

Report

	IDBA_UD	Ray	SOAPdenovo2	SPAdes
# contigs (>= 1000 bp)	67	32	37	60
# contigs (>= 5000 bp)	26	6	2	26
# contigs (>= 10000 bp)	14	3	0	16
# contigs (>= 25000 bp)	10	0	0	7
# contigs (>= 50000 bp)	4	0	0	5
Total length (>= 1000 bp)	872901	114746	79247	808908
Total length (>= 5000 bp)	780615	57193	14858	731474
Total length (>= 10000 bp)	689506	37891	0	654408
Total length (>= 25000 bp)	639378	0	0	481642
Total length (>= 50000 bp)	455274	0	0	411523
# contigs	86	43	74	75
Largest contig	180109	15783	8490	131559
Total length	886224	123028	104536	819235
Reference length	2496039	2496039	2496039	2496039
GC (%)	40.56	41.48	40.67	39.59
Reference GC (%)	37.75	37.75	37.75	37.75
N50	80507	4601	1749	58346
N75	12880	2299	1020	18130
L50	4	7	17	5
L75	12	17	37	14
# misassemblies	5	1	0	3
# misassembled contigs	4	1	0	3
Misassembled contigs length	28837	15783	0	20689
# local misassemblies	4	7	39	2
# structural variations	0	0	2	0
# unaligned contigs	0 + 55 part	0 + 19 part	0 + 25 part	0 + 44 part
Unaligned length	751404	45931	22394	693271
Genome fraction (%)	4.825	2.673	3.133	4.531
Duplication ratio	1.119	1.156	1.051	1.114
# N's per 100 kbp	56.53	1361.48	2159.06	206.53
# mismatches per 100 kbp	1603.31	1695.12	1726.54	1824.05
# indels per 100 kbp	55.63	22.48	23.02	56.59
Largest alignment	7714	7714	7714	7714
NA50	-	807	1049	-
NGA50	-	-	-	-
LA50	-	27	28	-

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

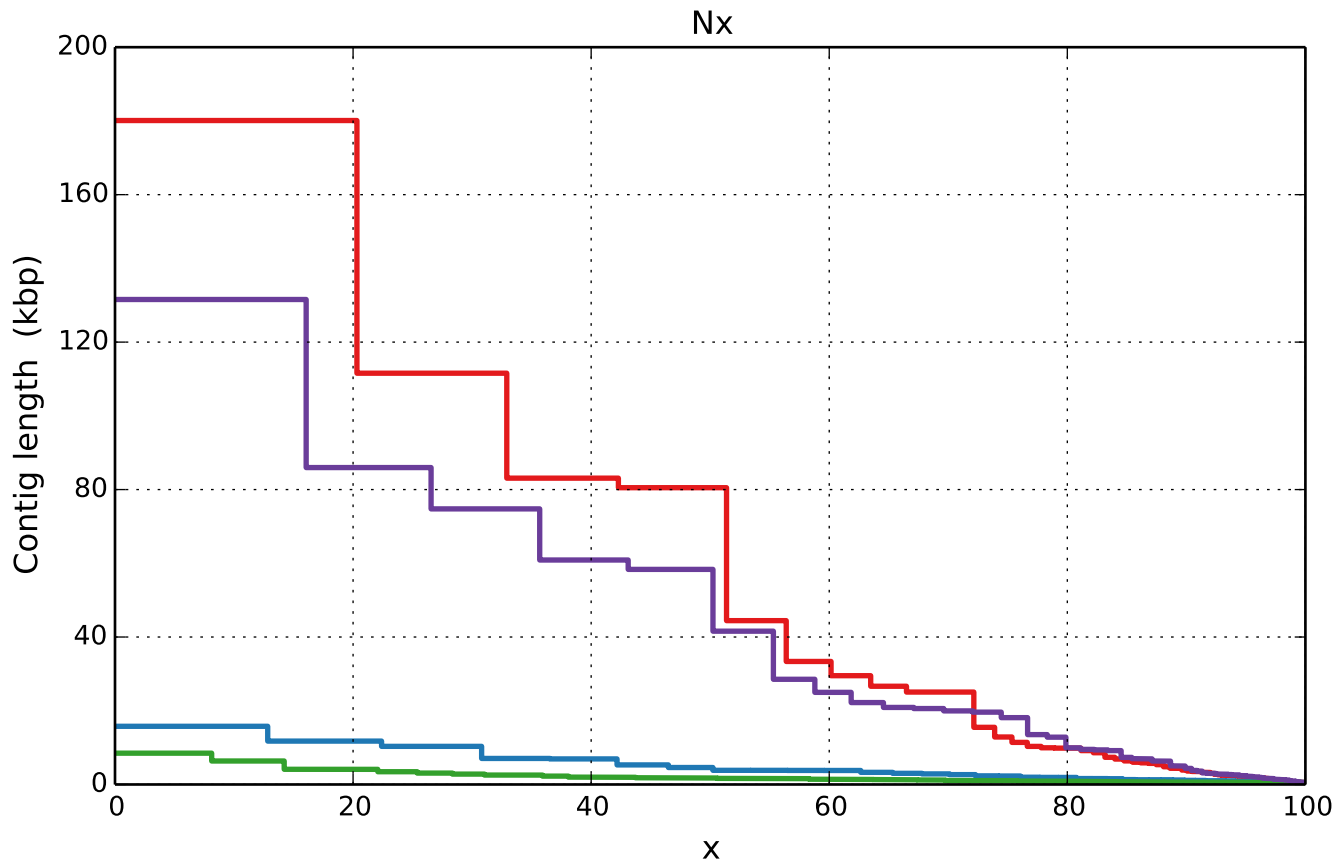
	IDBA_UD	Ray	SOAPdenovo2	SPAdes
# misassemblies	5	1	0	3
# relocations	4	1	0	2
# translocations	1	0	0	1
# inversions	0	0	0	0
# possibly misassembled contigs	19	10	8	24
# misassembled contigs	4	1	0	3
Misassembled contigs length	28837	15783	0	20689
# local misassemblies	4	7	39	2
# structural variations	0	0	2	0
# mismatches	1931	1131	1350	2063
# indels	67	15	18	64
# short indels	62	15	18	57
# long indels	5	0	0	7
Indels length	176	16	21	236

