

Report

	IDBA_UD	Ray	SOAPdenovo2	SPAdes
# contigs (>= 1000 bp)	136	51	60	189
# contigs (>= 5000 bp)	27	4	1	32
# contigs (>= 10000 bp)	16	3	0	19
# contigs (>= 25000 bp)	10	1	0	7
# contigs (>= 50000 bp)	4	0	0	3
Total length (>= 1000 bp)	847574	180525	110370	958773
Total length (>= 5000 bp)	632664	90020	5582	653825
Total length (>= 10000 bp)	555395	84723	0	563655
Total length (>= 25000 bp)	474747	42596	0	408862
Total length (>= 50000 bp)	287153	0	0	291186
# contigs	325	88	164	450
Largest contig	94894	42596	5582	135693
Total length	979681	206216	181591	1139422
Reference length	3242215	3242215	3242215	3242215
GC (%)	42.23	42.38	41.42	41.45
Reference GC (%)	42.49	42.49	42.49	42.49
N50	20242	3587	1150	9347
N75	2334	1638	748	1720
L50	11	8	43	20
L75	57	31	90	107
# misassemblies	15	3	4	9
# misassembled contigs	13	2	4	9
Misassembled contigs length	72260	4740	8991	59065
# local misassemblies	2	7	99	4
# structural variations	1	0	1	1
# unaligned contigs	0 + 147 part	0 + 26 part	0 + 47 part	0 + 236 part
Unaligned length	636239	116982	26461	698740
Genome fraction (%)	10.368	2.538	4.521	13.196
Duplication ratio	1.022	1.085	1.058	1.030
# N's per 100 kbp	243.14	1864.55	4762.35	1211.75
# mismatches per 100 kbp	1141.19	901.85	1007.55	1449.62
# indels per 100 kbp	76.46	71.71	60.71	107.28
Largest alignment	31794	3399	5185	31353
NA50	-	-	927	-
NGA50	-	-	-	-
NA75	-	-	393	-
LA50	-	-	52	-
LA75	-	-	129	-

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	15	3	4	9
# relocations	7	2	4	6
# translocations	7	1	0	3
# inversions	1	0	0	0
# possibly misassembled contigs	22	7	5	41
# misassembled contigs	13	2	4	9
Misassembled contigs length	72260	4740	8991	59065
# local misassemblies	2	7	99	4
# structural variations	1	0	1	1
# mismatches	3836	742	1477	6202
# indels	257	59	89	459
# short indels	241	55	87	393
# long indels	16	4	2	66
Indels length	566	166	128	1374

