

Report

	IDBA_UD	Ray	SOAPdenovo2	SPAdes
# contigs (>= 1000 bp)	34	15	3	90
# contigs (>= 5000 bp)	3	5	1	11
# contigs (>= 10000 bp)	2	2	0	5
# contigs (>= 25000 bp)	1	0	0	3
# contigs (>= 50000 bp)	0	0	0	0
Total length (>= 1000 bp)	106095	95971	7635	285471
Total length (>= 5000 bp)	53434	69545	5521	162459
Total length (>= 10000 bp)	44461	48023	0	119313
Total length (>= 25000 bp)	32007	0	0	87910
Total length (>= 50000 bp)	0	0	0	0
# contigs	233	16	23	438
Largest contig	32007	24860	5521	34694
Total length	235720	96930	19939	510102
Reference length	5205140	5205140	5205140	5205140
GC (%)	43.19	41.21	41.32	43.27
Reference GC (%)	43.19	43.19	43.19	43.19
N50	892	8454	887	1191
N75	636	4731	573	656
L50	47	3	6	62
L75	129	6	14	216
# misassemblies	0	0	0	0
# misassembled contigs	0	0	0	0
Misassembled contigs length	0	0	0	0
# local misassemblies	1	0	24	4
# structural variations	0	0	0	0
# unaligned contigs	0 + 53 part	0 + 15 part	0 + 8 part	0 + 105 part
Unaligned length	96852	91219	8951	233953
Genome fraction (%)	2.661	0.044	0.182	5.002
Duplication ratio	1.002	2.496	1.160	1.061
# N's per 100 kbp	217.63	1641.39	10547.17	3504.79
# mismatches per 100 kbp	983.95	2840.91	2290.24	996.65
# indels per 100 kbp	19.49	131.12	31.66	96.40
Largest alignment	1165	959	887	2458
NA50	527	-	-	270
NGA50	-	-	-	-
LA50	172	-	-	392

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

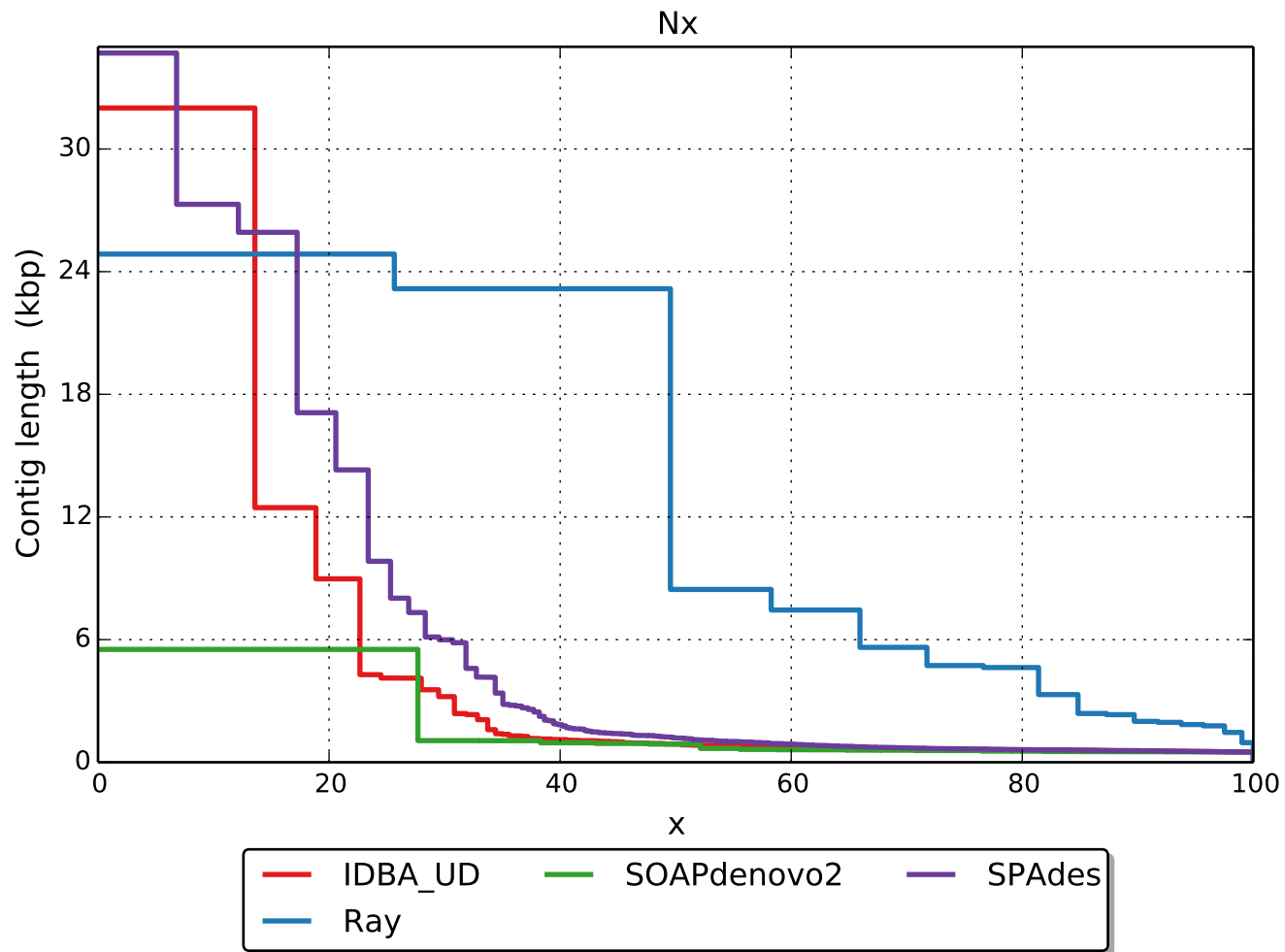
	IDBA_UD	Ray	SOAPdenovo2	SPAdes
# misassemblies	0	0	0	0
# relocations	0	0	0	0
# translocations	0	0	0	0
# inversions	0	0	0	0
# possibly misassembled contigs	3	0	1	14
# misassembled contigs	0	0	0	0
Misassembled contigs length	0	0	0	0
# local misassemblies	1	0	24	4
# structural variations	0	0	0	0
# mismatches	1363	65	217	2595
# indels	27	3	3	251
# short indels	23	3	3	165
# long indels	4	0	0	86
Indels length	107	3	5	1354

