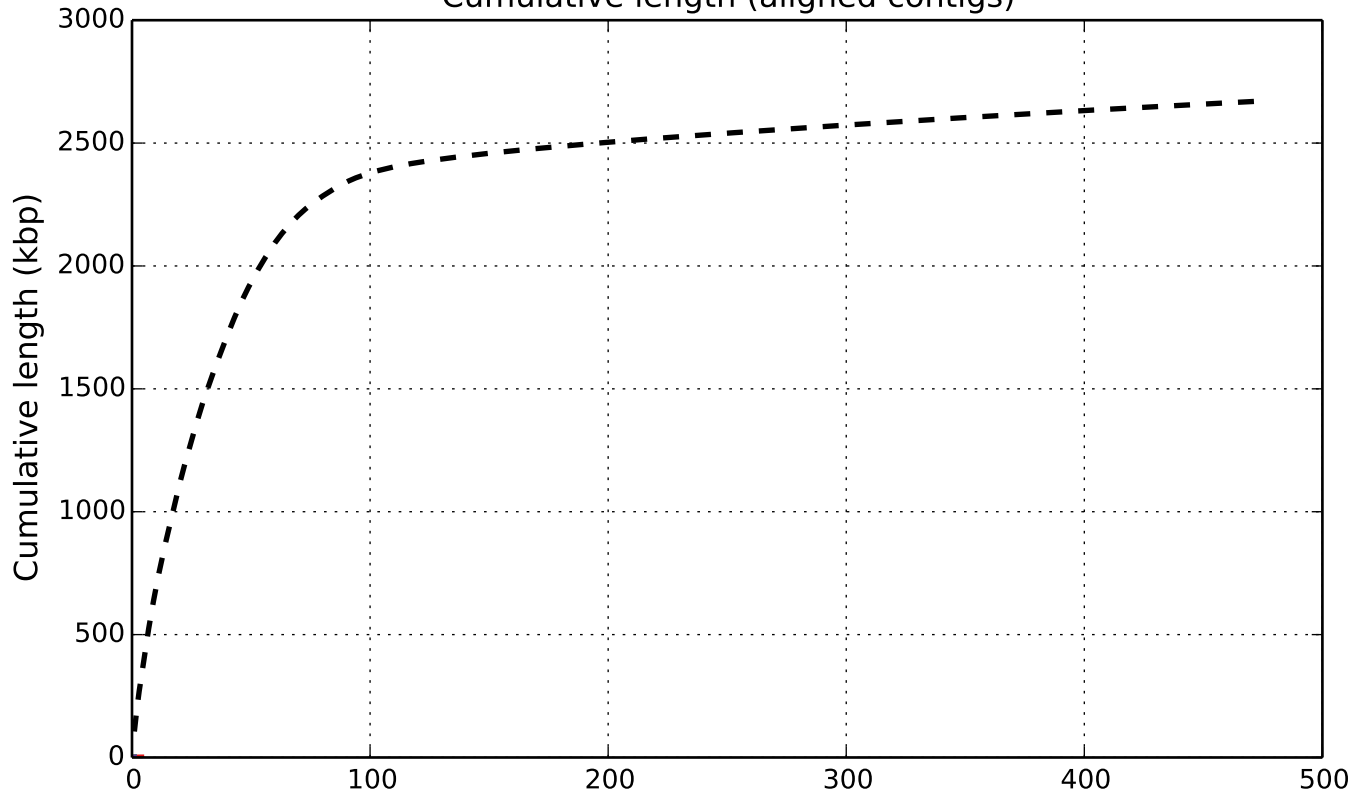
GC content



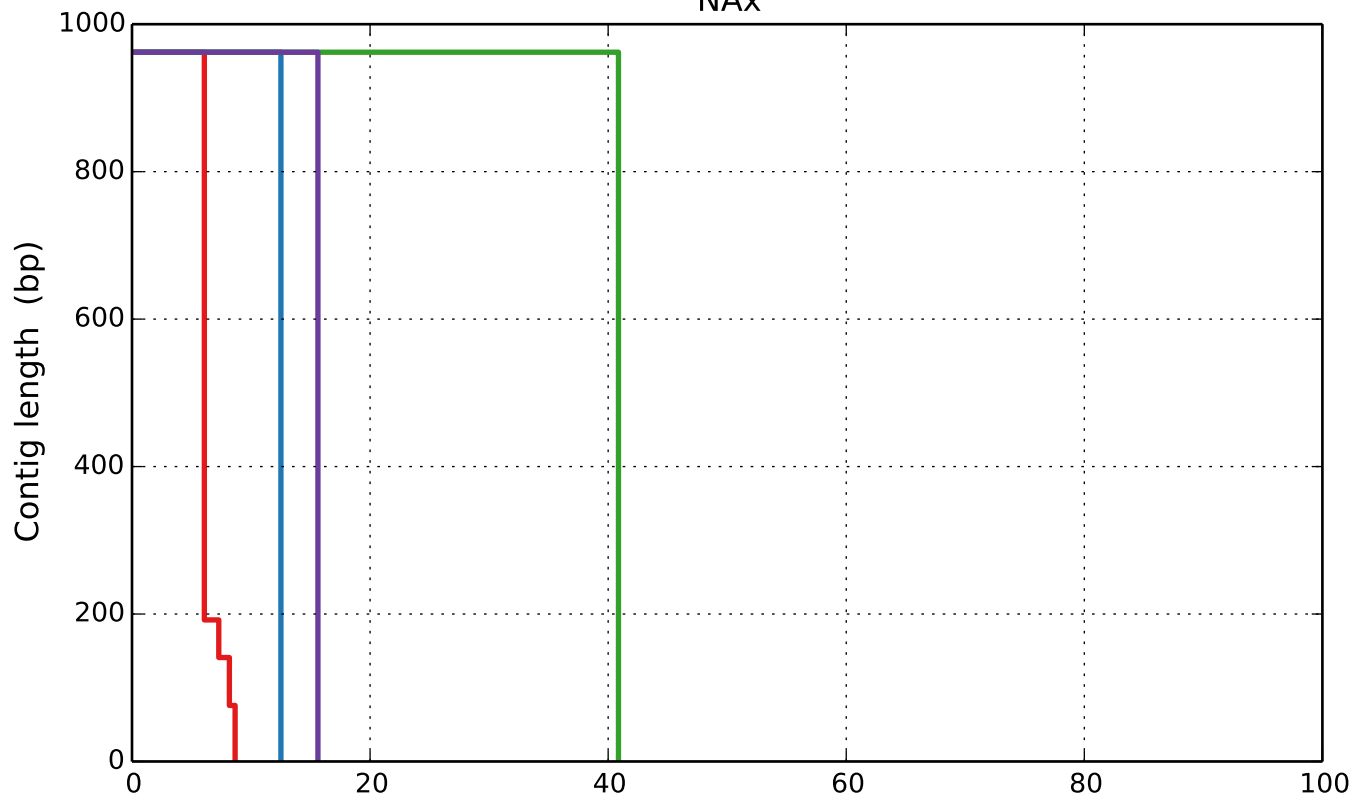




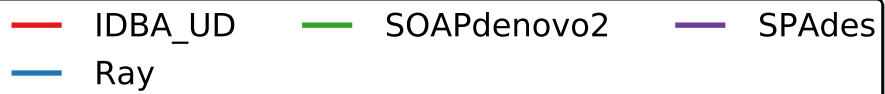