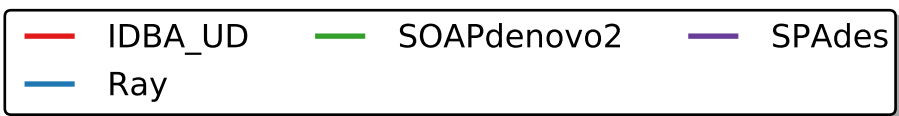
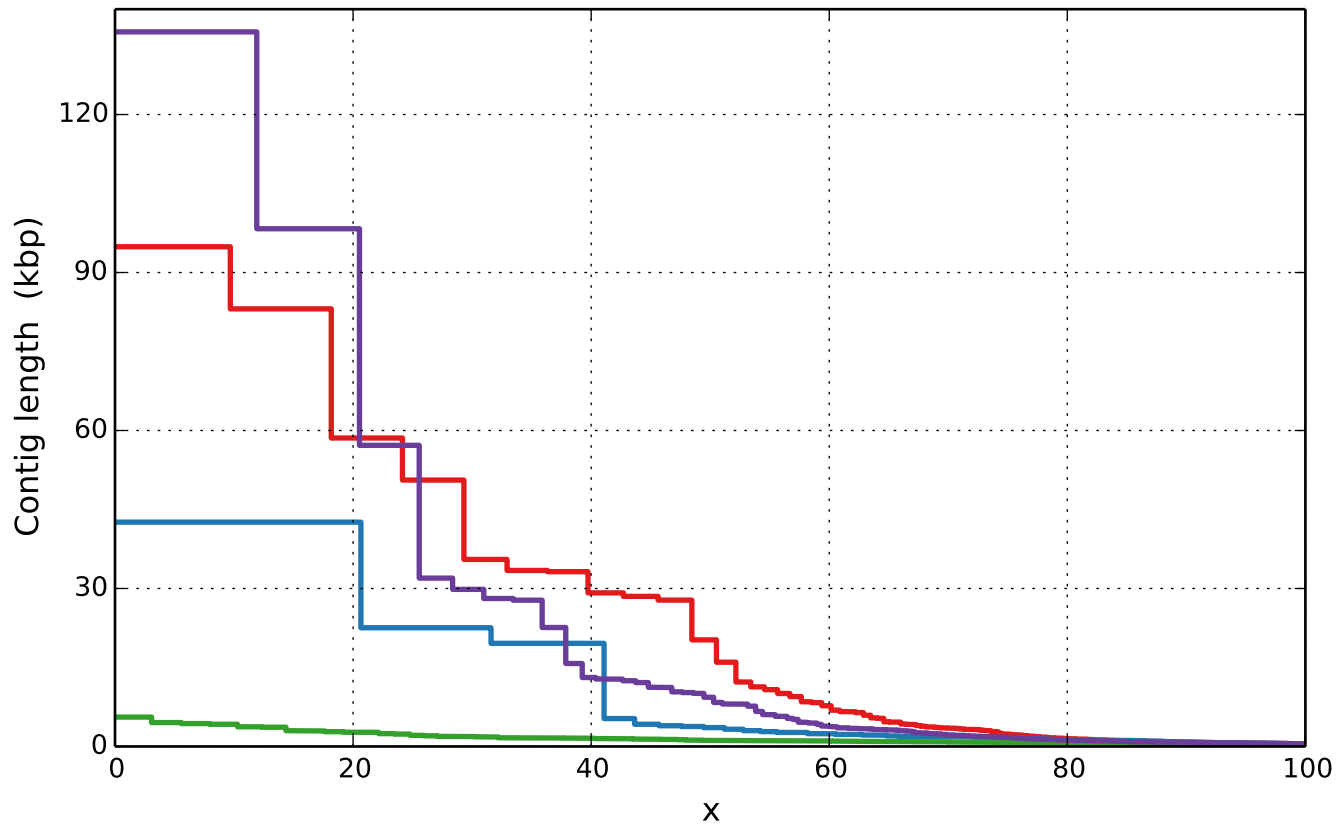
All statistics are based on contigs of size ≥ 500 bp, unless otherwise noted (e.g., "# contigs (≥ 0 bp)" and "Total length (≥ 0 bp)" include all contigs).

