

Report

	Gold_Assembly	IDBA_UD	Ray	SOAPdenovo2	SPAdes
# contigs (>= 1000 bp)	176	181	179	1012	178
# contigs (>= 5000 bp)	150	156	156	2	154
# contigs (>= 10000 bp)	128	133	134	0	134
# contigs (>= 25000 bp)	72	75	74	0	73
# contigs (>= 50000 bp)	27	27	28	0	27
Total length (>= 1000 bp)	4958761	4986408	5009957	1638928	4977064
Total length (>= 5000 bp)	4888840	4915851	4946022	10799	4907055
Total length (>= 10000 bp)	4717362	4732619	4772379	0	4753038
Total length (>= 25000 bp)	3766402	3746297	3742840	0	3714108
Total length (>= 50000 bp)	2206633	2073586	2131540	0	2112013
# contigs	182	187	187	2137	184
Largest contig	205290	146300	146299	5594	146301
Total length	4962448	4990311	5015092	2446056	4981427
Reference length	5771987	5771987	5771987	5771987	5771987
GC (%)	46.33	46.37	46.34	47.01	46.49
Reference GC (%)	46.44	46.44	46.44	46.44	46.44
N50	43347	42148	43017	1284	43018
NG50	39105	38690	39099	-	38690
N75	25913	25795	24600	879	24603
NG75	17624	17635	18467	-	17089
L50	34	37	37	644	36
LG50	43	46	46	-	45
L75	71	75	75	1221	74
LG75	99	103	102	-	103
# misassemblies	33	34	32	3	36
# misassembled contigs	23	25	24	3	26
Misassembled contigs length	1110222	1105783	1086886	7183	1158240
# local misassemblies	47	44	50	31	44
# structural variations	7	7	7	5	7
# unaligned contigs	0 + 92 part	0 + 94 part	0 + 94 part	0 + 323 part	0 + 96 part
Unaligned length	2019926	2031453	2042270	159065	2031276
Genome fraction (%)	45.040	44.928	44.902	39.412	44.882
Duplication ratio	1.132	1.141	1.147	1.005	1.139
# N's per 100 kbp	0.00	0.00	5.88	0.00	1.45
# mismatches per 100 kbp	3667.80	3669.19	3666.72	3323.46	3667.86
# indels per 100 kbp	121.05	121.47	120.89	70.69	121.52
Largest alignment	134457	134457	134456	5588	134457
NA50	2200	1839	2247	1151	1851
NGA50	-	-	-	-	-
NA75	-	-	-	748	-
LA50	191	201	192	713	199
LA75	-	-	-	1373	-

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

	Gold_Assembly	IDBA_UD	Ray	SOAPdenovo2	SPAdes
# misassemblies	33	34	32	3	36
# relocations	24	24	25	2	25
# translocations	9	10	7	1	11
# inversions	0	0	0	0	0
# possibly misassembled contigs	115	121	122	72	120
# misassembled contigs	23	25	24	3	26
Misassembled contigs length	1110222	1105783	1086886	7183	1158240
# local misassemblies	47	44	50	31	44
# structural variations	7	7	7	5	7
# mismatches	95351	95150	95031	75604	95020
# indels	3147	3150	3133	1608	3148
# short indels	2782	2776	2771	1514	2779
# long indels	365	374	362	94	369
Indels length	9228	9352	9159	2966	9273