Cumulative length (aligned contigs)



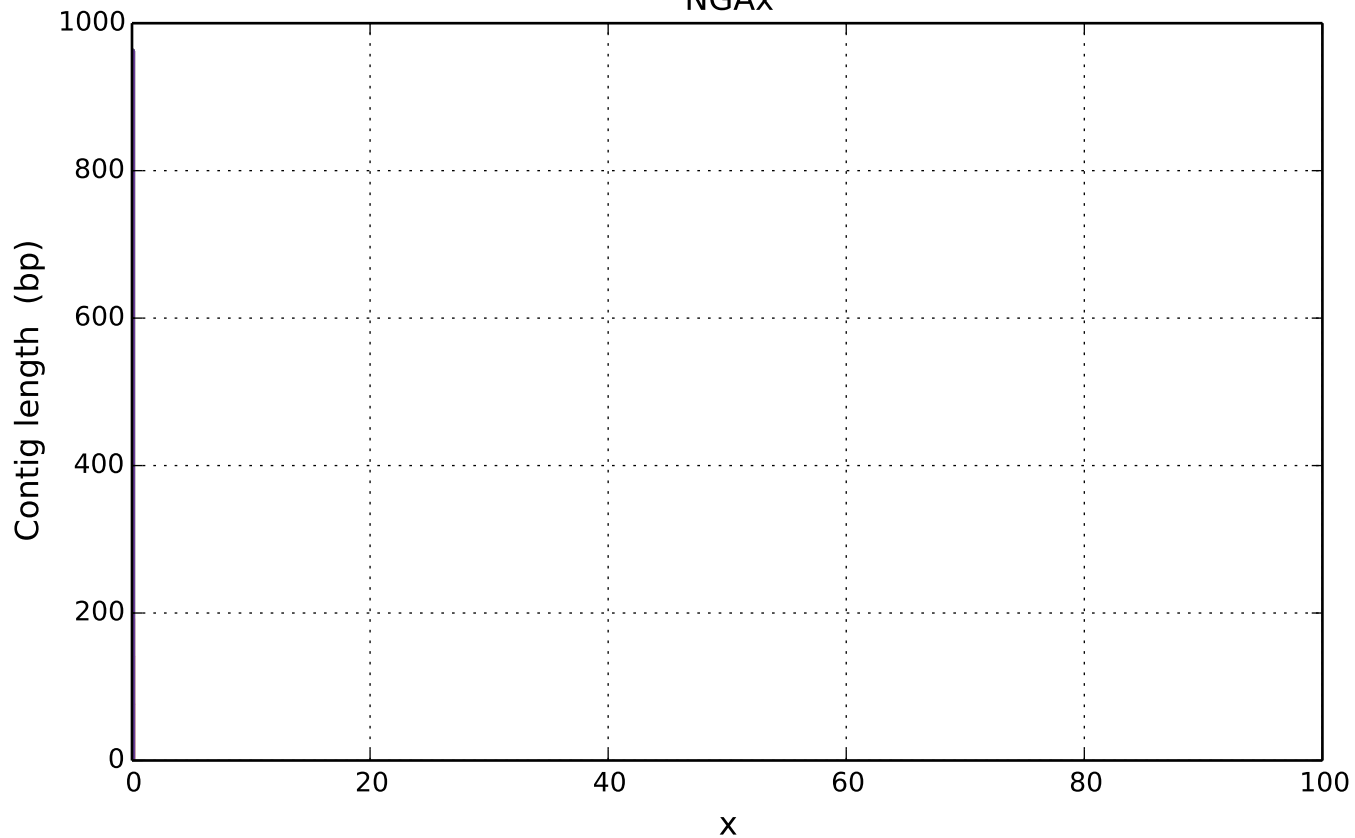
NAx



x



NGAx



— IDBA\_UD

— SOAPdenovo2

— SPAdes

— Ray