Unaligned report

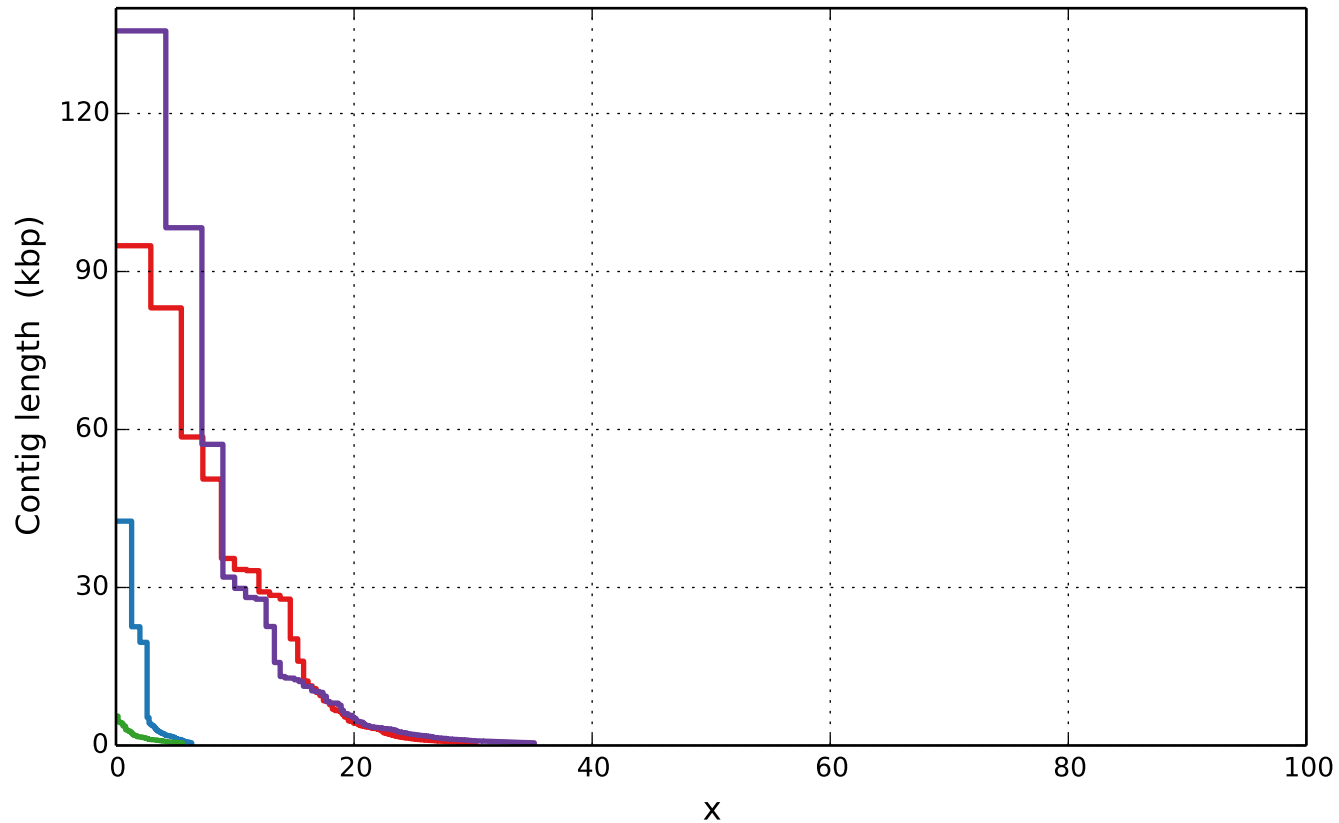
	IDBA_UD	Ray	SOAPdenovo2	SPAdes
# fully unaligned contigs	0	0	0	0
Fully unaligned length	0	0	0	0
# partially unaligned contigs	147	26	47	236
# with misassembly	7	2	10	9
# both parts are significant	20	6	4	38
Partially unaligned length	636239	116982	26461	698740
# N's	2382	3845	8648	13807

