

# Report

	IDBA_UD	Ray	SOAPdenovo2	SPAdes
# contigs (>= 1000 bp)	229	10	3	159
# contigs (>= 5000 bp)	8	9	0	7
# contigs (>= 10000 bp)	4	9	0	6
# contigs (>= 25000 bp)	1	7	0	1
# contigs (>= 50000 bp)	0	4	0	1
Total length (>= 1000 bp)	412043	992370	4925	380195
Total length (>= 5000 bp)	101820	991285	0	172566
Total length (>= 10000 bp)	76327	991285	0	163024
Total length (>= 25000 bp)	27573	950972	0	71020
Total length (>= 50000 bp)	0	854951	0	71020
# contigs	914	24	33	846
Largest contig	27573	431523	2760	71020
Total length	885347	1000362	23719	843673
Reference length	2506025	2506025	2506025	2506025
GC (%)	53.20	59.84	52.17	53.38
Reference GC (%)	53.69	53.69	53.69	53.69
N50	946	198752	677	925
N75	691	144408	570	665
L50	261	2	12	203
L75	538	3	22	477
# misassemblies	9	0	0	3
# misassembled contigs	9	0	0	3
Misassembled contigs length	11754	0	0	3809
# local misassemblies	6	0	0	4
# structural variations	1	0	0	2
# unaligned contigs	0 + 155 part	0 + 13 part	0 + 11 part	0 + 128 part
Unaligned length	153886	992368	7837	211195
Genome fraction (%)	28.998	0.306	0.628	25.166
Duplication ratio	1.007	1.041	1.010	1.003
# N's per 100 kbp	0.00	301.59	3271.64	21.81
# mismatches per 100 kbp	2419.71	1888.02	1691.36	2394.00
# indels per 100 kbp	67.84	104.17	89.02	68.66
Largest alignment	3547	638	875	2501
NA50	737	-	526	655
NGA50	-	-	-	-
NA75	534	-	-	-
LA50	417	-	19	450
LA75	769	-	-	-

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	9	0	0	3
# relocations	8	0	0	3
# translocations	0	0	0	0
# inversions	1	0	0	0
# possibly misassembled contigs	14	0	0	12
# misassembled contigs	9	0	0	3
Misassembled contigs length	11754	0	0	3809
# local misassemblies	6	0	0	4
# structural variations	1	0	0	2
# mismatches	17584	145	266	15098
# indels	493	8	14	433
# short indels	471	8	10	413
# long indels	22	0	4	20
Indels length	826	9	131	723

