

# Report

	Gold_Assembly	IDBA_UD	Ray	SOAPdenovo2	SPAdes
# contigs (>= 1000 bp)	411	1429	391	1996	1566
# contigs (>= 5000 bp)	293	311	0	10	273
# contigs (>= 10000 bp)	195	43	0	0	39
# contigs (>= 25000 bp)	71	1	0	0	1
# contigs (>= 50000 bp)	12	0	0	0	0
Total length (>= 1000 bp)	5912170	5237871	494190	3557238	5226688
Total length (>= 5000 bp)	5583738	2387794	0	59178	2077816
Total length (>= 10000 bp)	4860409	555086	0	0	540268
Total length (>= 25000 bp)	2885765	28881	0	0	49165
Total length (>= 50000 bp)	861752	0	0	0	0
# contigs	447	1690	3041	3891	1978
Largest contig	143040	28881	3154	7658	49165
Total length	5938654	5431012	2264306	4907211	5533131
Reference length	5961098	5961098	5961098	5961098	5961098
GC (%)	64.24	64.10	64.39	64.18	64.28
Reference GC (%)	64.23	64.23	64.23	64.23	64.23
N50	24106	4554	733	1465	4019
NG50	24106	4184	-	1218	3746
N75	12862	2644	599	940	2277
NG75	12835	2157	-	657	1912
L50	75	380	1149	1081	427
LG50	75	441	-	1476	482
L75	160	766	2005	2124	882
LG75	162	932	-	3128	1036
# misassemblies	0	36	1	4	11
# misassembled contigs	0	36	1	4	11
Misassembled contigs length	0	205128	986	6015	69419
# local misassemblies	0	3	3	0	1
# structural variations	0	0	0	0	0
# unaligned contigs	0 + 0 part	0 + 127 part	0 + 0 part	0 + 18 part	0 + 155 part
Unaligned length	0	92351	0	1557	158368
Genome fraction (%)	99.623	88.737	37.819	82.055	89.276
Duplication ratio	1.000	1.009	1.004	1.003	1.010
# N's per 100 kbp	0.00	0.00	5.79	99.16	35.06
# mismatches per 100 kbp	0.00	102.61	1.38	178.35	292.42
# indels per 100 kbp	0.00	2.78	0.00	35.65	4.08
Largest alignment	143040	24606	3154	7658	19191
NA50	24106	4375	733	1464	3786
NGA50	24106	4021	-	1218	3450
NA75	12862	2449	599	938	2068
NGA75	12835	1967	-	655	1710
LA50	75	397	1150	1082	458
LGA50	75	461	-	1477	518
LA75	160	806	2005	2126	950
LGA75	162	985	-	3133	1120

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	36	1	4	11
# relocations	0	1	0	1	1
# translocations	0	35	1	3	10
# inversions	0	0	0	0	0
# possibly misassembled contigs	0	40	0	0	32
# misassembled contigs	0	36	1	4	11
Misassembled contigs length	0	205128	986	6015	69419
# local misassemblies	0	3	3	0	1
# structural variations	0	0	0	0	0
# mismatches	0	5428	31	8724	15562
# indels	0	147	0	1744	217
# short indels	0	144	0	797	205
# long indels	0	3	0	947	12
Indels length	0	193	0	13253	790