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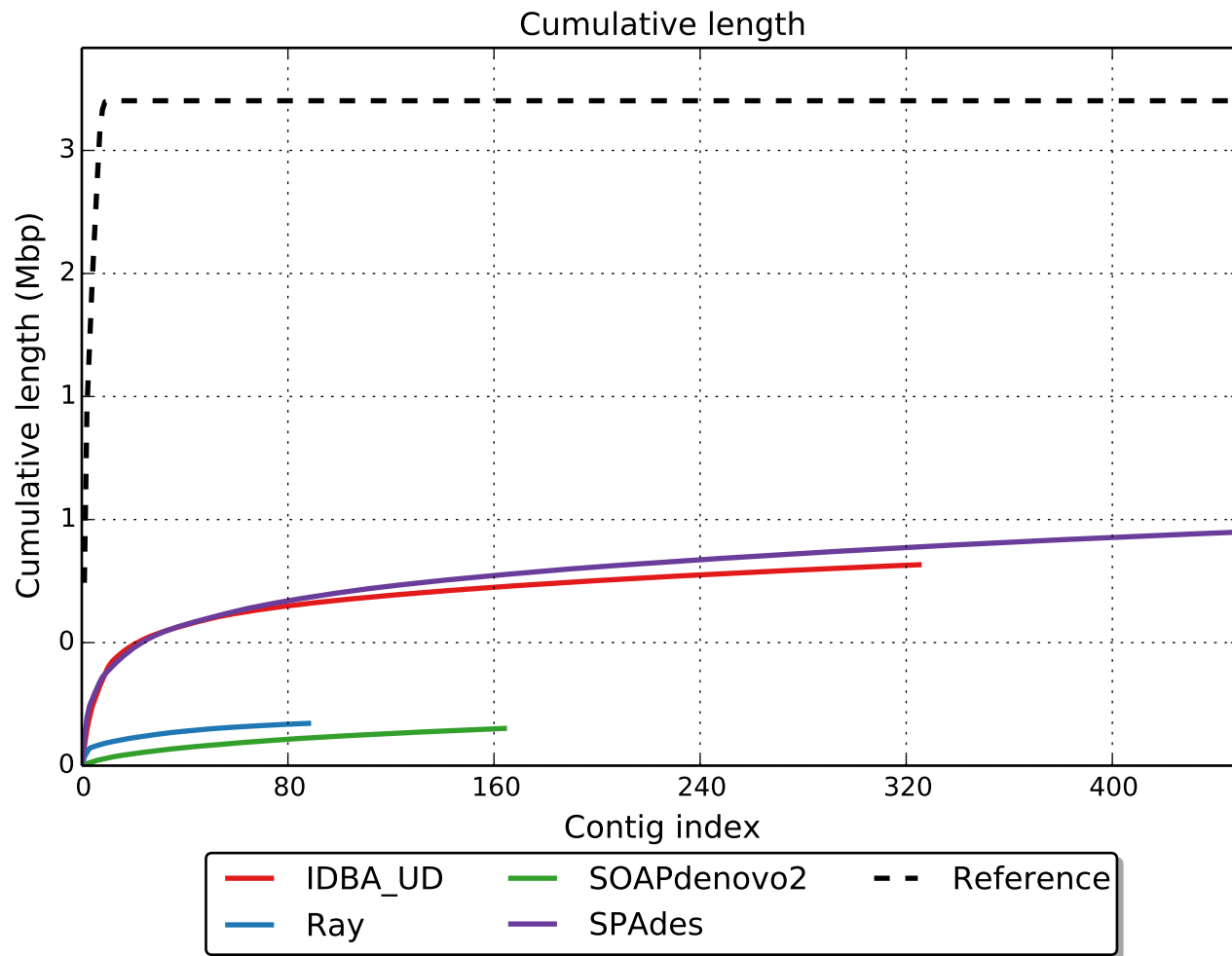
Nx