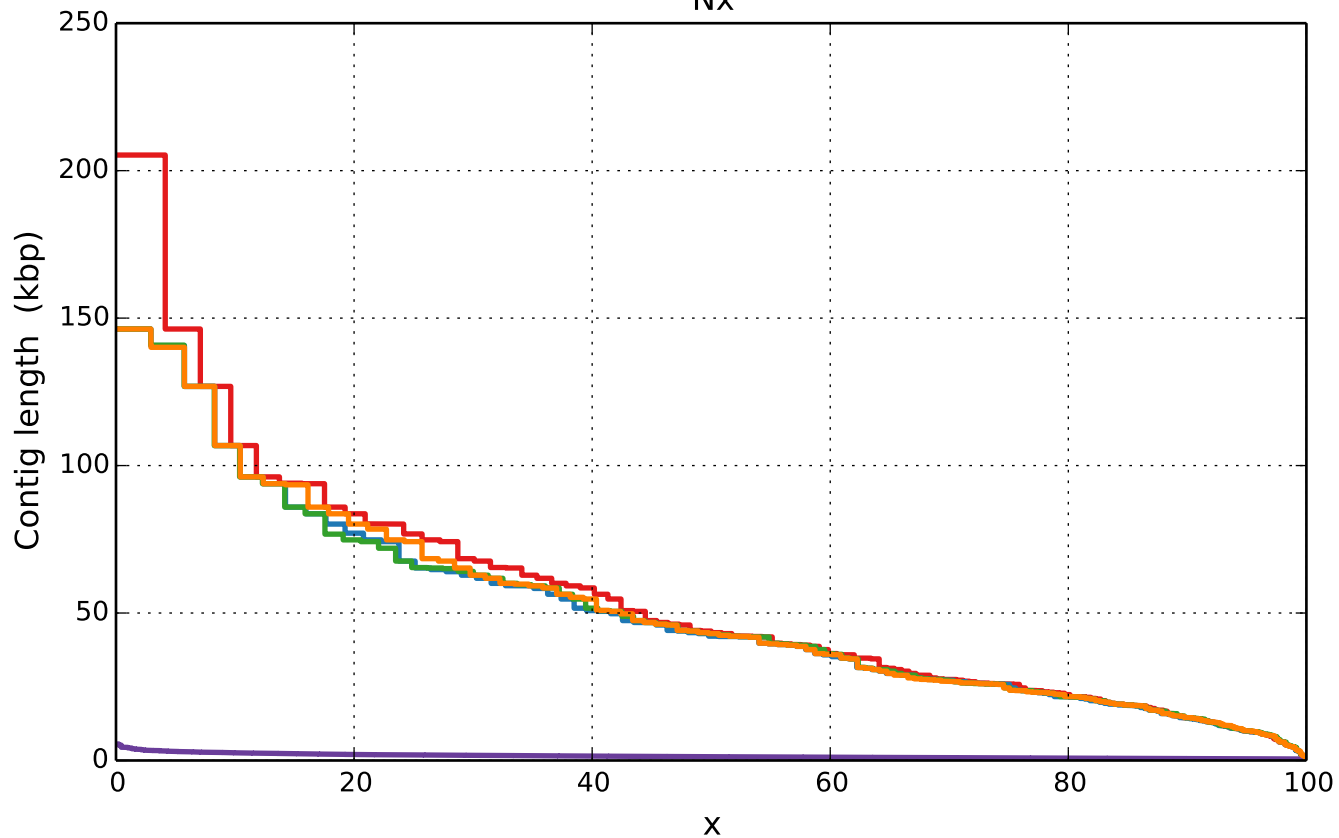
All statistics are based on contigs of size ≥ 500 bp, unless otherwise noted (e.g., "# contigs (≥ 0 bp)" and "Total length (≥ 0 bp)" include all contigs).

Unaligned report

	Gold_Assembly	IDBA_UD	Ray	SOAPdenovo2	SPAdes
# fully unaligned contigs	0	0	0	0	0
Fully unaligned length	0	0	0	0	0
# partially unaligned contigs	92	94	94	323	96
# with misassembly	43	40	43	1	43
# both parts are significant	82	85	85	70	86
Partially unaligned length	2019926	2031453	2042270	159065	2031276
# N's	0	0	295	0	72

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).