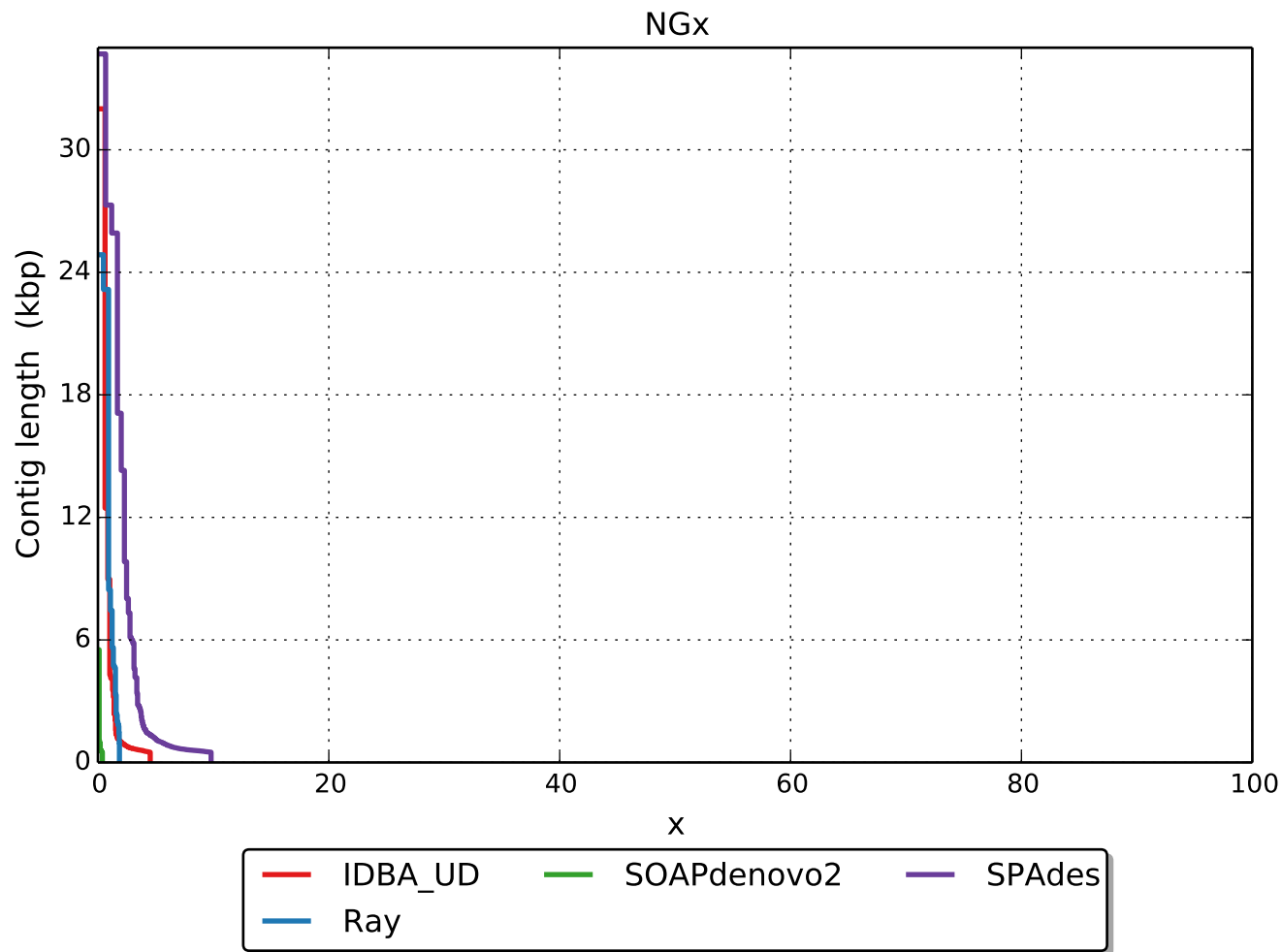
All statistics are based on contigs of size ≥ 500 bp, unless otherwise noted (e.g., "# contigs (≥ 0 bp)" and "Total length (≥ 0 bp)" include all contigs).