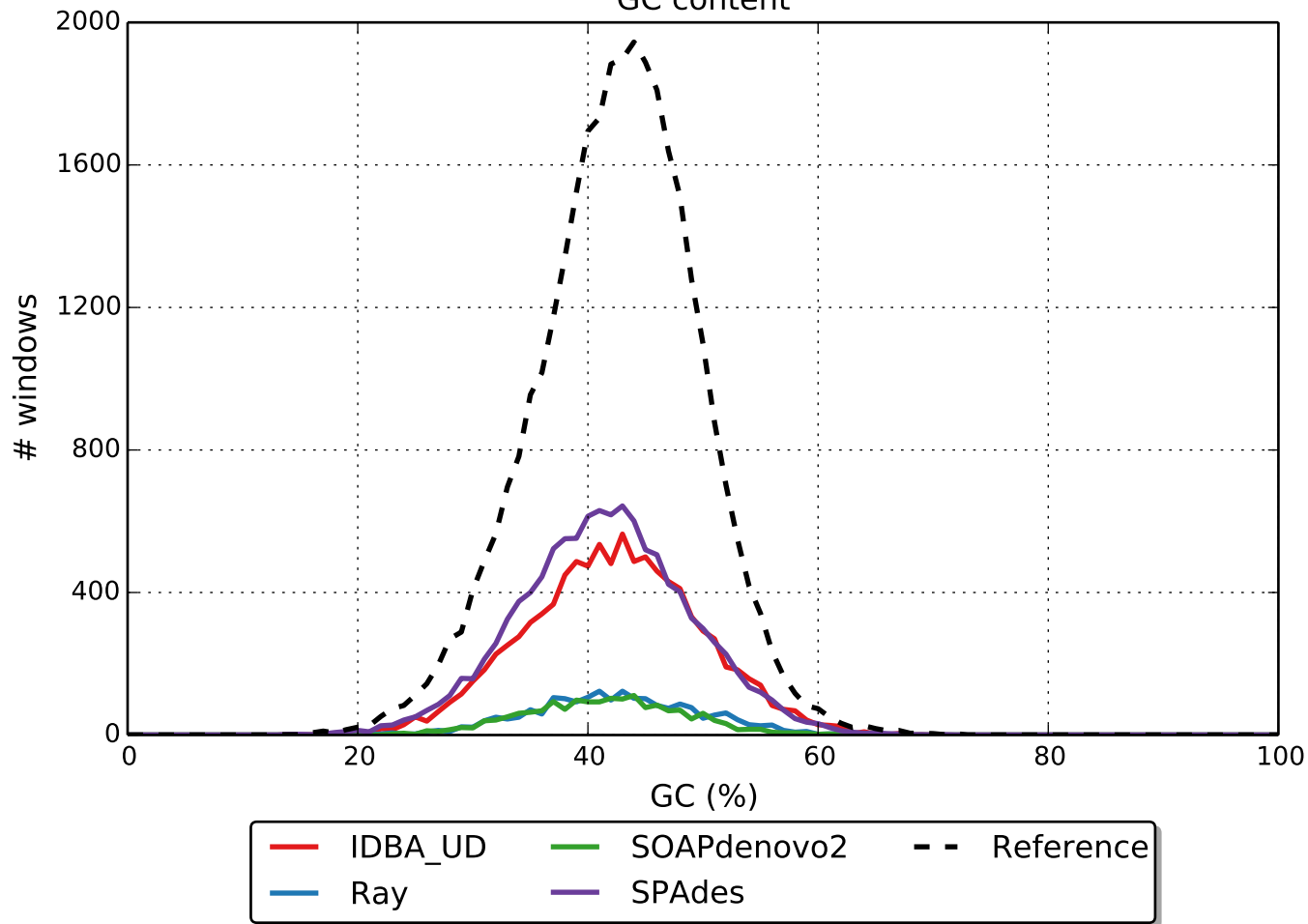
NGx



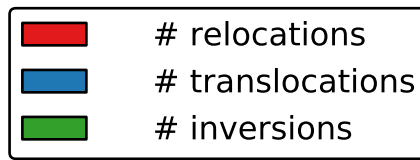
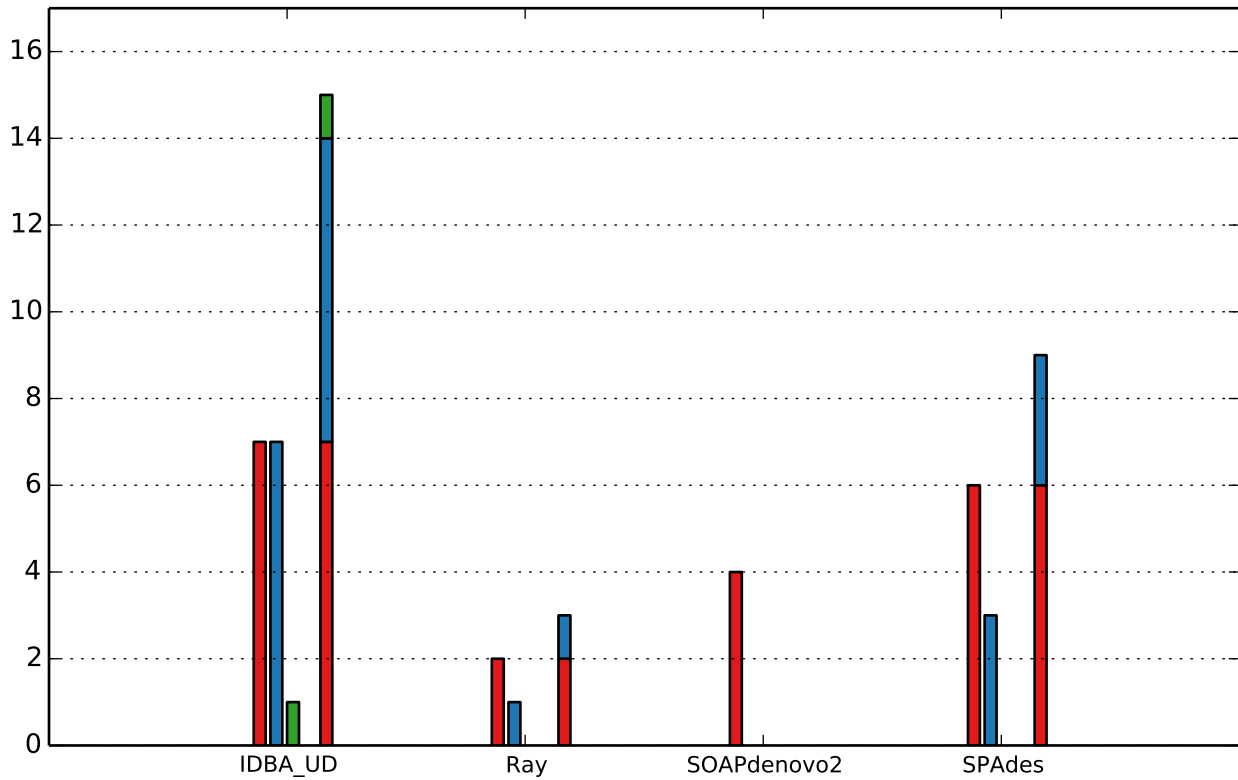
— IDBA_UD — SOAPdenovo2 — SPAdes
— Ray

