

Report

	Gold_Assembly	IDBA_UD	Ray	SOAPdenovo2	SPAdes
# contigs (>= 1000 bp)	330	345	341	704	420
# contigs (>= 5000 bp)	230	240	238	337	275
# contigs (>= 10000 bp)	167	165	173	152	184
# contigs (>= 25000 bp)	61	56	61	20	48
# contigs (>= 50000 bp)	14	16	15	2	7
Total length (>= 1000 bp)	5073854	5115381	5664723	4982065	5173923
Total length (>= 5000 bp)	4817623	4851000	5399546	3989583	4796866
Total length (>= 10000 bp)	4355207	4297273	4919274	2645816	4144952
Total length (>= 25000 bp)	2516543	2419024	2975884	721610	1874765
Total length (>= 50000 bp)	925969	1075668	1384379	121470	482618
# contigs	348	363	357	779	444
Largest contig	100092	100092	454778	66697	100092
Total length	5087205	5129804	5677313	5036628	5192746
Reference length	5092500	5092500	5092500	5092500	5092500
GC (%)	74.07	73.93	74.09	74.05	73.94
Reference GC (%)	74.08	74.08	74.08	74.08	74.08
N50	24674	23511	27533	10720	20296
NG50	24674	23585	30170	10389	20552
N75	16059	14976	16549	5869	11945
NG75	16059	15272	20102	5705	12736
L50	63	63	56	140	80
LG50	63	62	46	143	78
L75	126	130	124	299	162
LG75	126	128	99	306	156
# misassemblies	0	14	29	3	15
# misassembled contigs	0	11	23	3	15
Misassembled contigs length	0	386544	578770	6135	295491
# local misassemblies	0	0	1	0	0
# structural variations	0	0	0	0	0
# unaligned contigs	0 + 0 part	0 + 25 part	0 + 3 part	0 + 15 part	0 + 106 part
Unaligned length	0	48244	511546	1827	124176
Genome fraction (%)	99.896	99.724	99.552	98.562	99.418
Duplication ratio	1.000	1.001	1.019	1.003	1.001
# N's per 100 kbp	0.00	0.00	1.55	17.53	0.00
# mismatches per 100 kbp	0.00	3.56	0.16	18.03	46.55
# indels per 100 kbp	0.02	0.51	0.02	10.78	1.80
Largest alignment	100092	100092	100081	66696	100092
NA50	24674	22802	21842	10720	18977
NGA50	24674	22912	23646	10376	19372
NA75	16059	14045	11070	5869	10830
NGA75	16059	14303	14496	5705	11278
LA50	63	68	79	140	85
LGA50	63	67	66	143	83
LA75	126	138	167	299	173
LGA75	126	136	133	306	166

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	0	14	29	3	15
# relocations	0	0	0	0	0
# translocations	0	14	29	3	15
# inversions	0	0	0	0	0
# possibly misassembled contigs	0	14	3	1	39
# misassembled contigs	0	11	23	3	15
Misassembled contigs length	0	386544	578770	6135	295491
# local misassemblies	0	0	1	0	0
# structural variations	0	0	0	0	0
# mismatches	0	181	8	905	2357
# indels	1	26	1	541	91
# short indels	0	24	0	227	89
# long indels	1	2	1	314	2
Indels length	31	87	31	11347	180