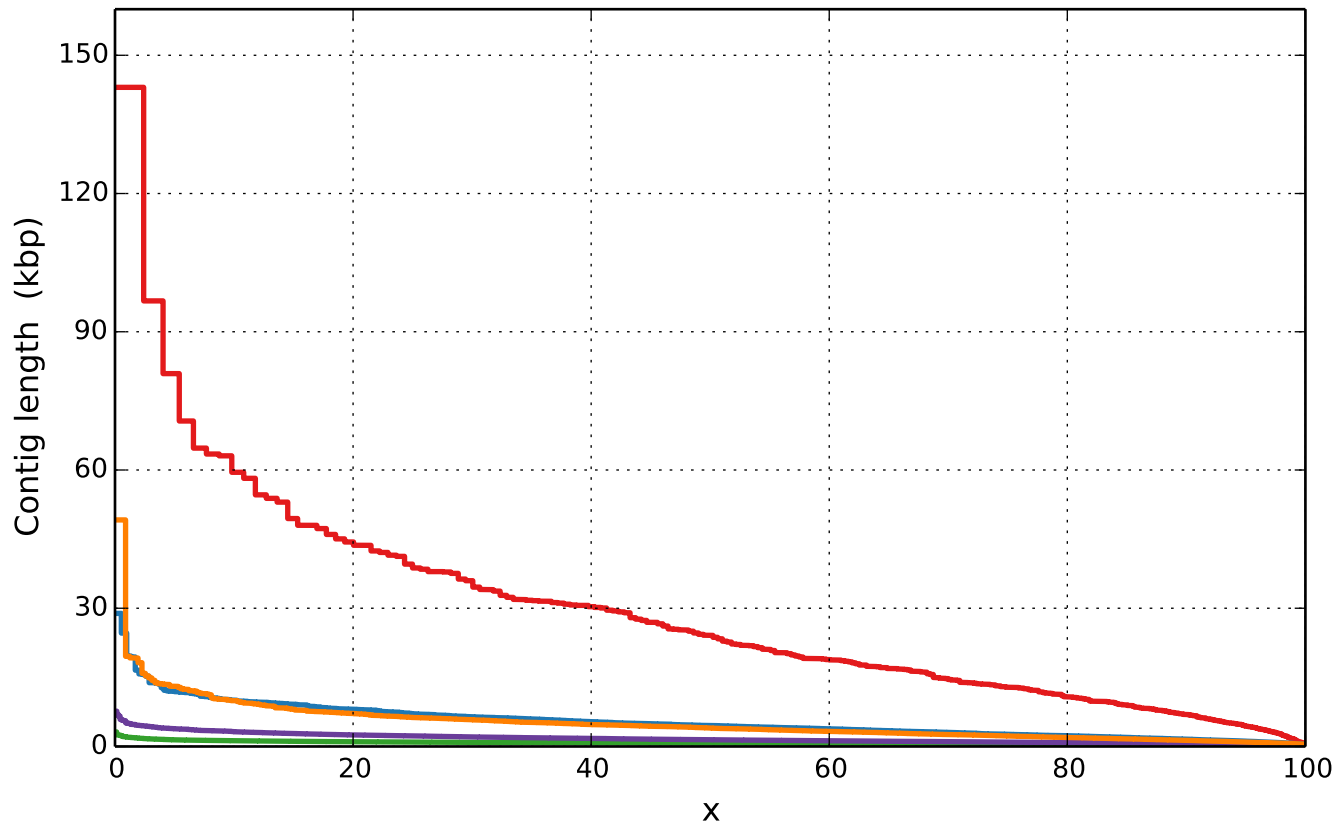
All statistics are based on contigs of size  $\geq 500$  bp, unless otherwise noted (e.g., "# contigs ( $\geq 0$  bp)" and "Total length ( $\geq 0$  bp)" include all contigs).