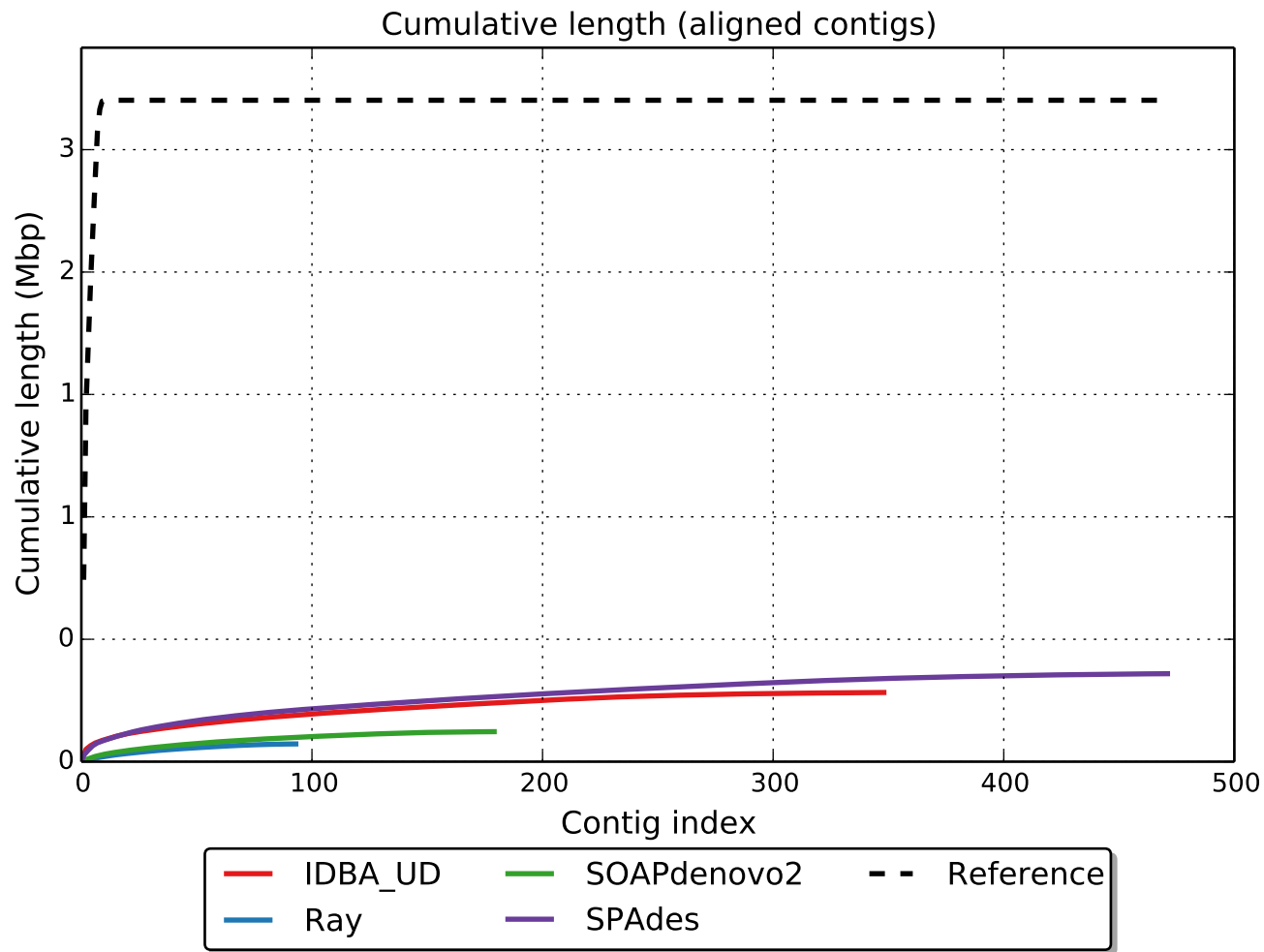


GC content