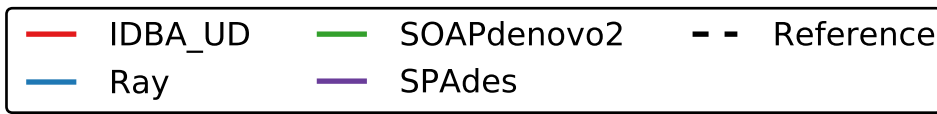
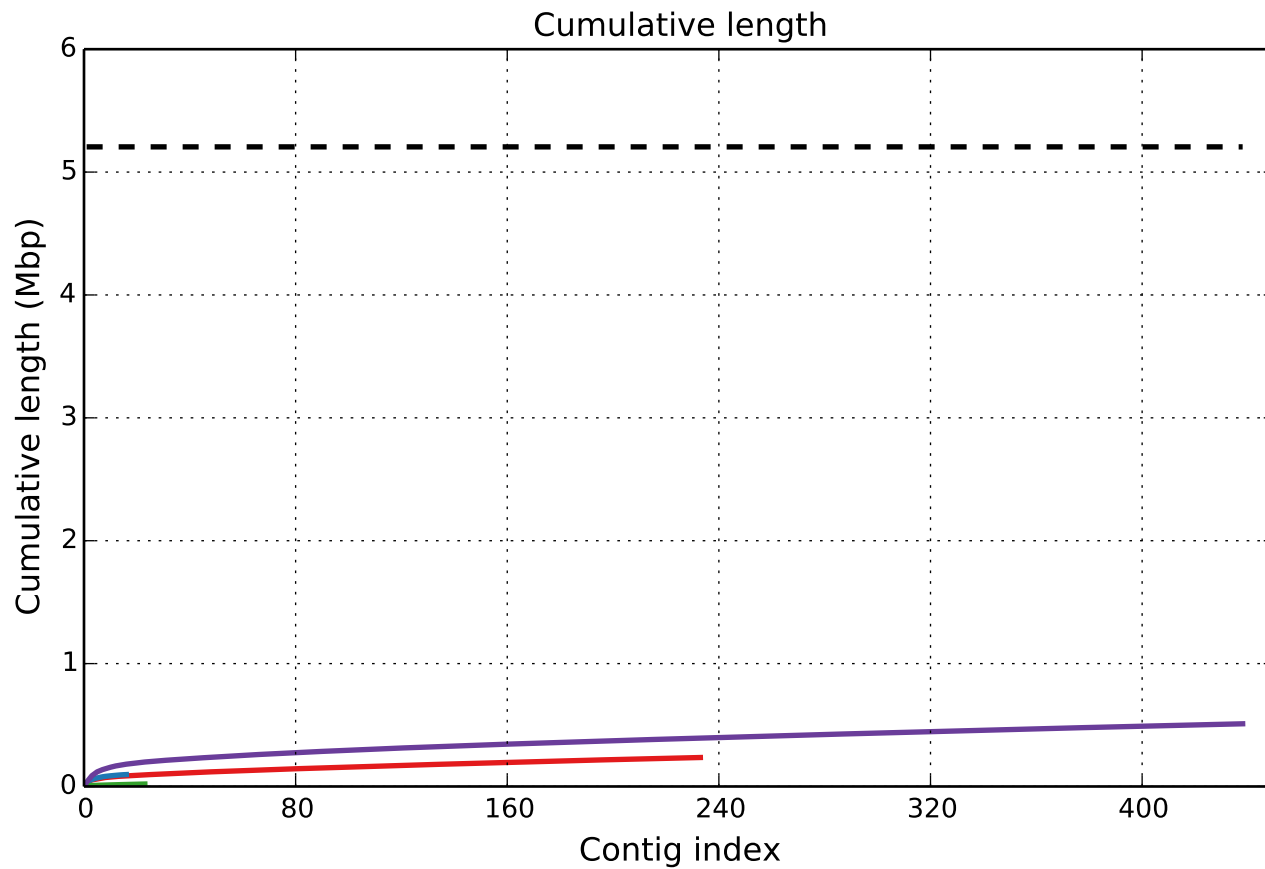
Unaligned report

