

Report

	IDBA_UD	Ray	SOAPdenovo2	SPAdes
# contigs (>= 1000 bp)	19	23	34	14
# contigs (>= 5000 bp)	7	17	6	6
# contigs (>= 10000 bp)	5	12	3	6
# contigs (>= 25000 bp)	4	7	0	4
# contigs (>= 50000 bp)	2	2	0	2
Total length (>= 1000 bp)	220031	468854	132397	296917
Total length (>= 5000 bp)	196592	454988	69091	280212
Total length (>= 10000 bp)	183329	422061	47482	280212
Total length (>= 25000 bp)	168984	339377	0	251109
Total length (>= 50000 bp)	109347	142882	0	178946
# contigs	28	30	55	23
Largest contig	54922	88128	19665	118876
Total length	226371	473951	147104	303488
Reference length	4041504	4041504	4041504	4041504
GC (%)	43.85	44.19	45.13	45.46
Reference GC (%)	45.72	45.72	45.72	45.72
N50	33404	43176	4638	60070
N75	14345	23163	2186	30960
L50	3	5	7	2
L75	5	8	19	4
# misassemblies	3	7	1	5
# misassembled contigs	3	4	1	4
Misassembled contigs length	8107	148285	2018	126074
# local misassemblies	0	6	1	1
# structural variations	0	0	0	0
# unaligned contigs	0 + 14 part	0 + 24 part	0 + 9 part	0 + 15 part
Unaligned length	170342	310402	40715	162466
Genome fraction (%)	1.330	3.467	2.617	2.331
Duplication ratio	1.042	1.167	1.006	1.497
# N's per 100 kbp	19.44	973.31	88.37	180.57
# mismatches per 100 kbp	643.71	691.52	530.49	544.65
# indels per 100 kbp	35.35	25.69	27.42	31.85
Largest alignment	26174	42912	19665	40708
NA50	-	-	1720	-
NGA50	-	-	-	-
LA50	-	-	19	-