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).

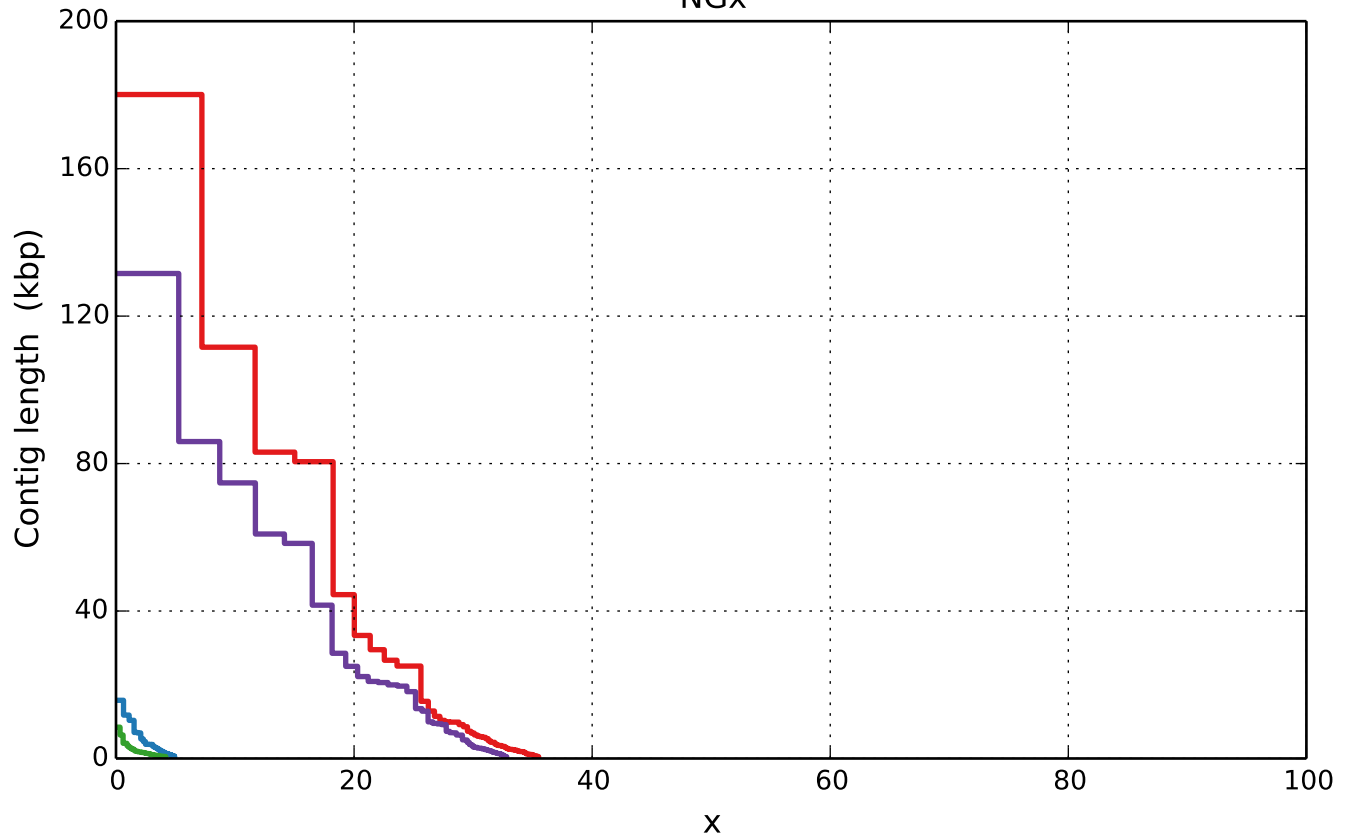
Unaligned report

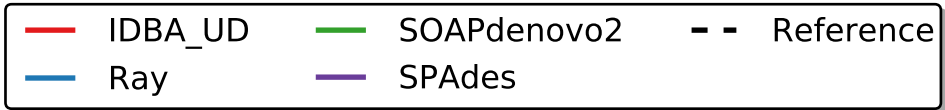
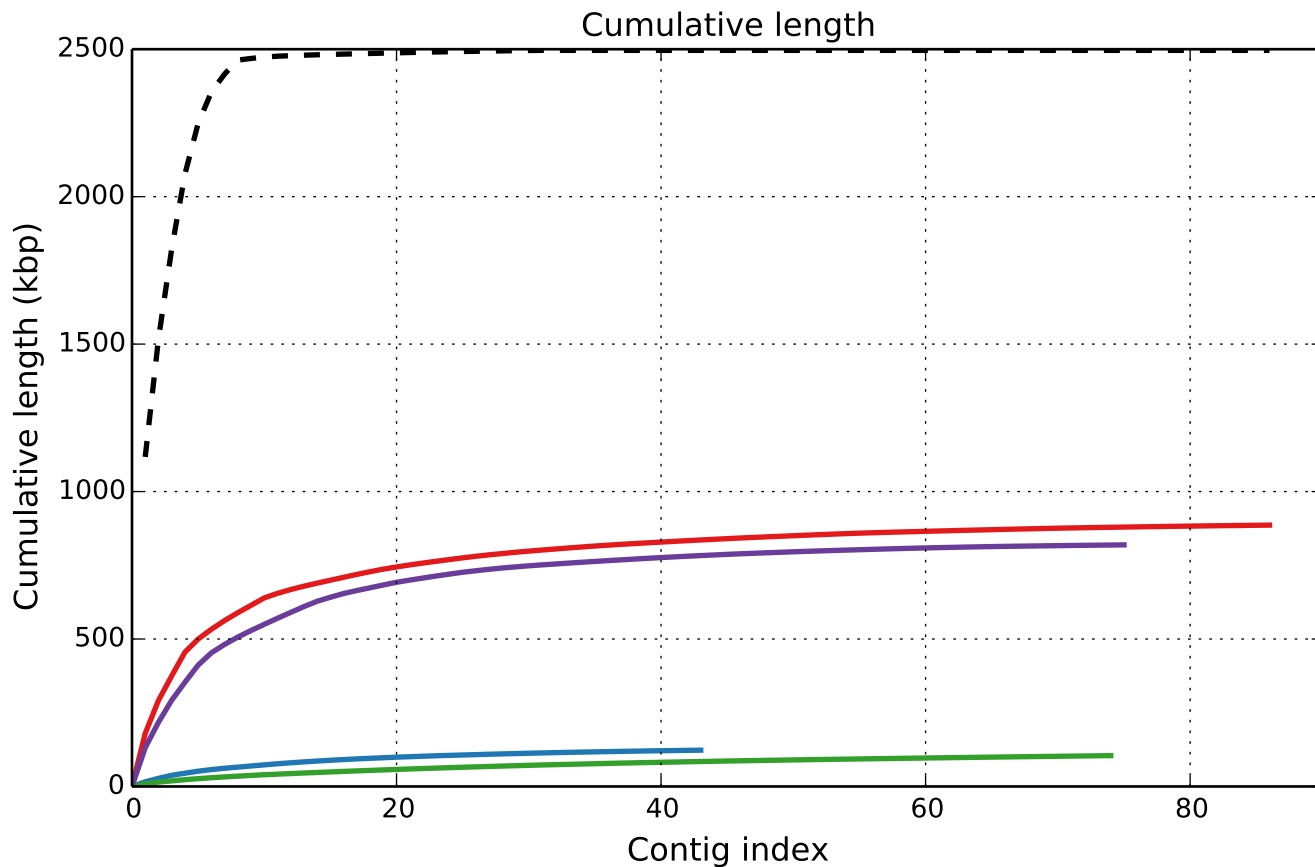
	IDBA_UD	Ray	SOAPdenovo2	SPAdes
# fully unaligned contigs	0	0	0	0
Fully unaligned length	0	0	0	0
# partially unaligned contigs	55	19	25	44
# with misassembly	2	2	5	4
# both parts are significant	16	8	8	20
Partially unaligned length	751404	45931	22394	693271
# N's	501	1675	2257	1692