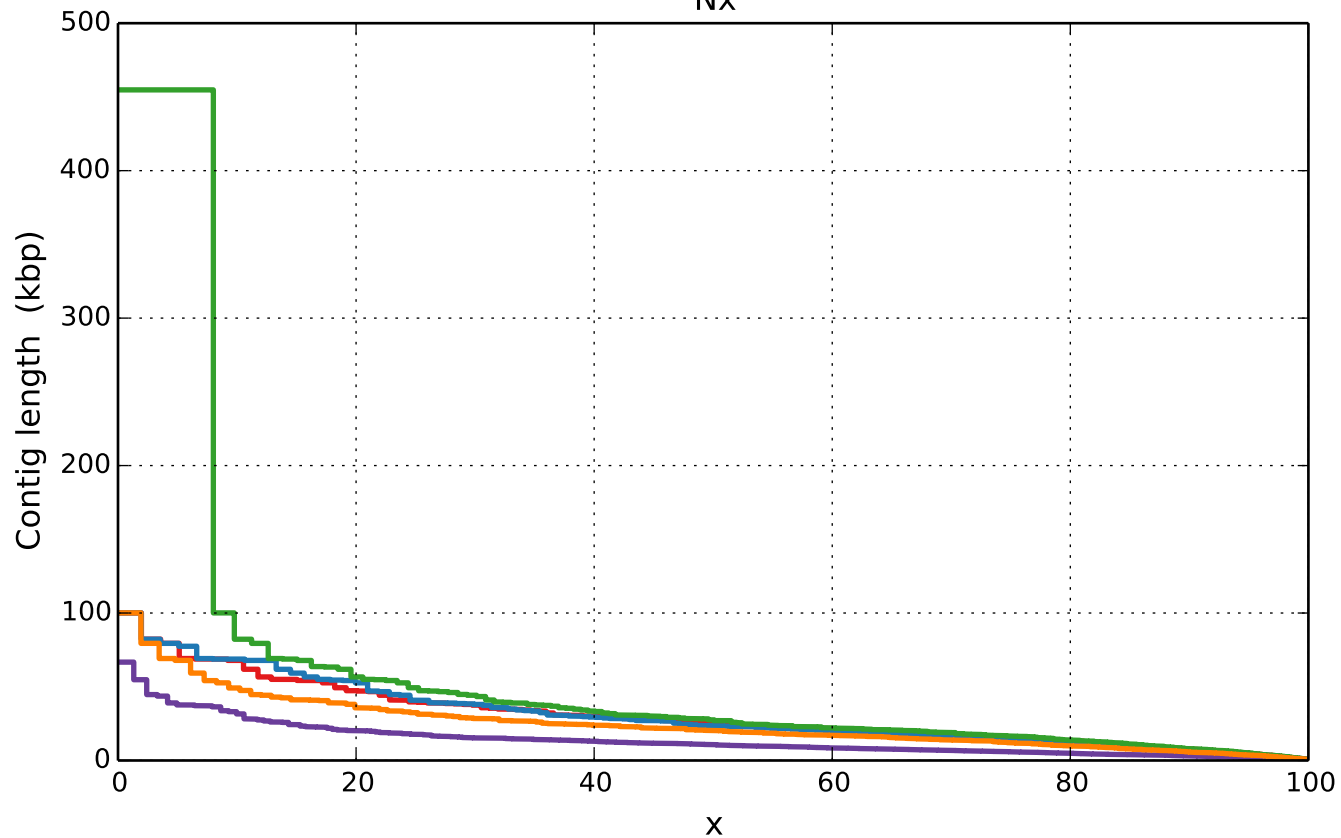
All statistics are based on contigs of size ≥ 500 bp, unless otherwise noted (e.g., "# contigs (≥ 0 bp)" and "Total length (≥ 0 bp)" include all contigs).