## Unaligned report

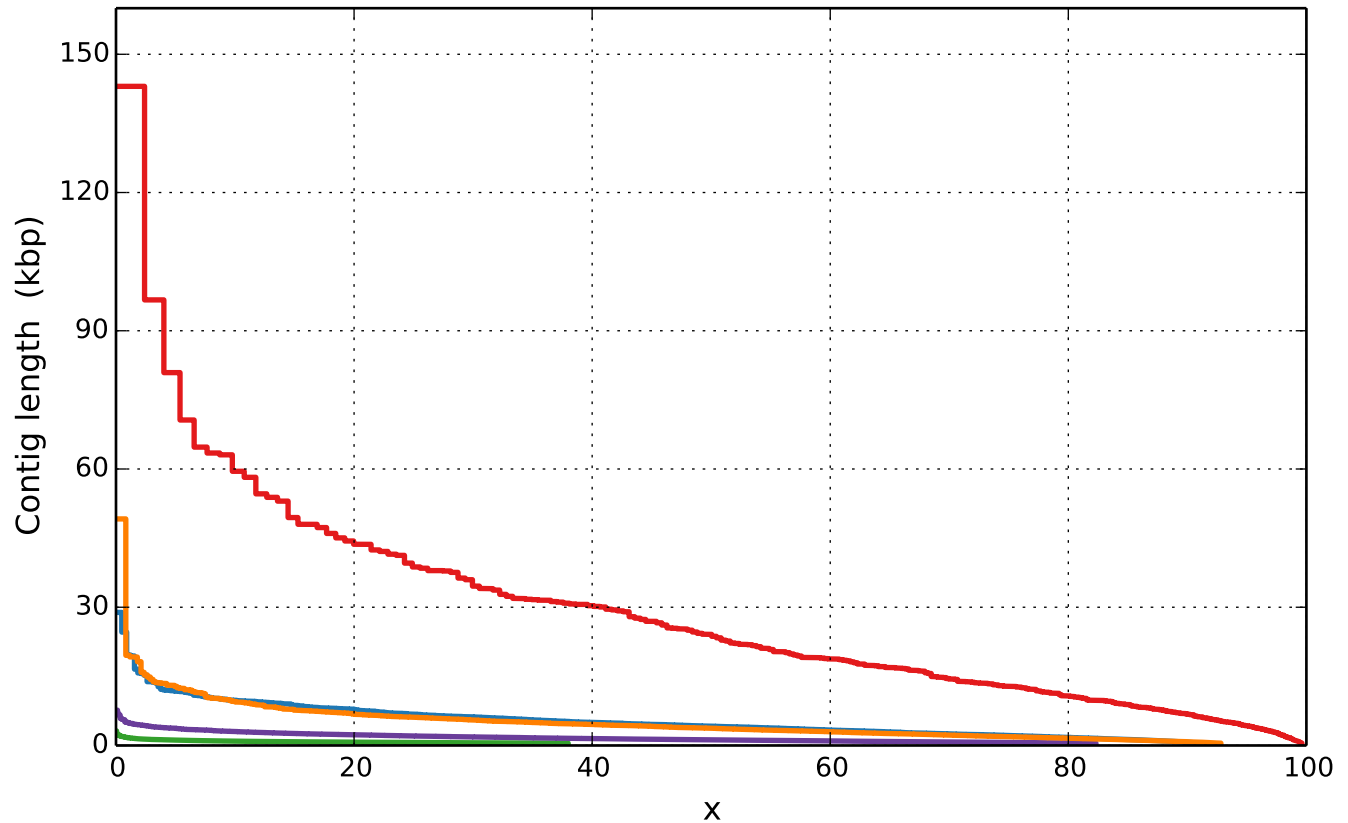
	Gold_Assembly	IDBA_UD	Ray	SOAPdenovo2	SPAdes
# fully unaligned contigs	0	0	0	0	0
Fully unaligned length	0	0	0	0	0
# partially unaligned contigs	0	127	0	18	155
# with misassembly	0	0	0	0	0
# both parts are significant	0	37	0	0	31
Partially unaligned length	0	92351	0	1557	158368
# N's	0	0	131	4866	1940