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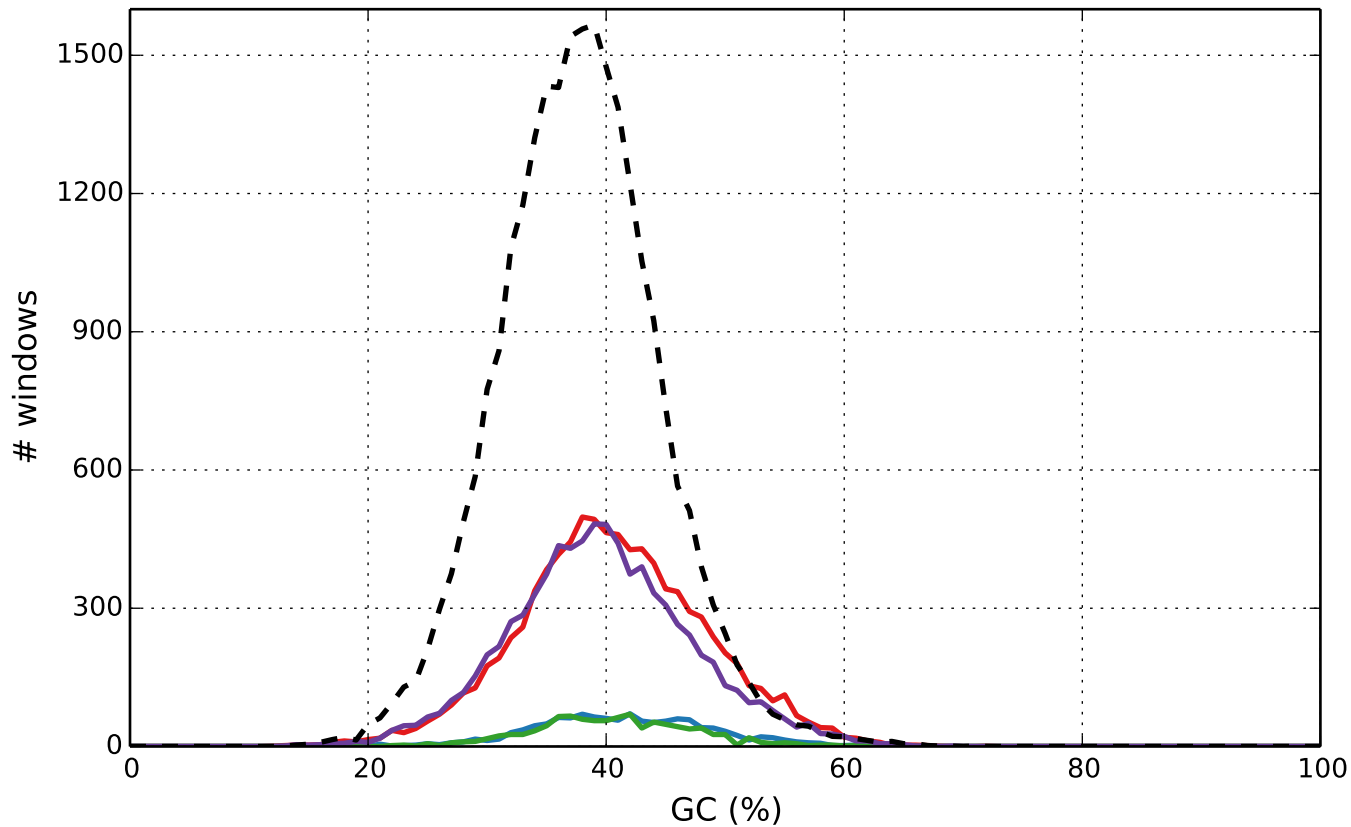