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

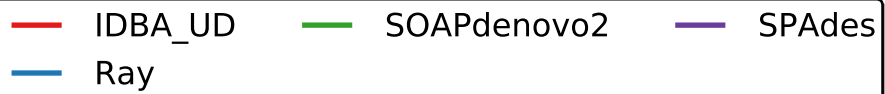
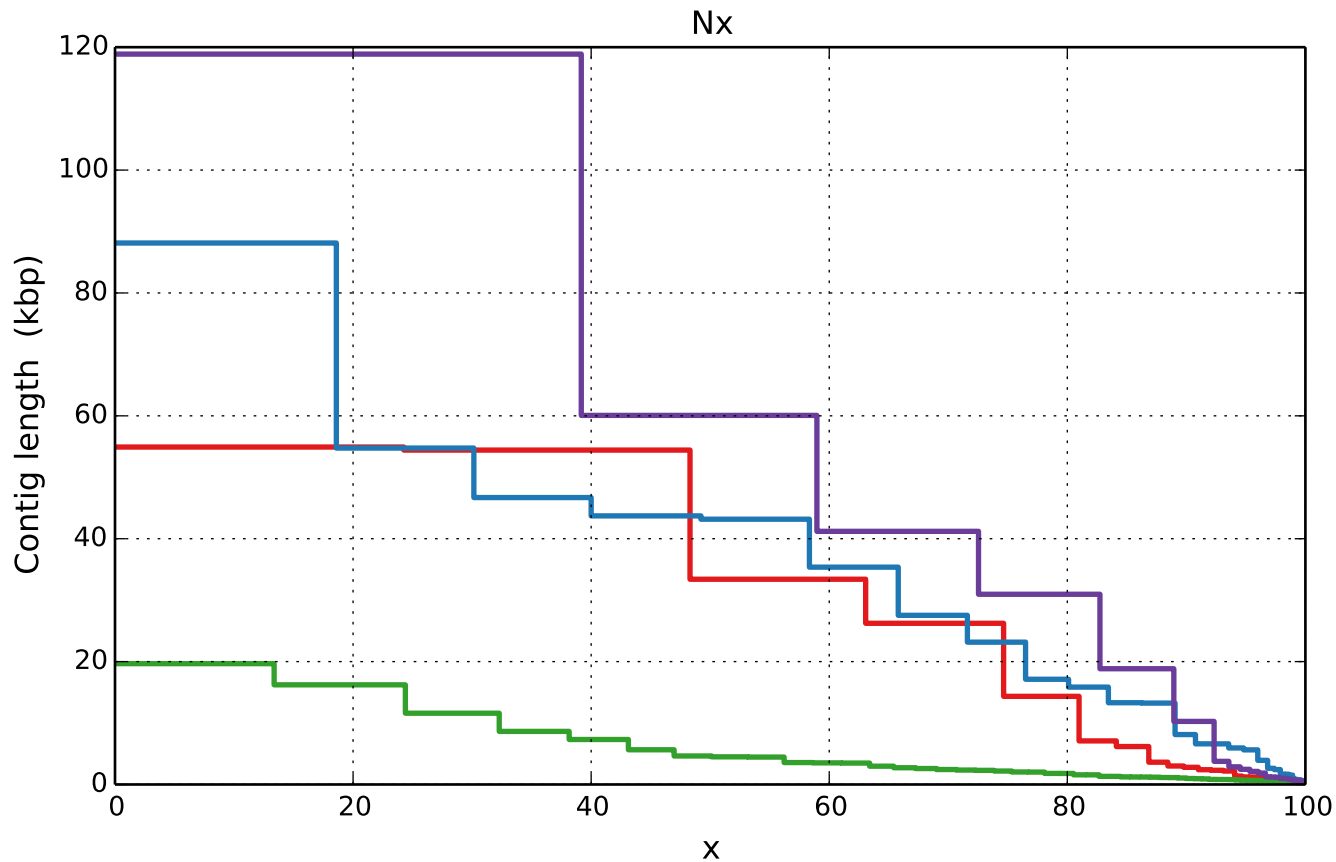
	IDBA_UD	Ray	SOAPdenovo2	SPAdes
# misassemblies	3	7	1	5
# relocations	1	5	1	3
# translocations	2	2	0	2
# inversions	0	0	0	0
# possibly misassembled contigs	5	6	7	7
# misassembled contigs	3	4	1	4
Misassembled contigs length	8107	148285	2018	126074
# local misassemblies	0	6	1	1
# structural variations	0	0	0	0
# mismatches	346	969	561	513
# indels	19	36	29	30
# short indels	19	35	28	29
# long indels	0	1	1	1
Indels length	26	53	44	47

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).