Unaligned report

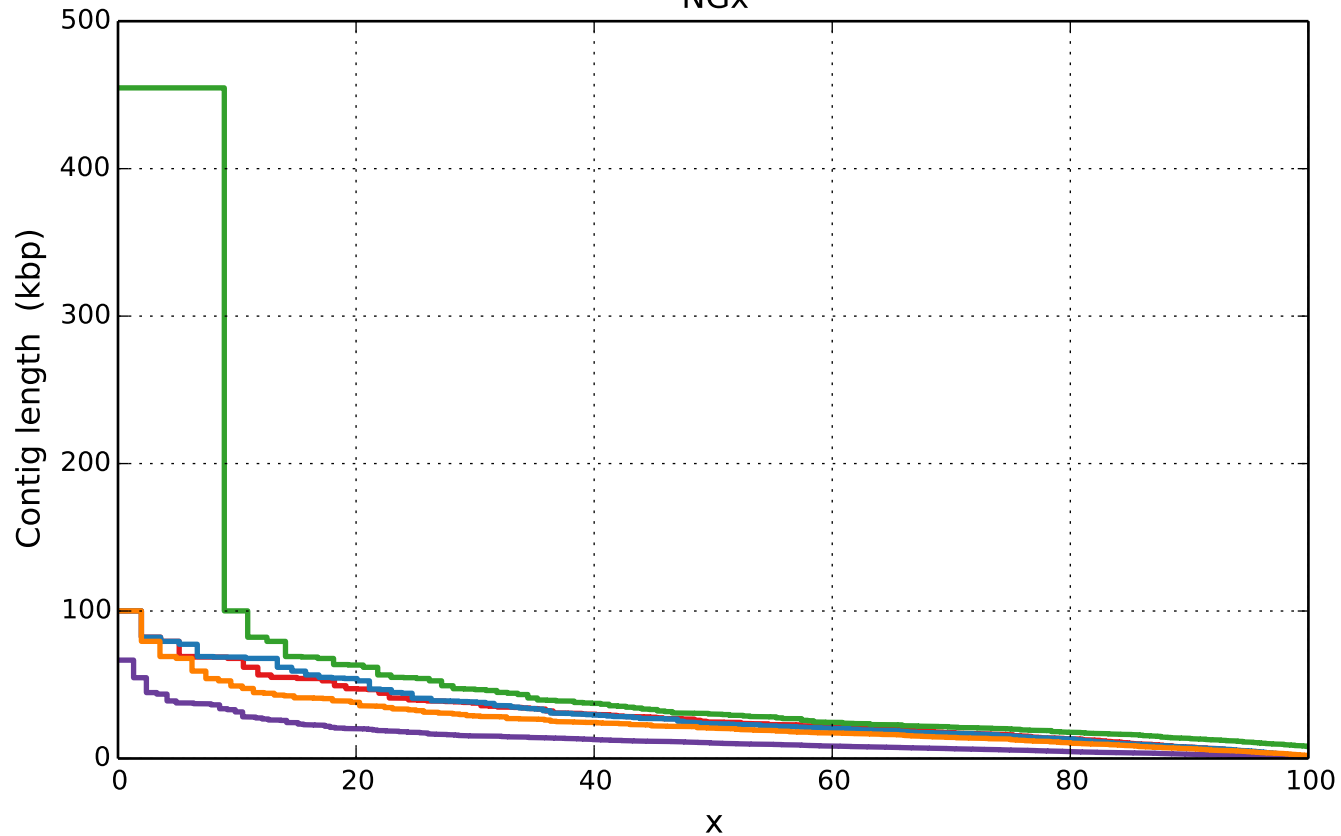
	Gold_Assembly	IDBA_UD	Ray	SOAPdenovo2	SPAdes
# fully unaligned contigs	0	0	0	0	0
Fully unaligned length	0	0	0	0	0
# partially unaligned contigs	0	25	3	15	106
# with misassembly	0	0	1	0	0
# both parts are significant	0	14	3	1	38
Partially unaligned length	0	48244	511546	1827	124176
# N's	0	0	88	883	0