Nx



Gold_Assembly

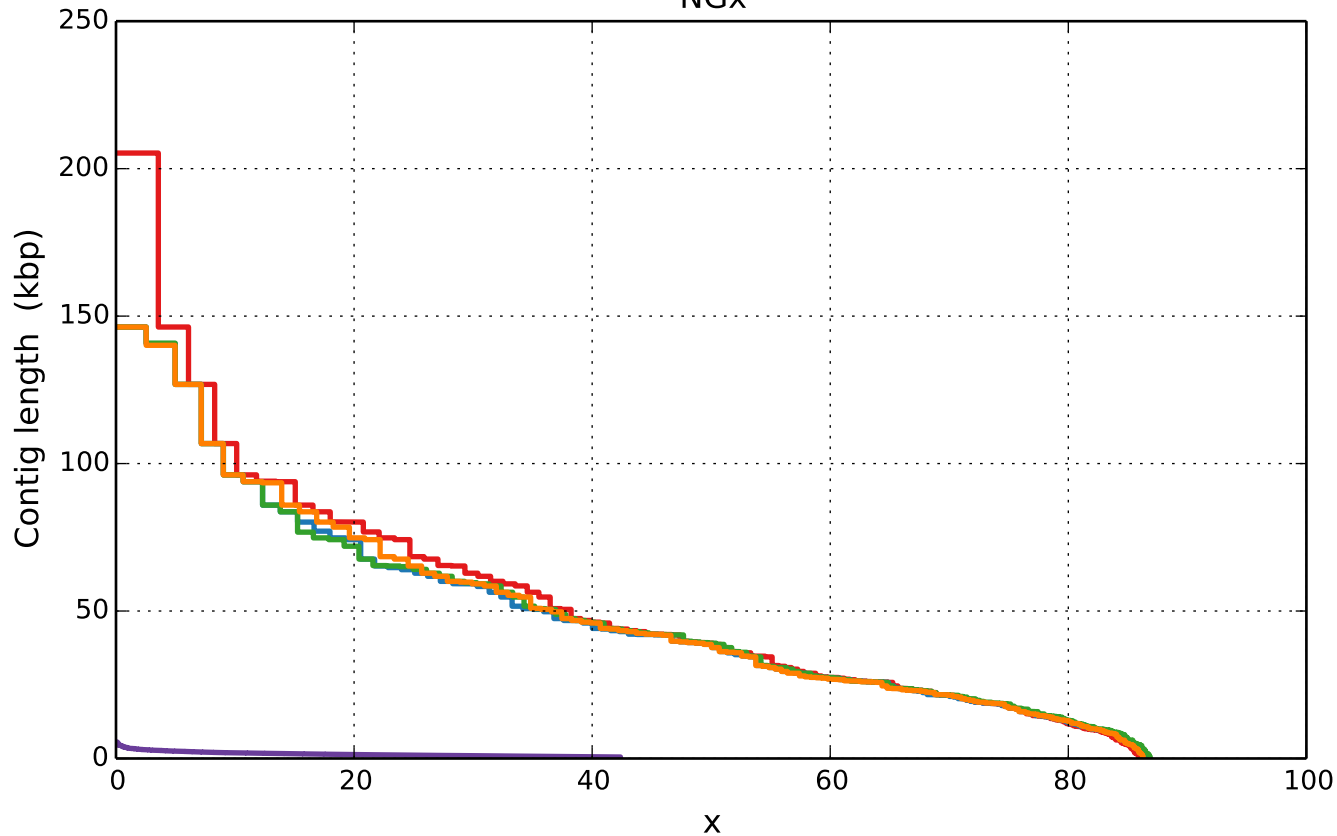