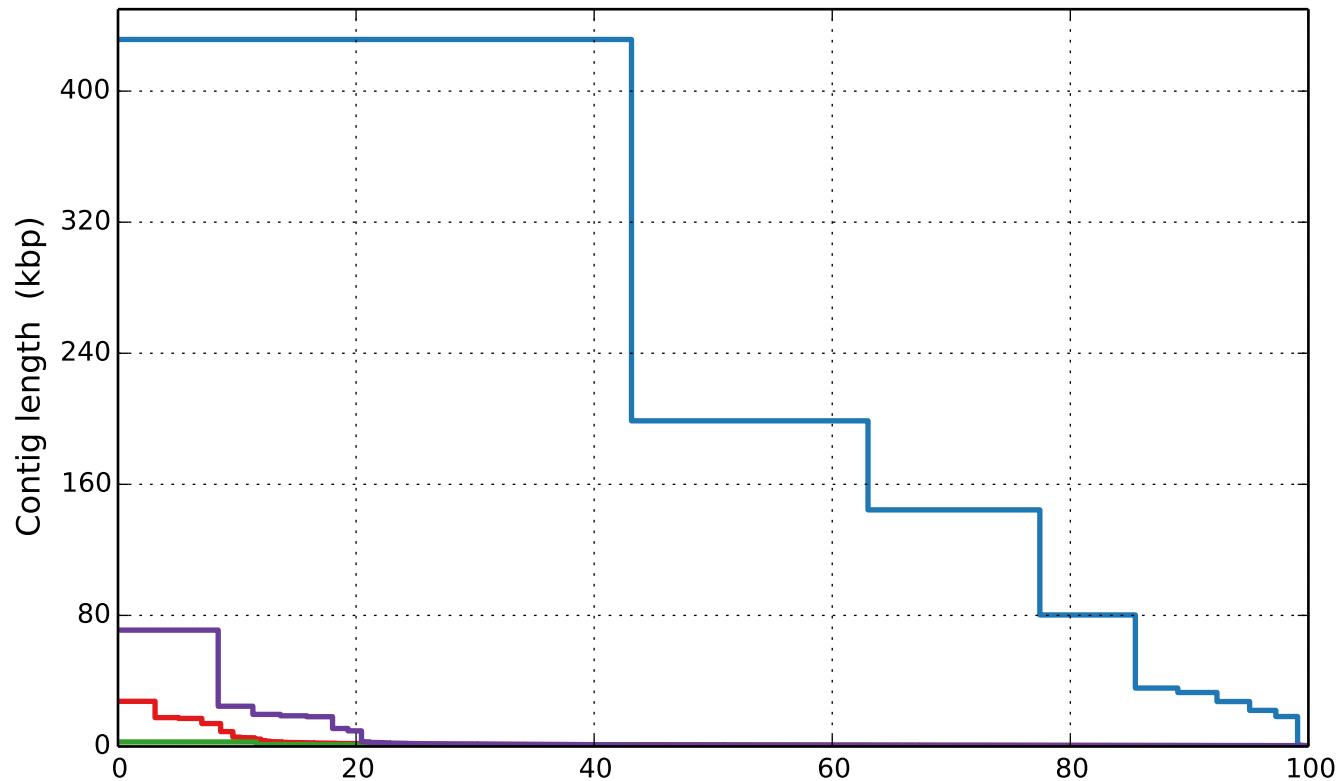
All statistics are based on contigs of size  $\geq 500$  bp, unless otherwise noted (e.g., "# contigs ( $\geq 0$  bp)" and "Total length ( $\geq 0$  bp)" include all contigs).

## Unaligned report

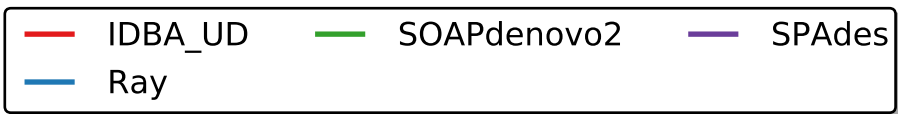
	IDBA_UD	Ray	SOAPdenovo2	SPAdes
# fully unaligned contigs	0	0	0	0
Fully unaligned length	0	0	0	0
# partially unaligned contigs	155	13	11	128
# with misassembly	1	6	0	2
# both parts are significant	12	0	0	12
Partially unaligned length	153886	992368	7837	211195
# N's	0	3017	776	184

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).