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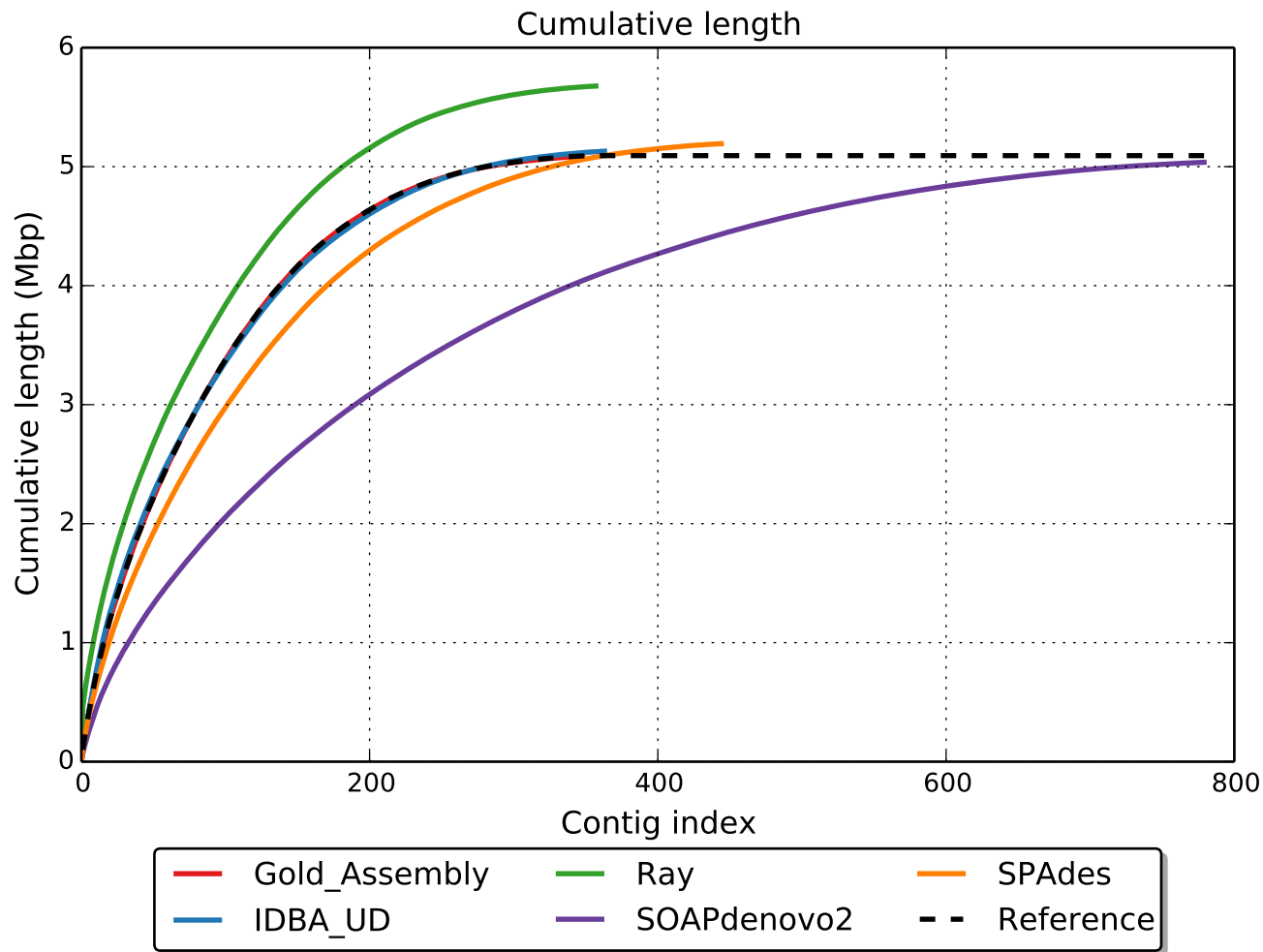
Nx