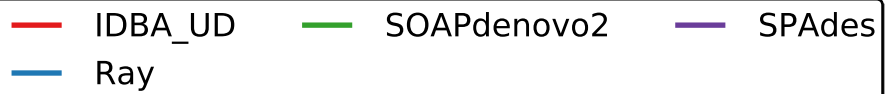
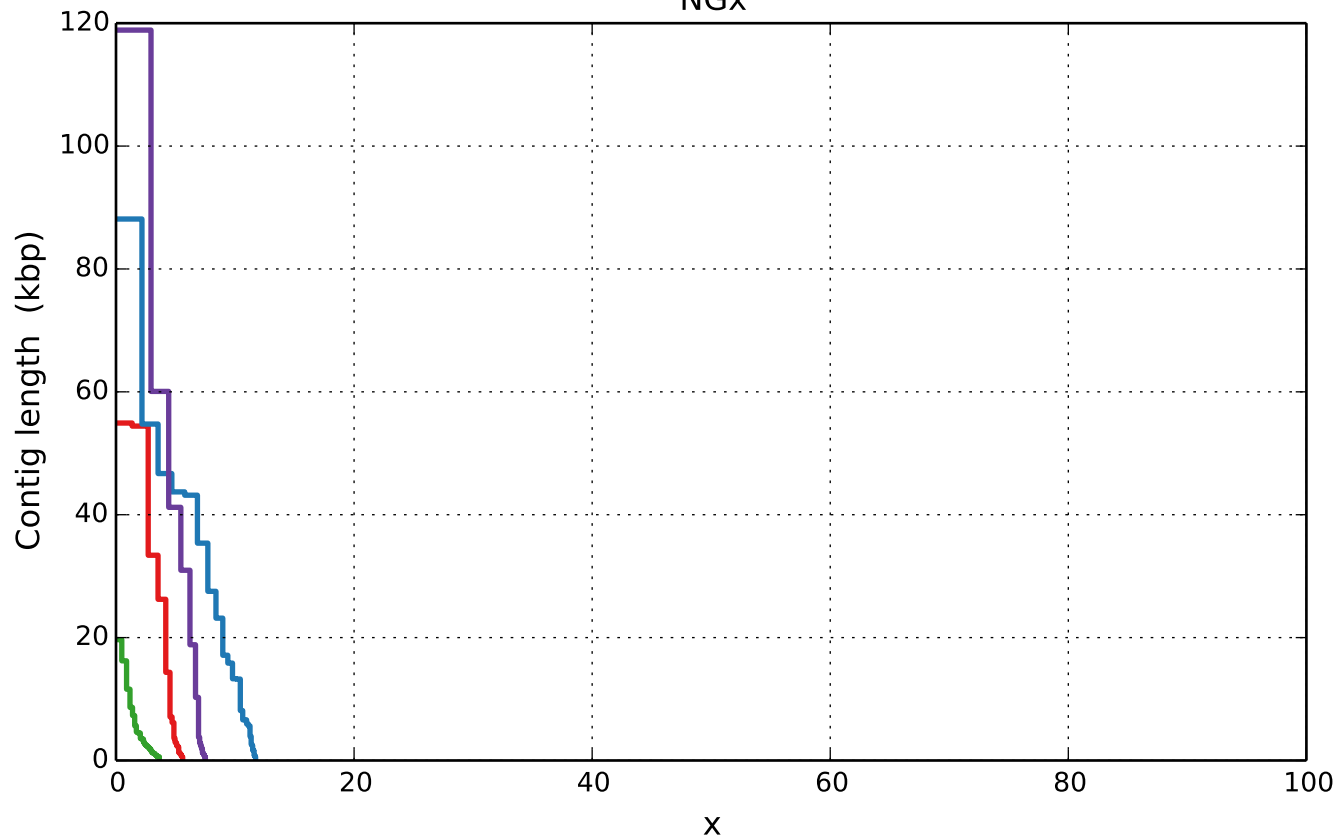
Unaligned report

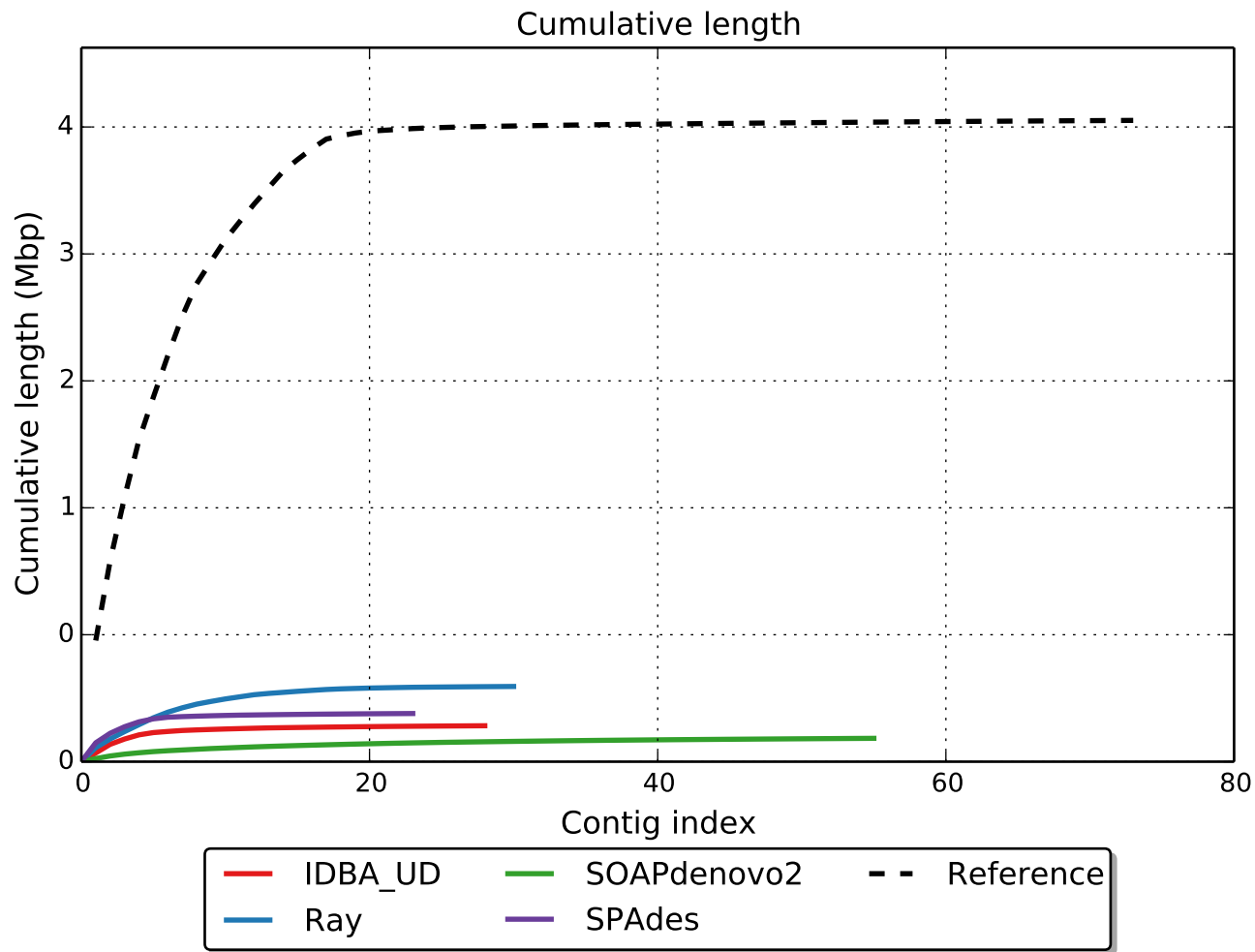
	IDBA_UD	Ray	SOAPdenovo2	SPAdes
# fully unaligned contigs	0	0	0	0
Fully unaligned length	0	0	0	0
# partially unaligned contigs	14	24	9	15
# with misassembly	1	1	0	0
# both parts are significant	3	3	7	5
Partially unaligned length	170342	310402	40715	162466
# N's	44	4613	130	548