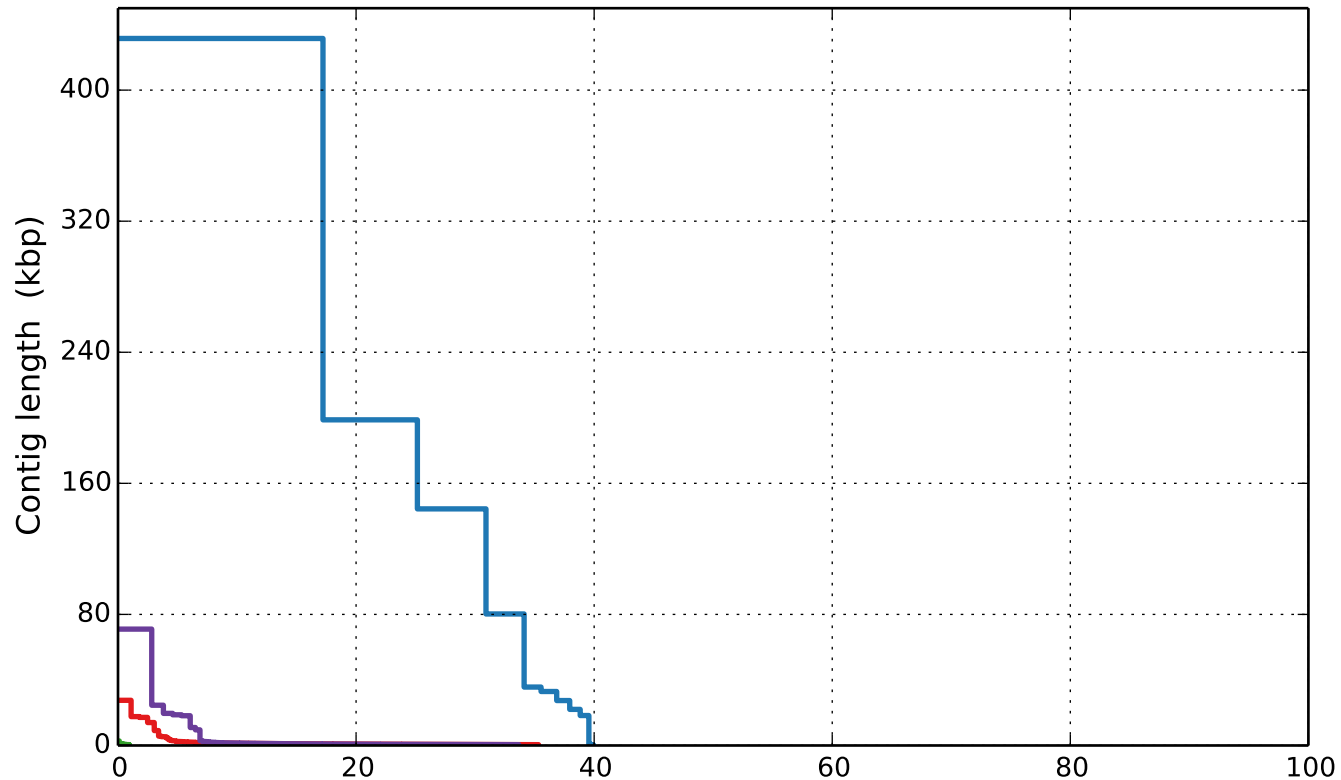
Nx



x



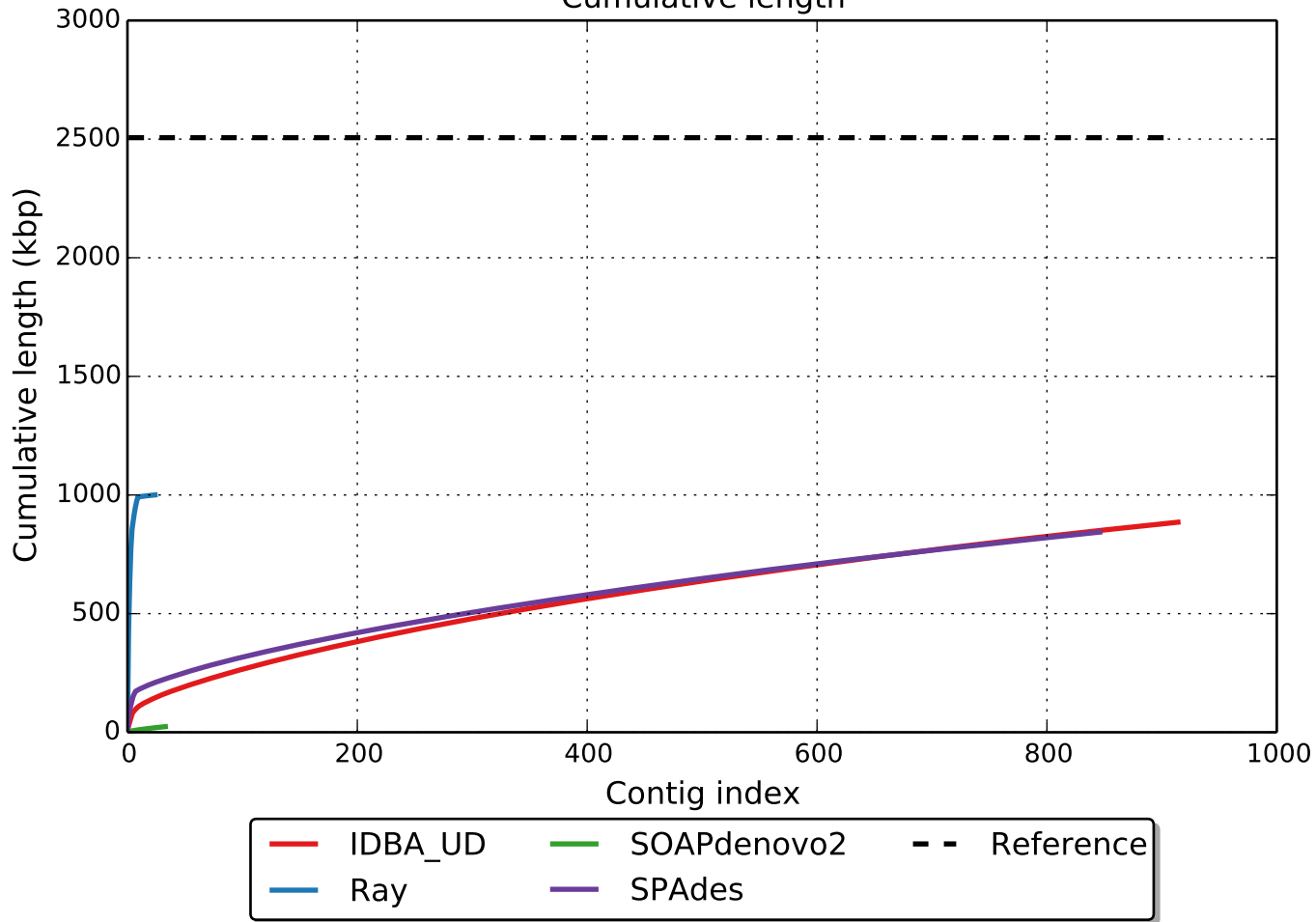