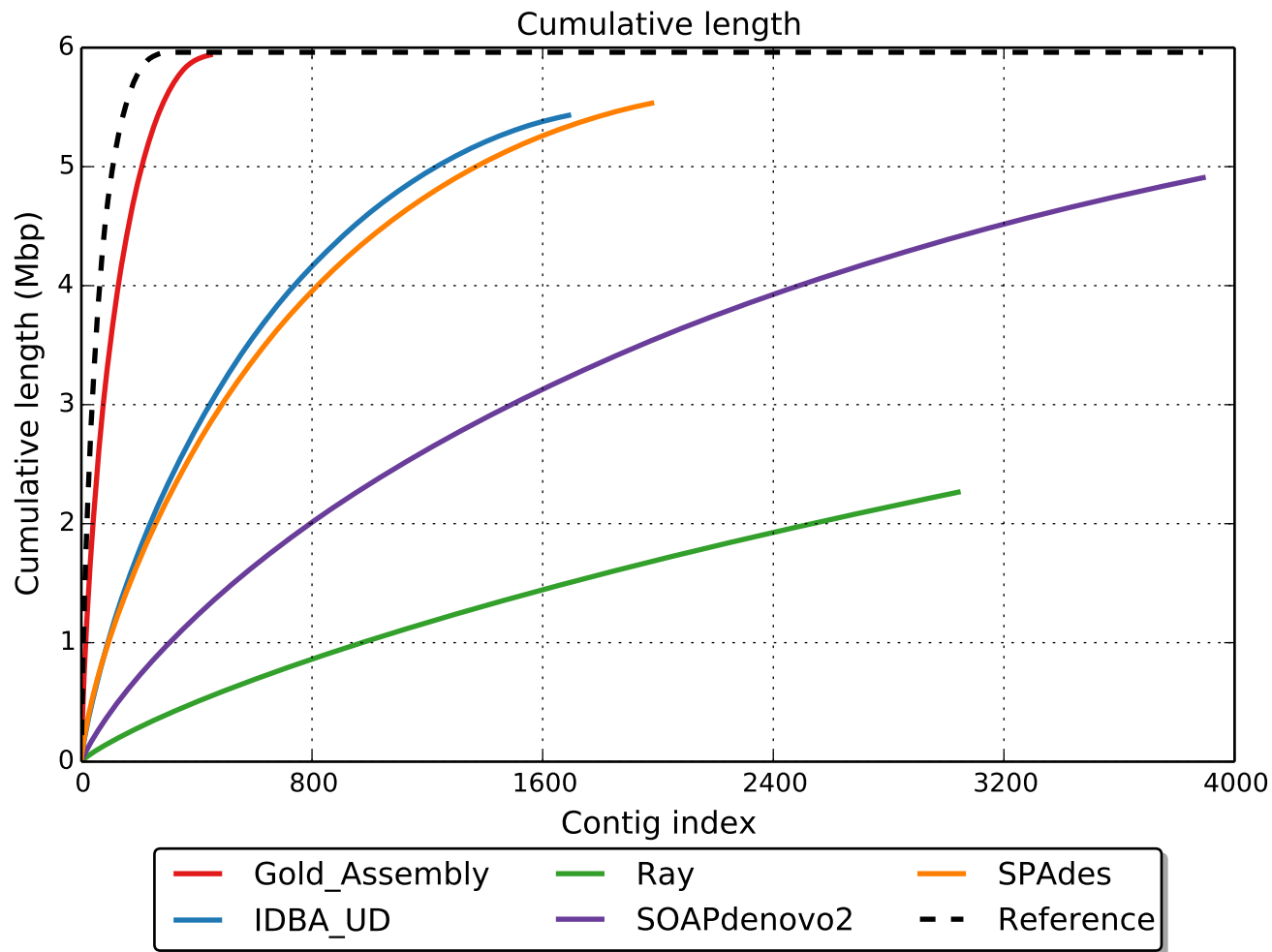
All statistics are based on contigs of size  $\geq 500$  bp, unless otherwise noted (e.g., "# contigs ( $\geq 0$  bp)" and "Total length ( $\geq 0$  bp)" include all contigs).