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).

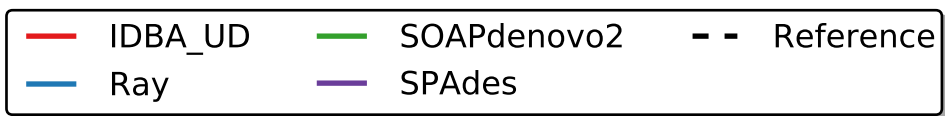
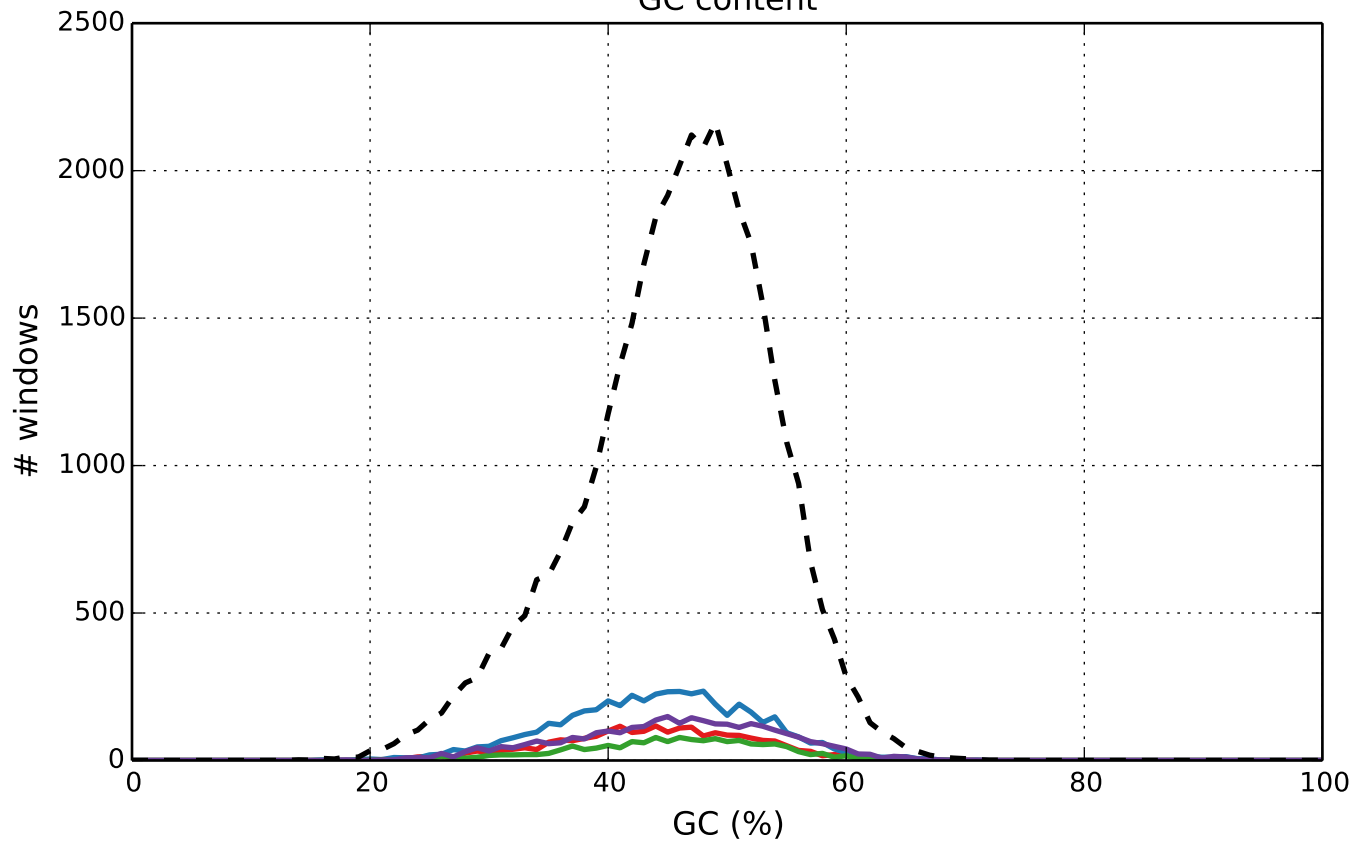