NGx



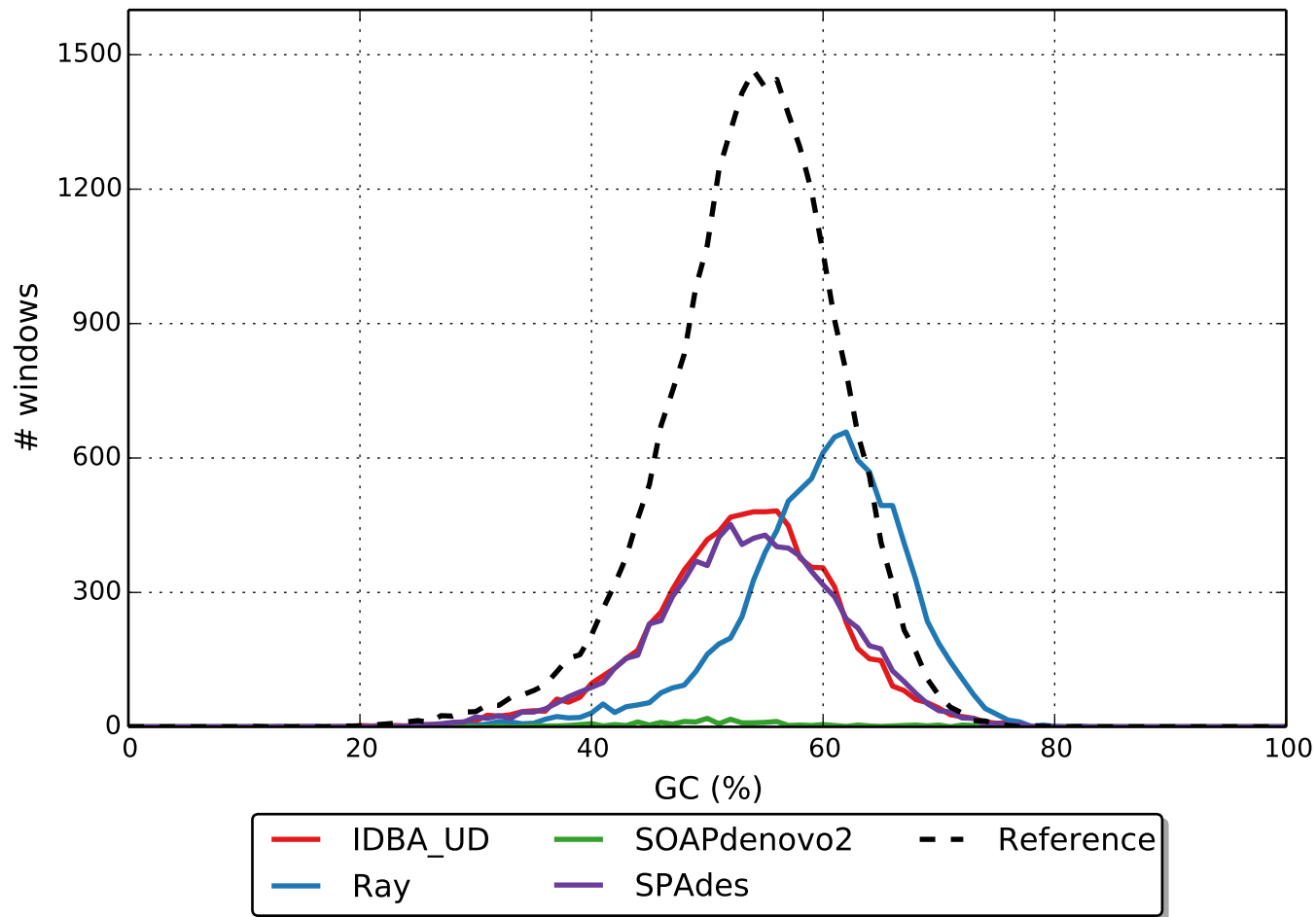
x