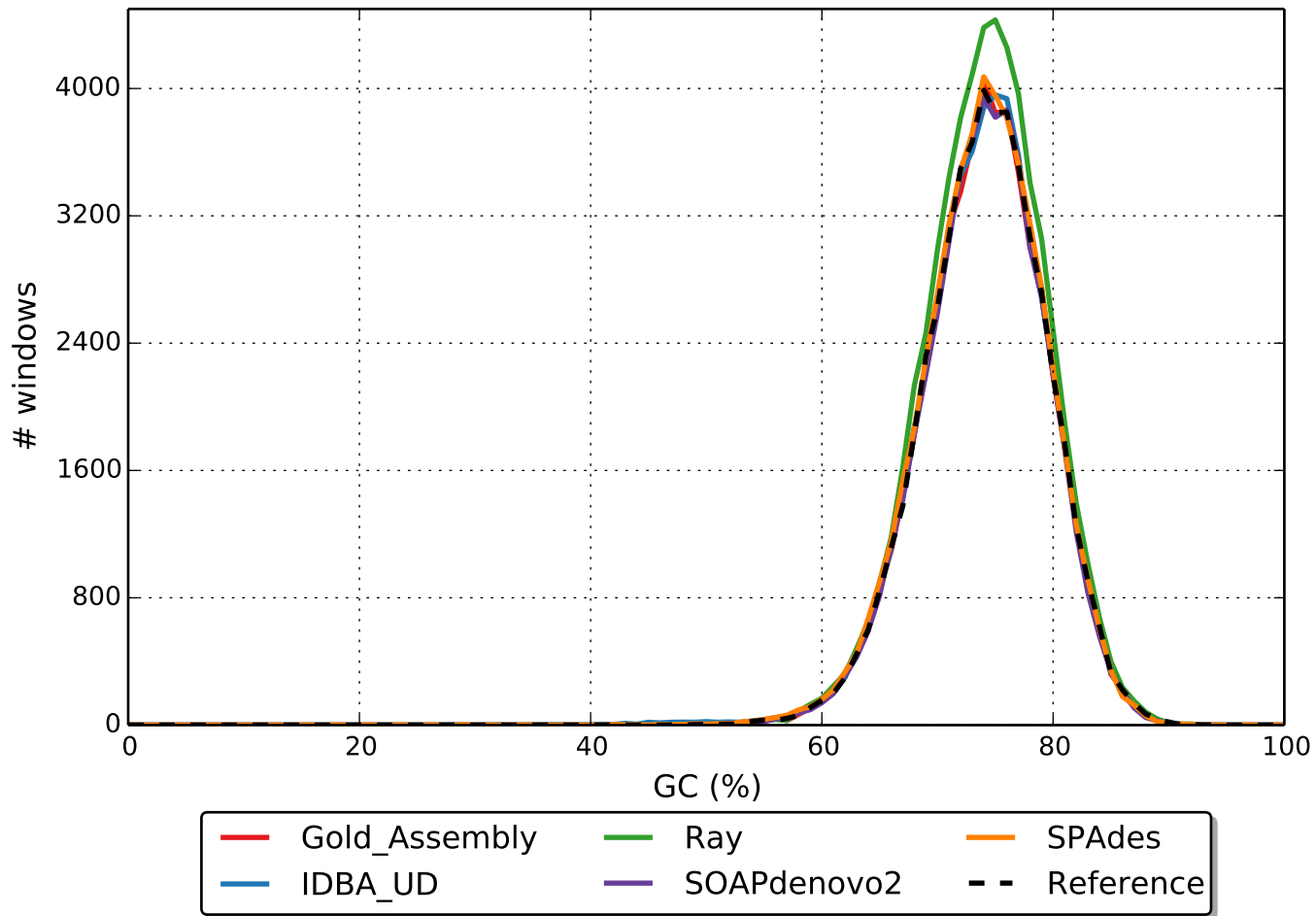
NGx



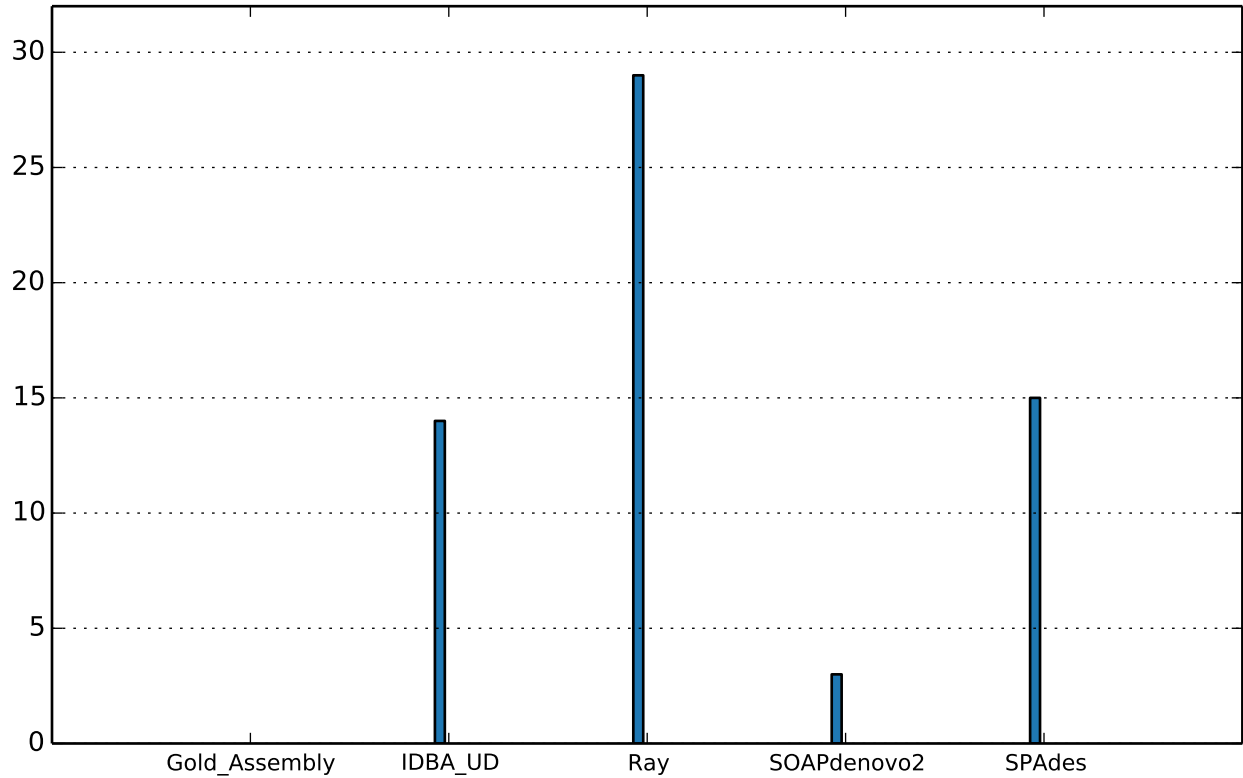
Gold_Assembly Ray SPAdes
IDBA_UD SOAPdenovo2