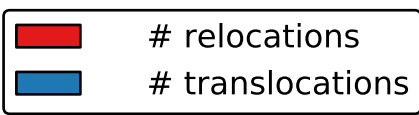
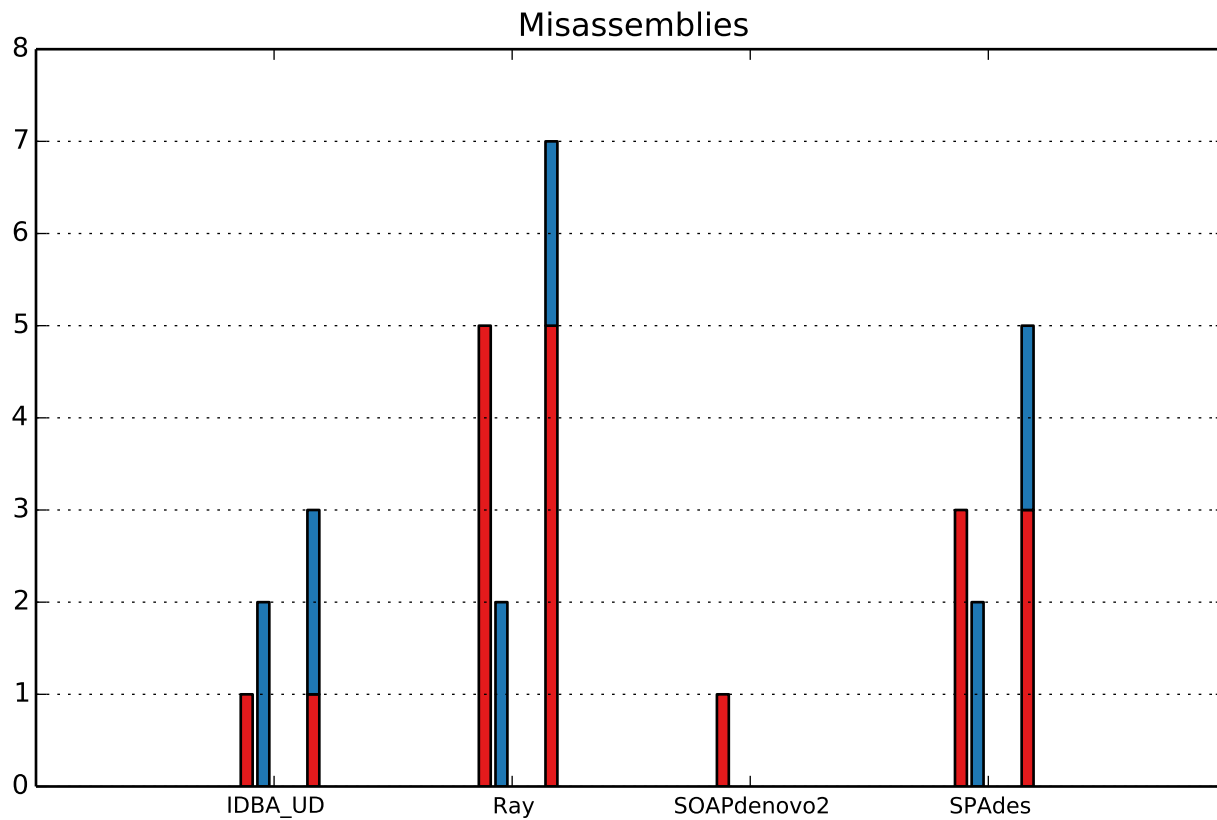
NGx