NGx

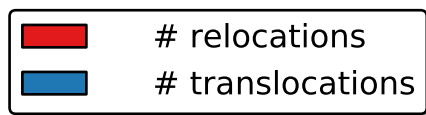
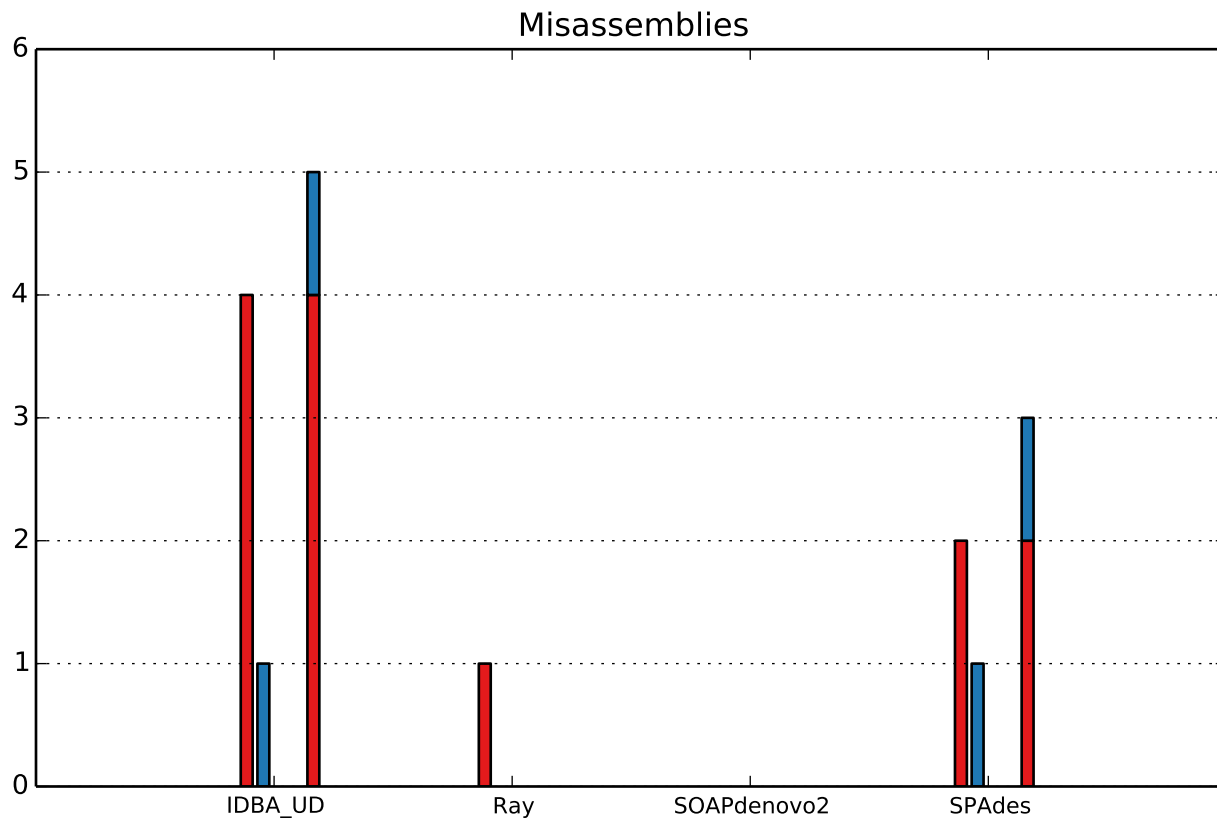