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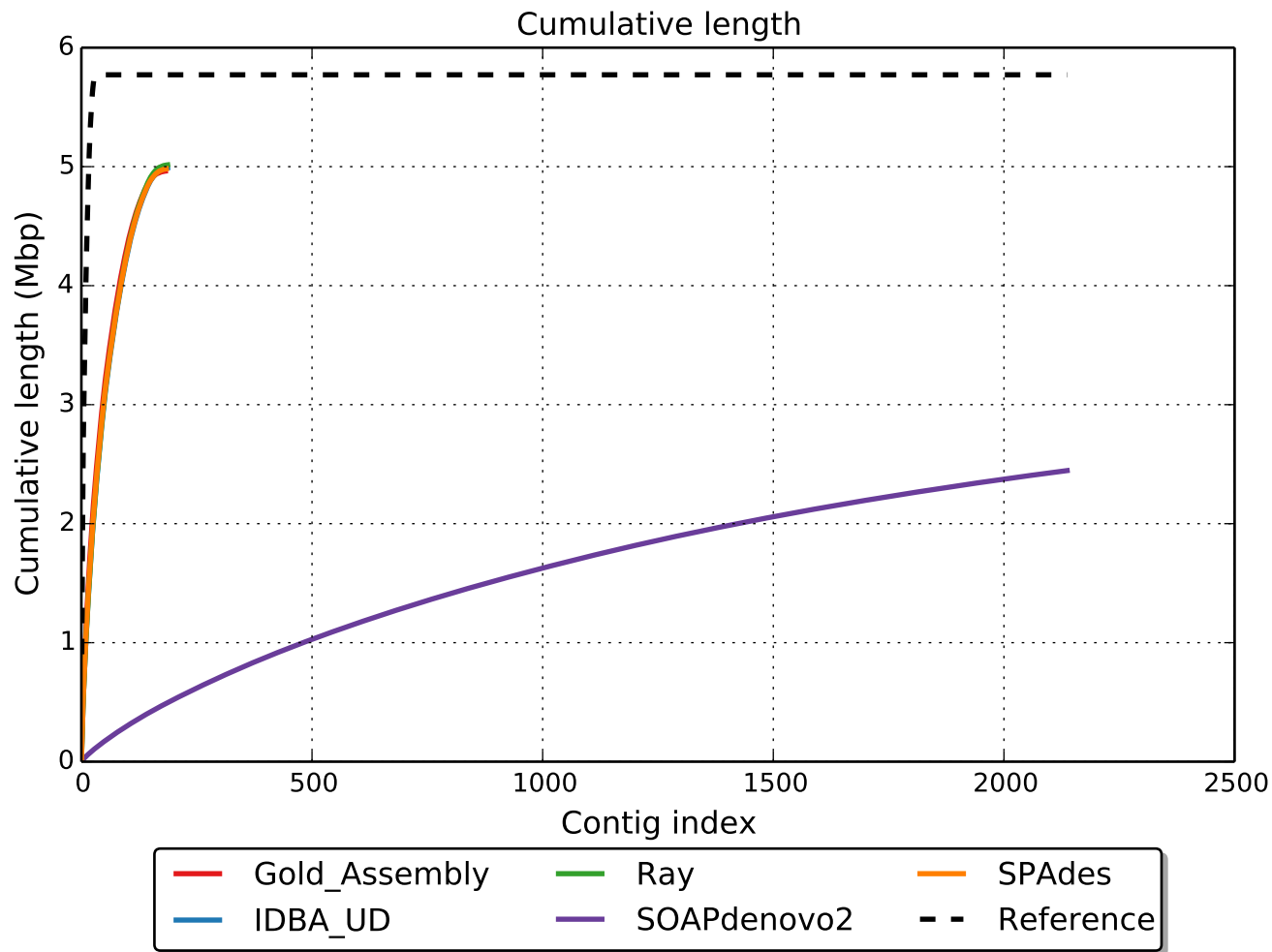
SPAdes