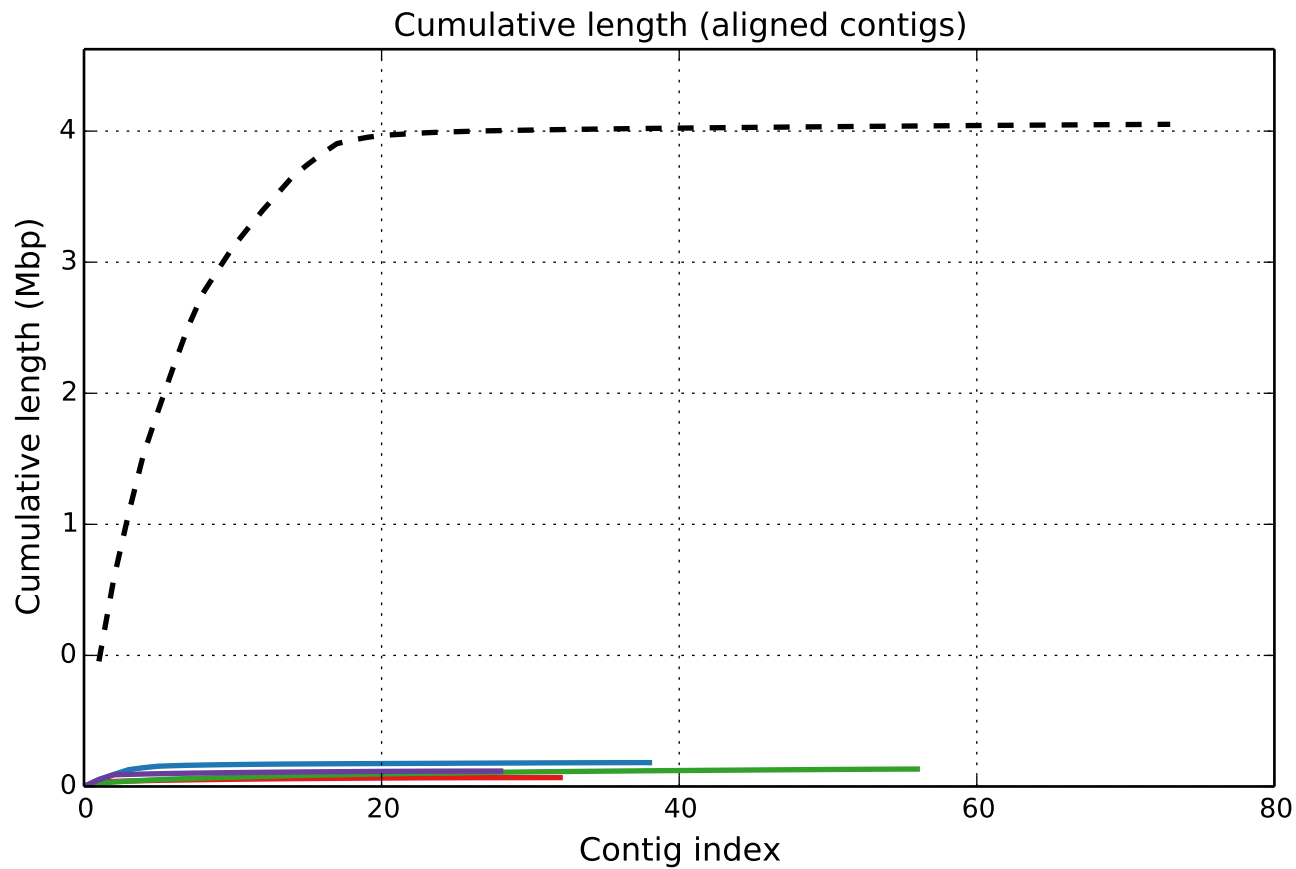




GC content

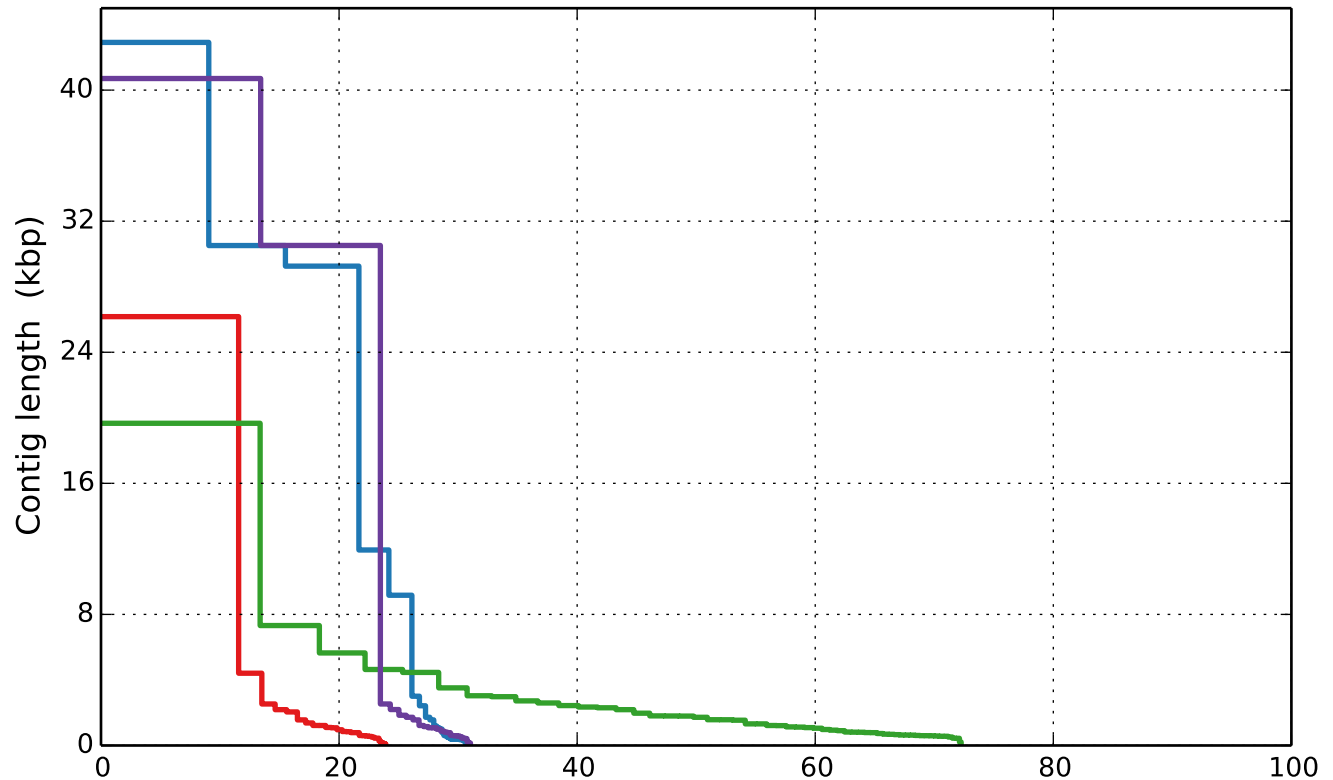






— IDBA_UD	— SOAPdenovo2	- - Reference
— Ray	— SPAdes	

NAx



NGAx