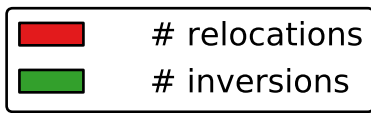
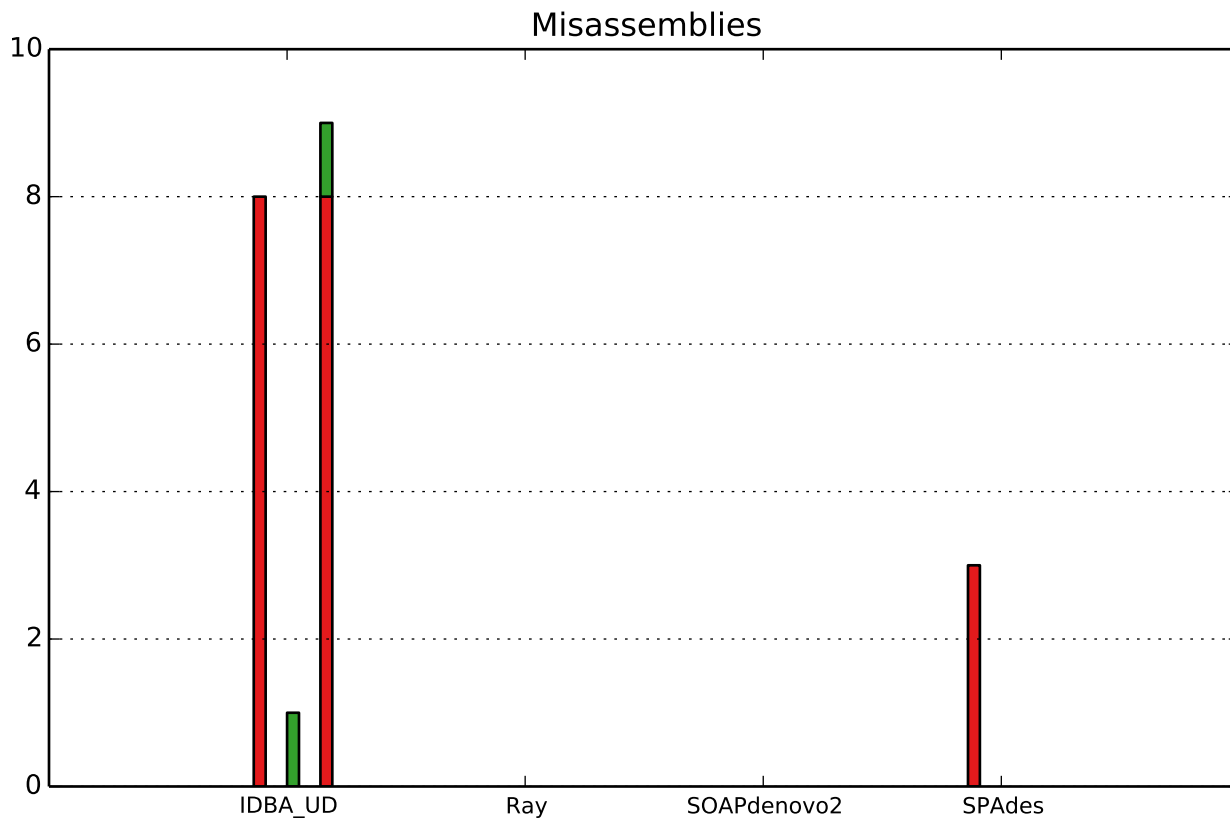