IDBA_UD

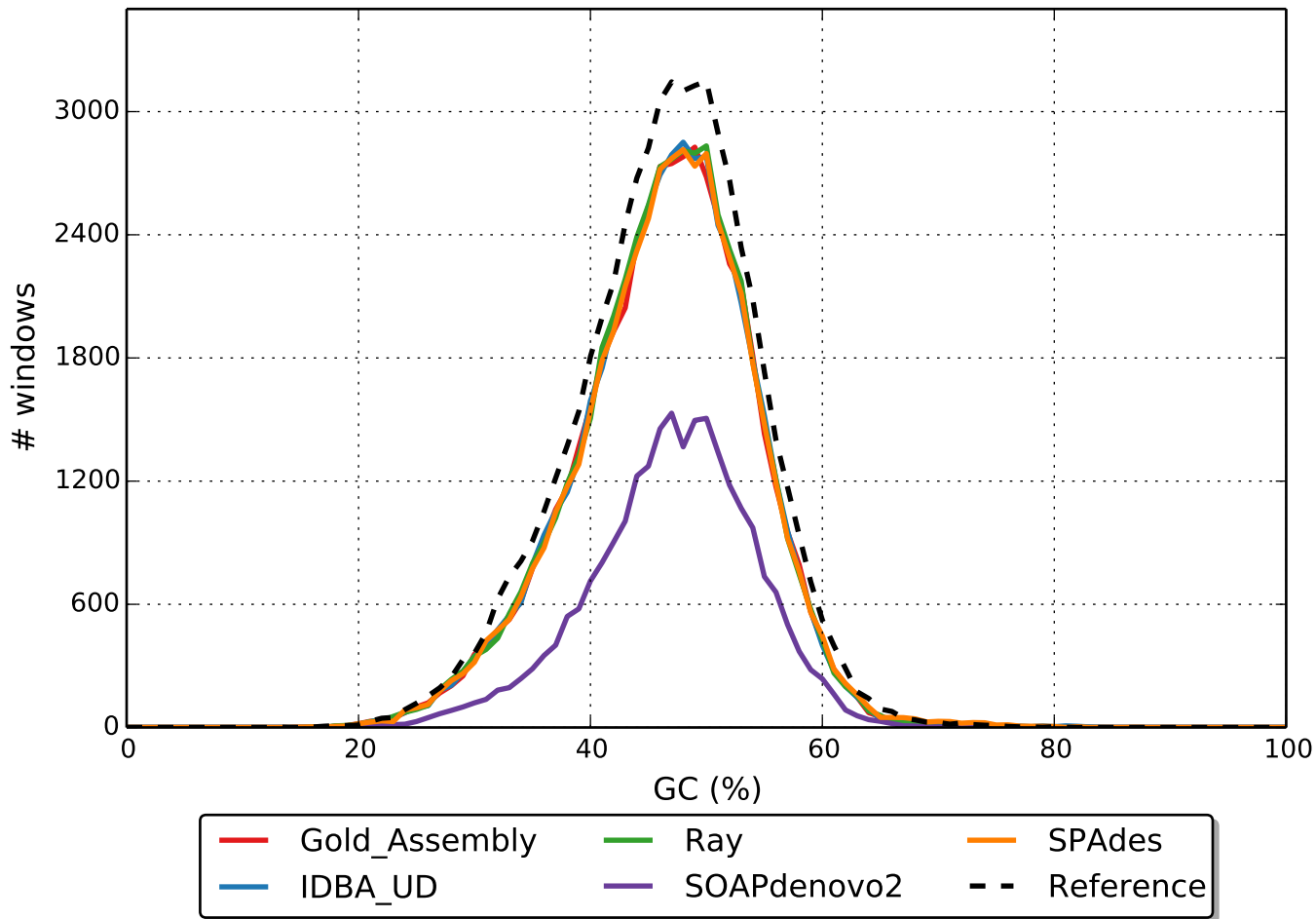
SOAPdenovo2

NGx

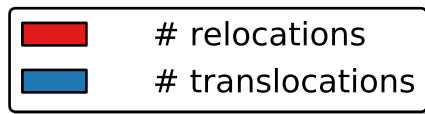
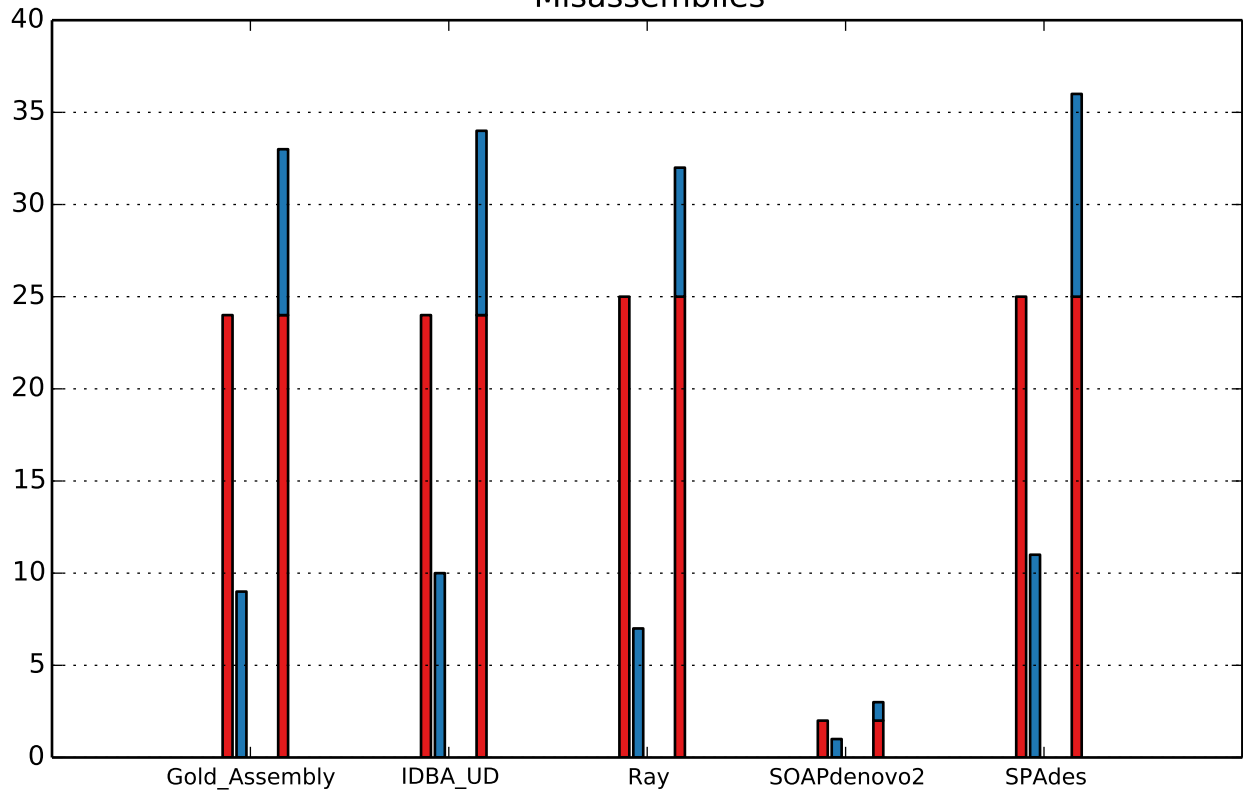