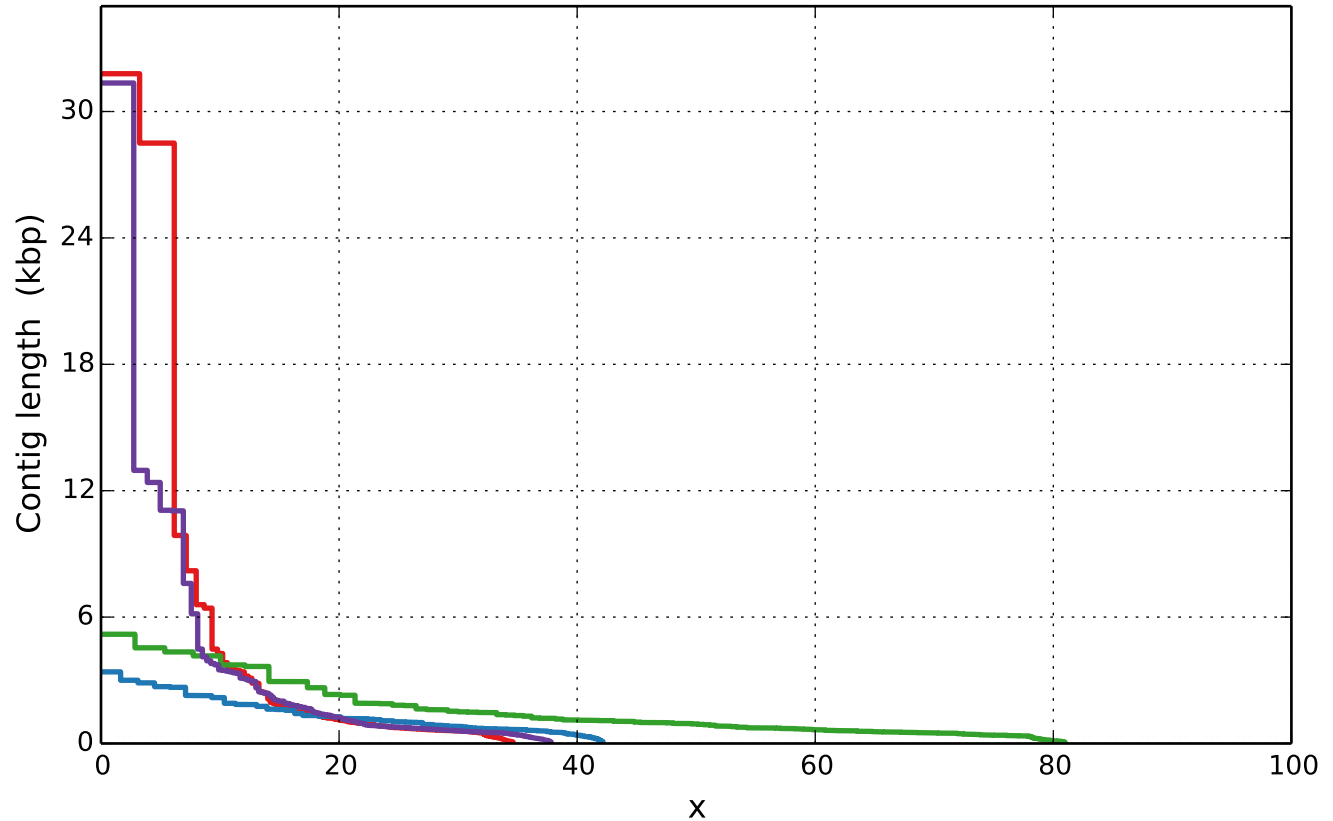


Misassemblies





NAx



NGAx