Cumulative length



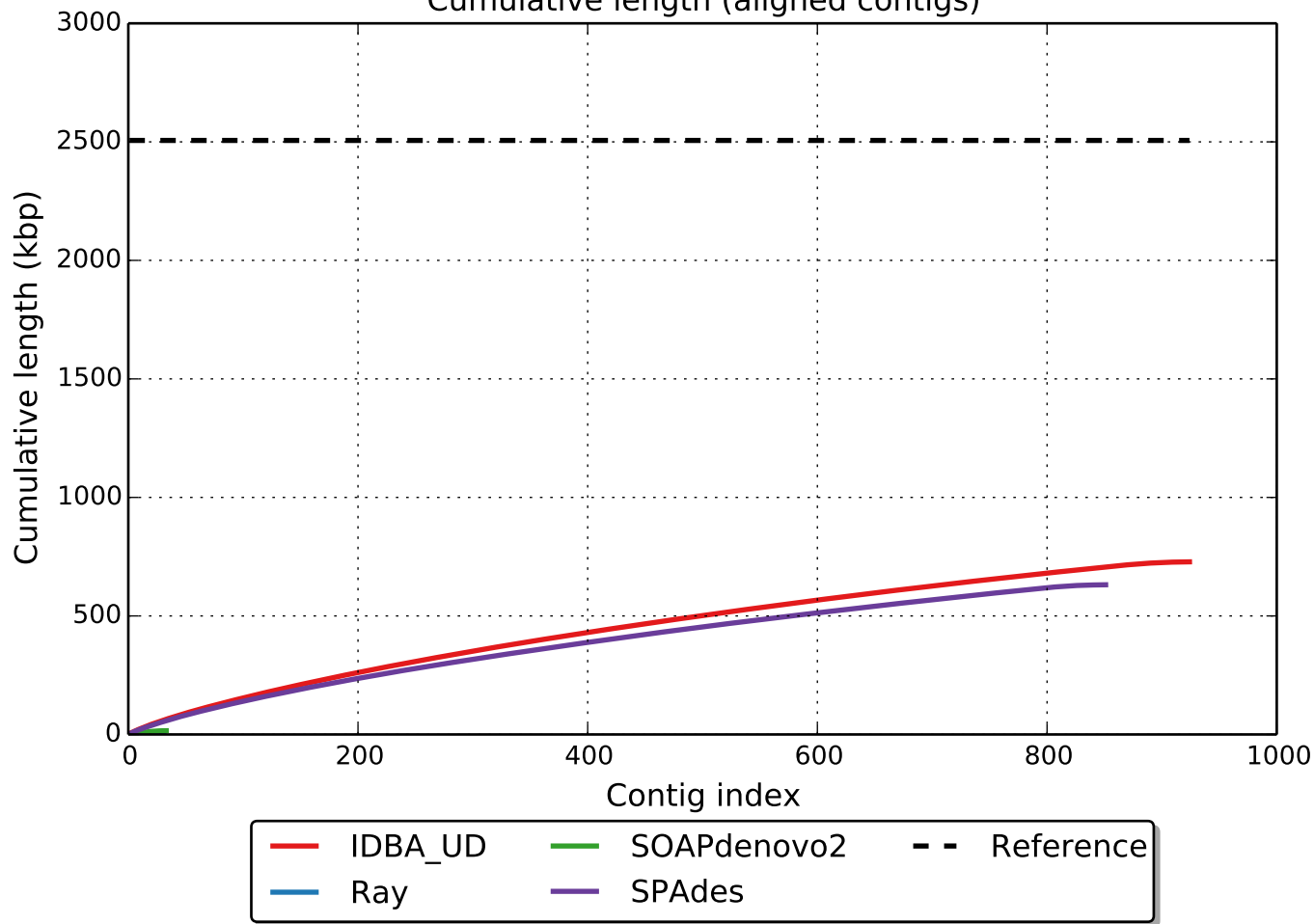
GC content