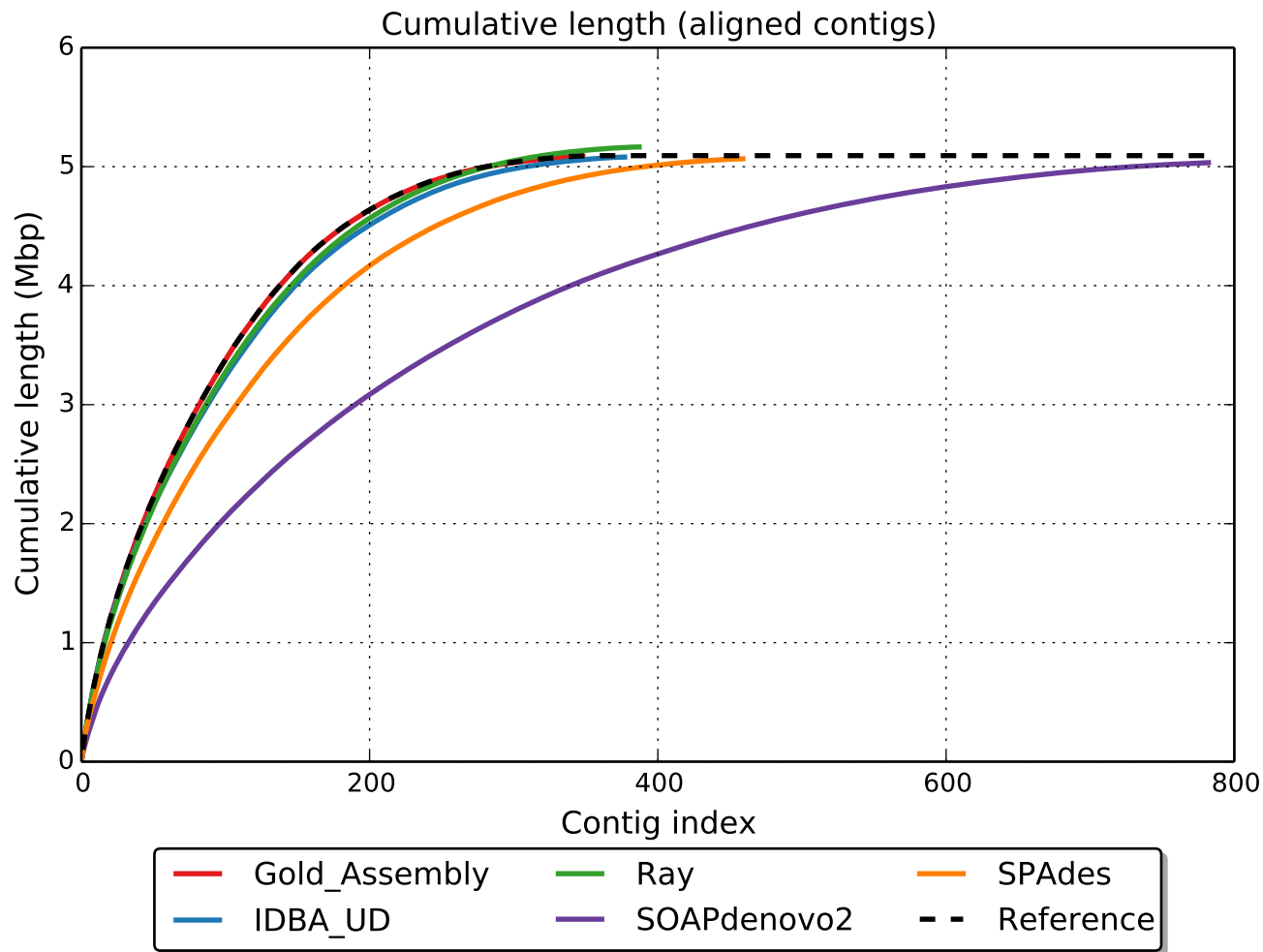
GC content