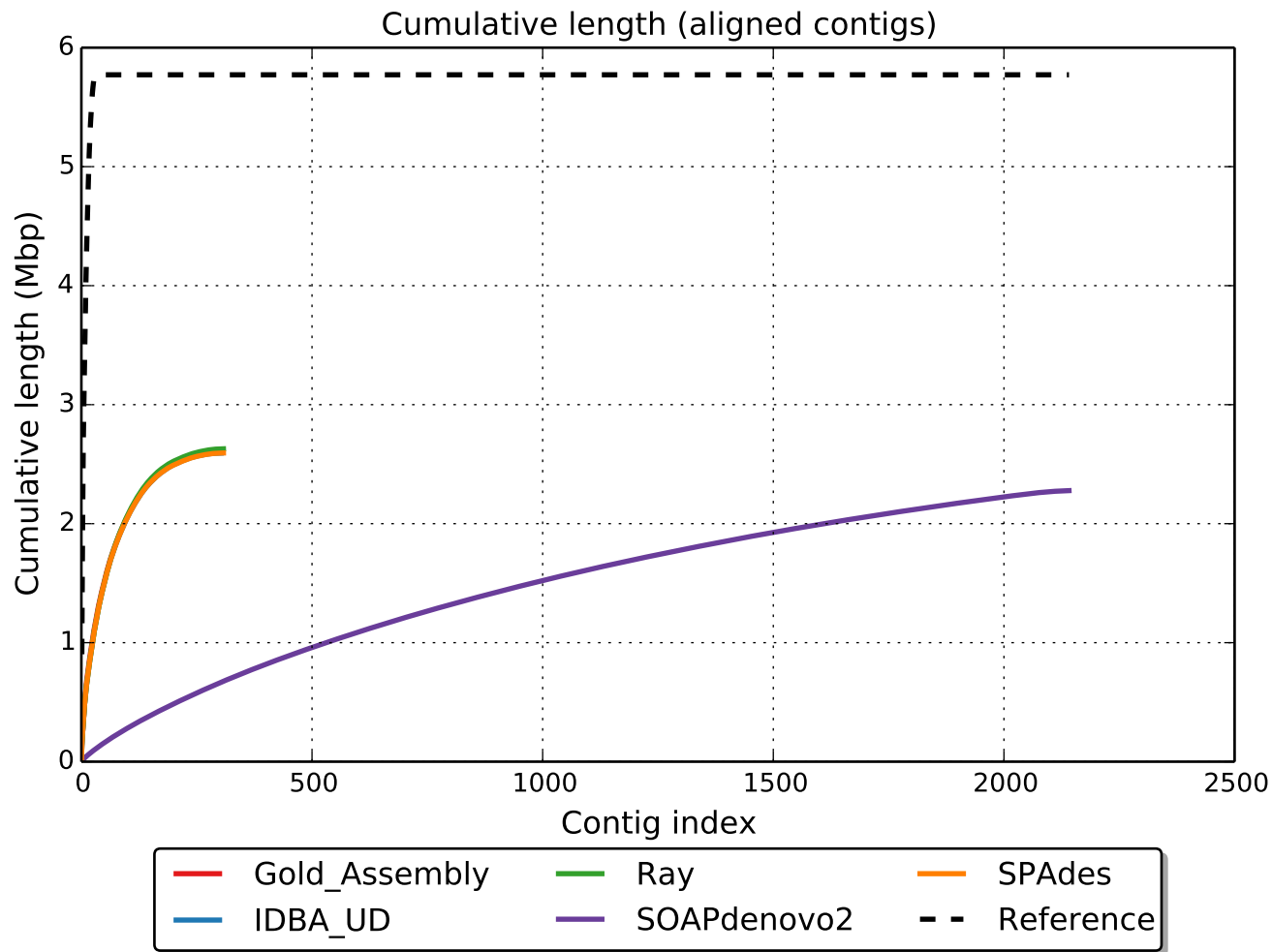


GC content