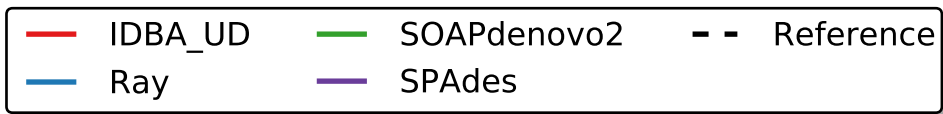
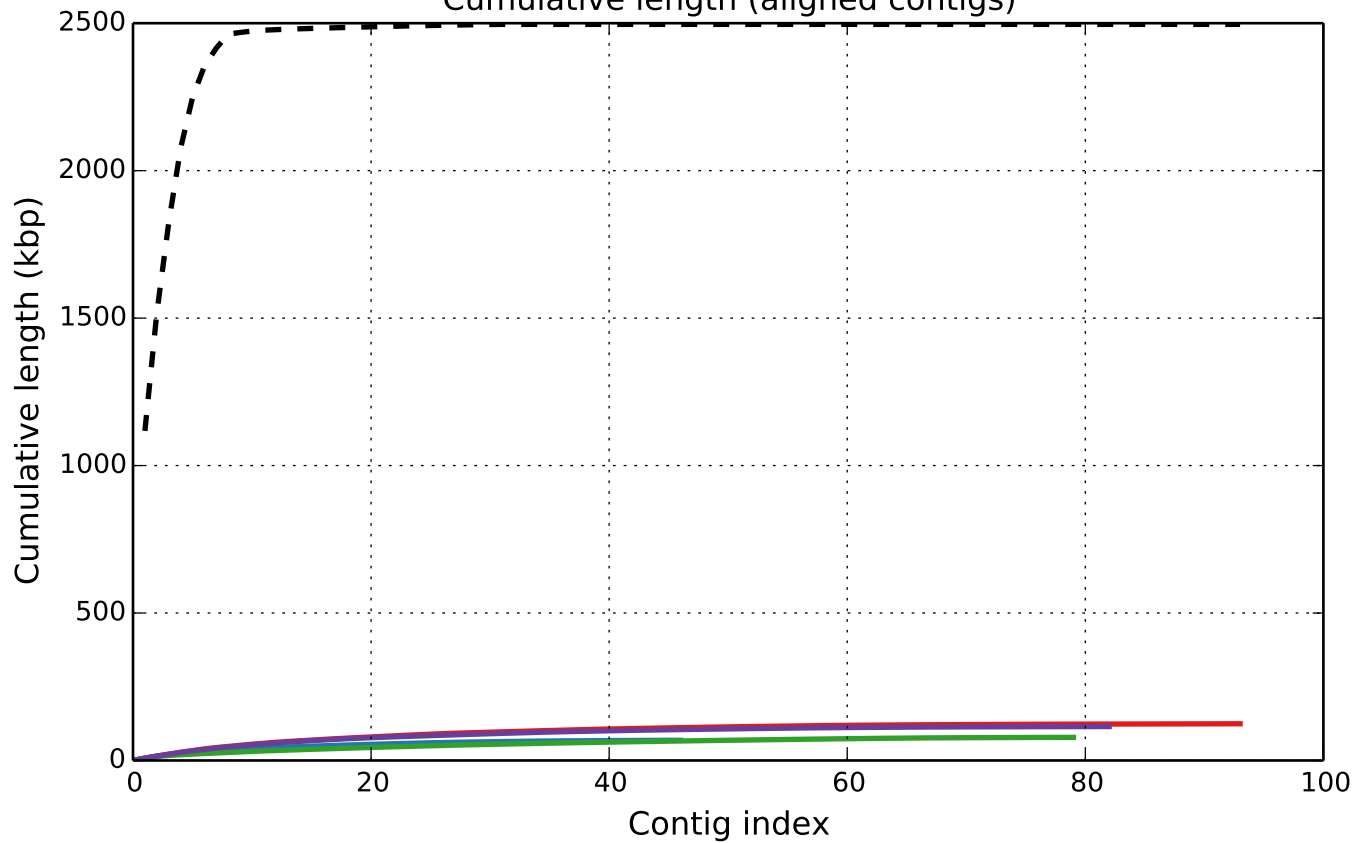
GC content