	IDBA_UD	Ray	SOAPdenovo2	SPAdes
# fully unaligned contigs	0	0	0	0
Fully unaligned length	0	0	0	0
# partially unaligned contigs	53	15	8	105
# with misassembly	1	1	2	5
# both parts are significant	3	0	1	13
Partially unaligned length	96852	91219	8951	233953
# N's	513	1591	2103	17878

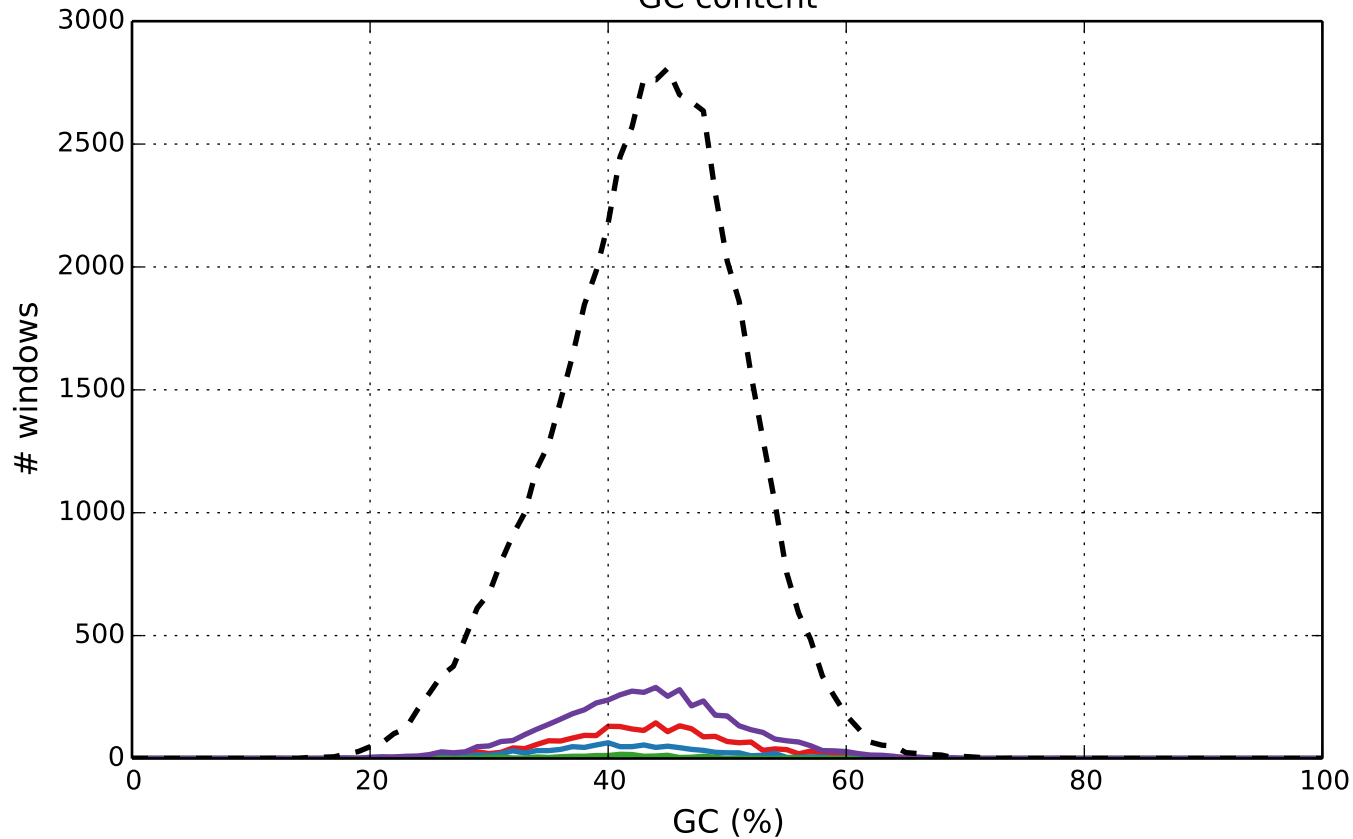
All statistics are based on contigs of size ≥ 500 bp, unless otherwise noted (e.g., "# contigs (≥ 0 bp)" and "Total length (≥ 0 bp)" include all contigs).