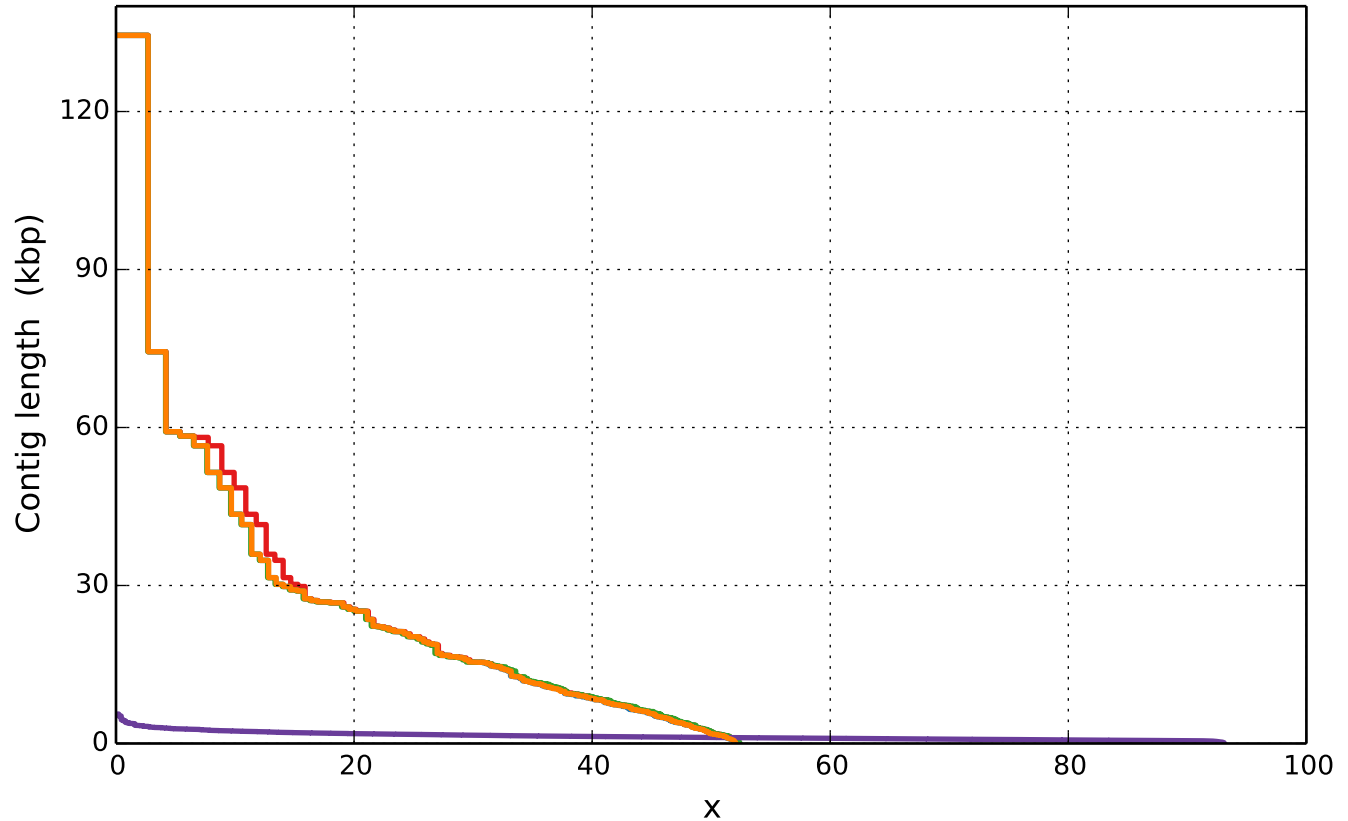


Misassemblies





NAx



NGAx