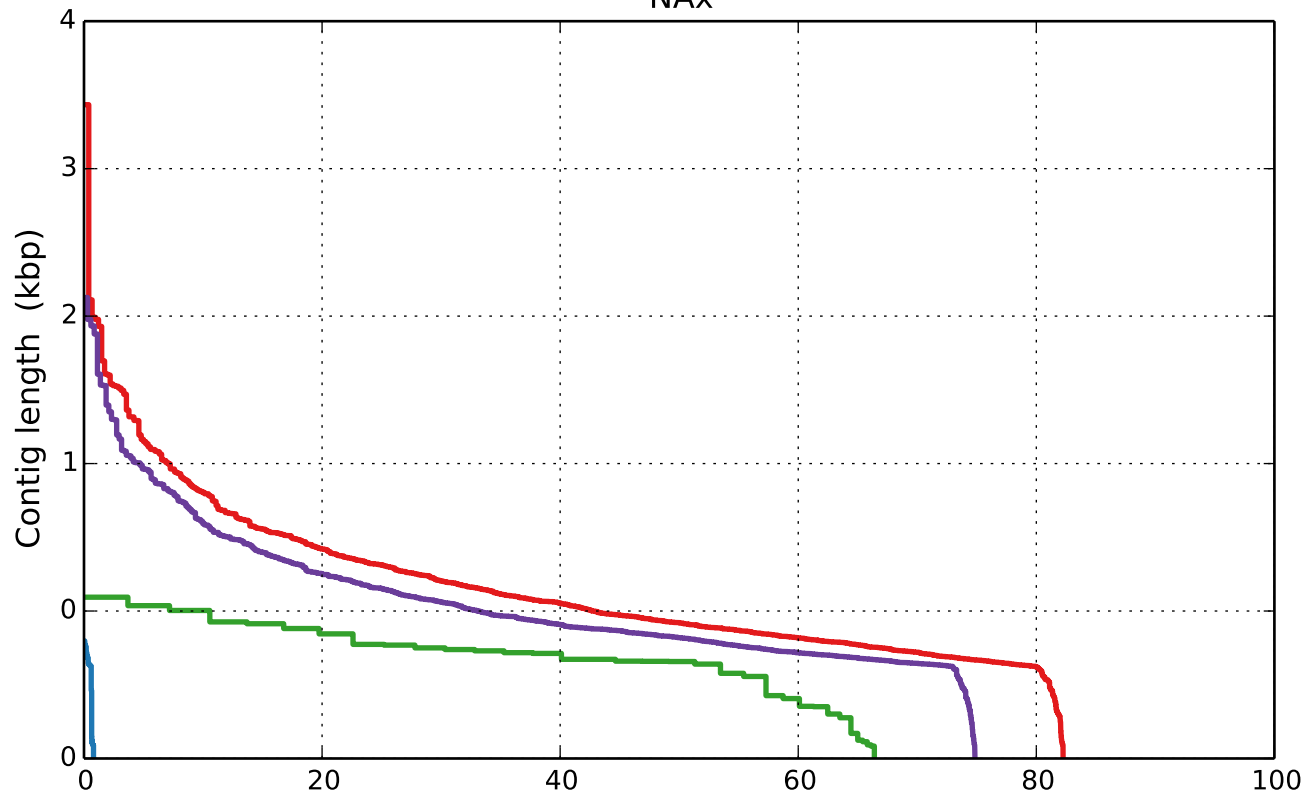




Cumulative length (aligned contigs)



NAx



NGAx