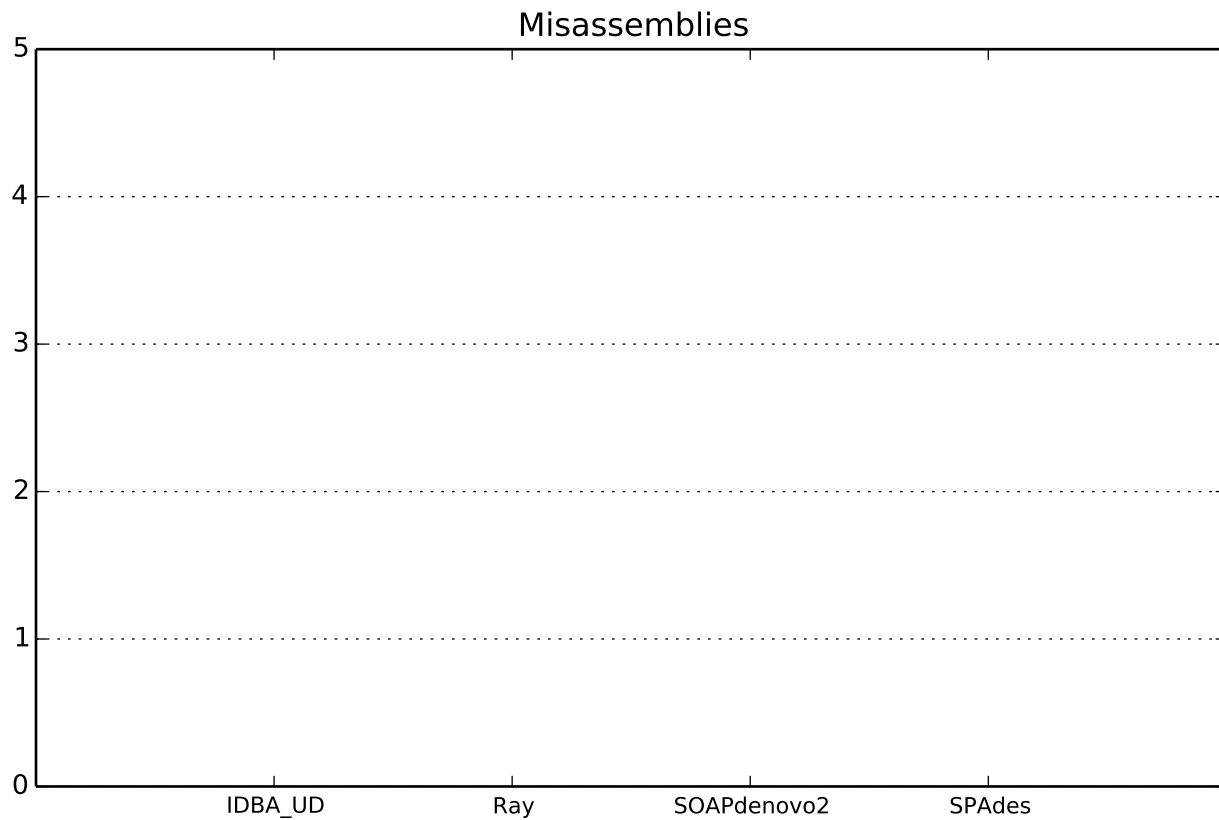


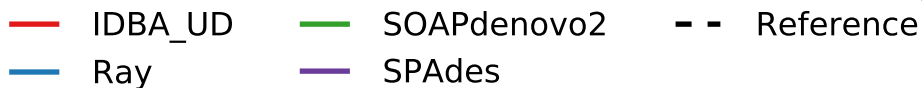