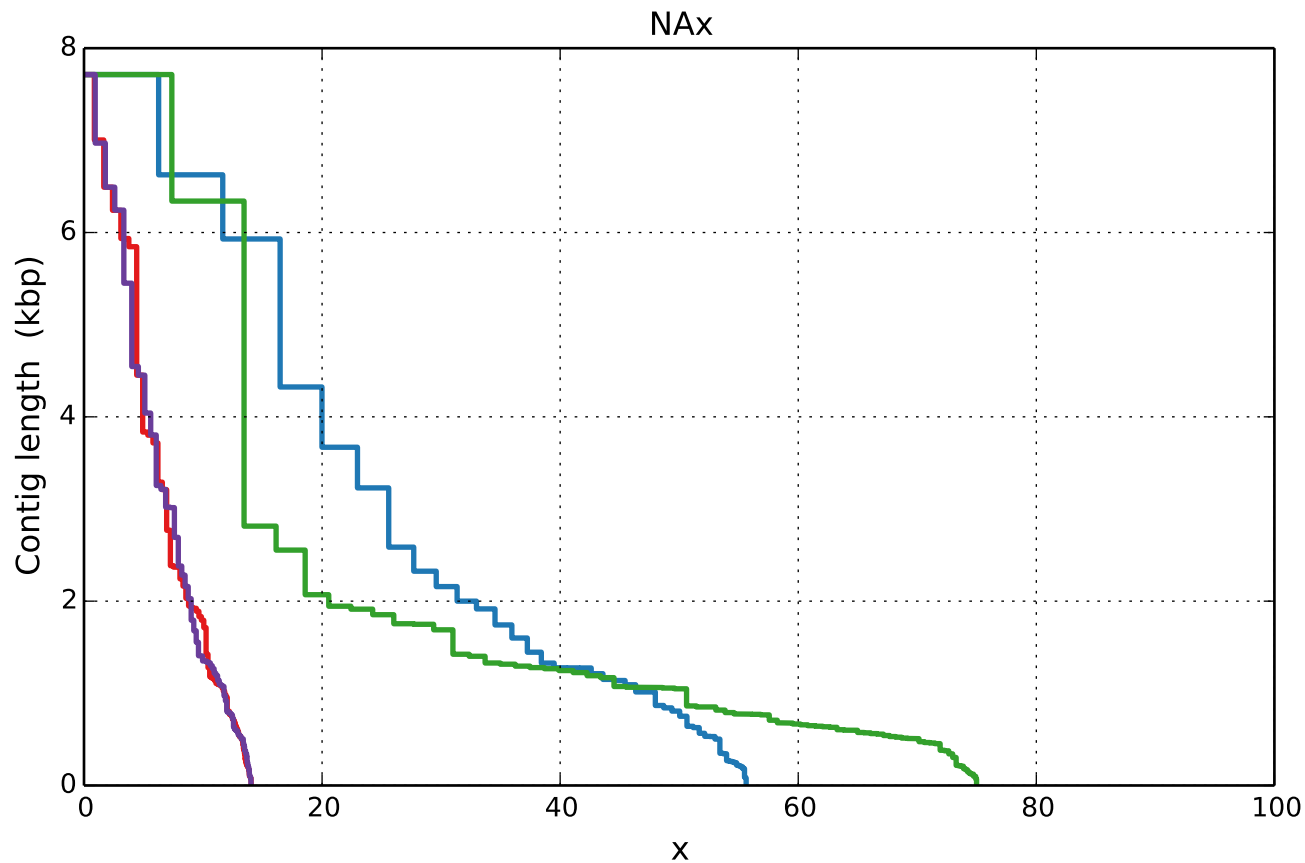


— IDBA_UD — SOAPdenovo2 - - Reference
— Ray — SPAdes



Cumulative length (aligned contigs)





— IDBA_UD — SOAPdenovo2 — SPAdes
— Ray