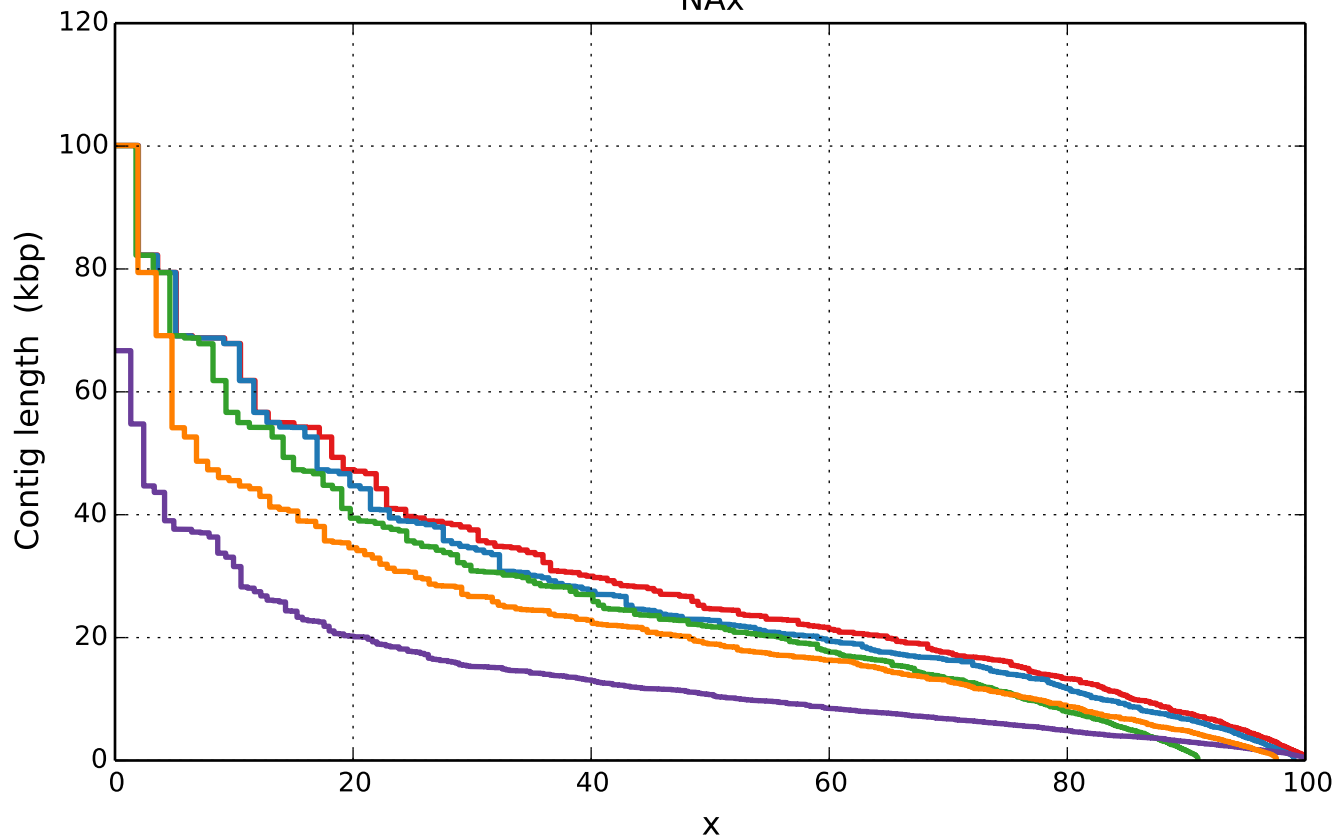
Misassemblies



 # translocations



NAx



NGAx