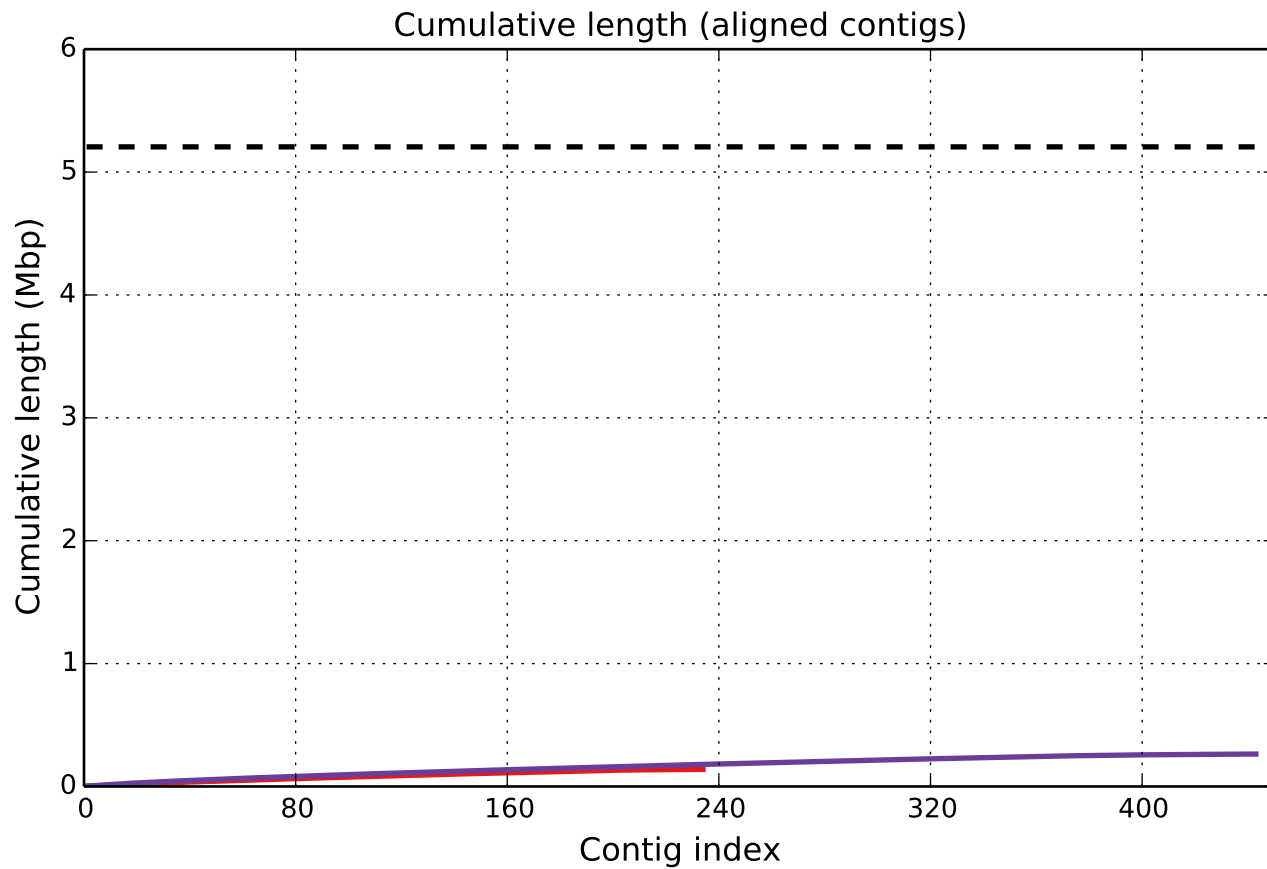


GC content

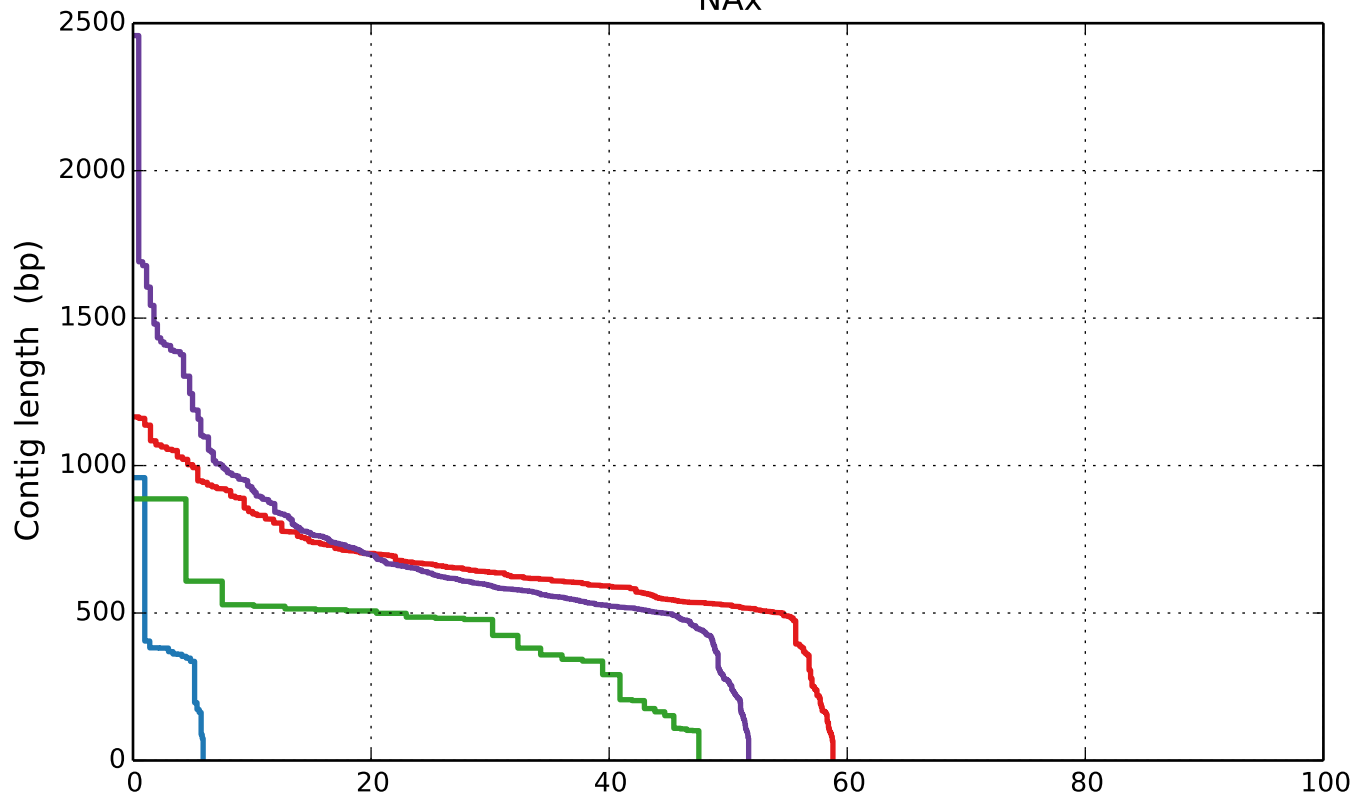


— IDBA_UD — SOAPdenovo2 - - Reference
— Ray — SPAdes





NAx



NGAx