Nx

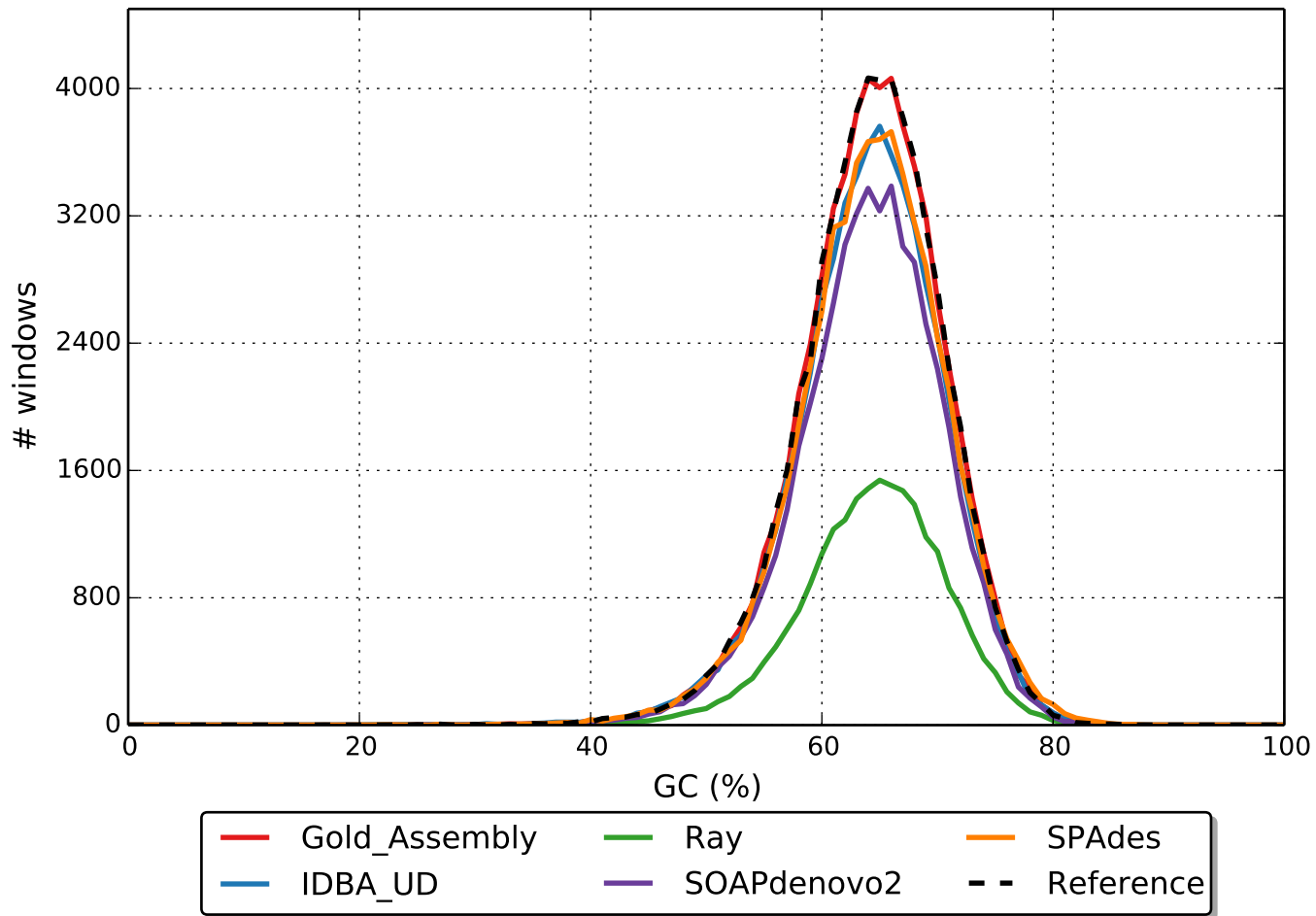


NGx

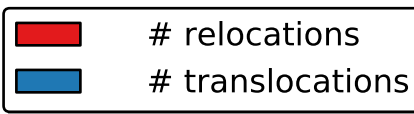
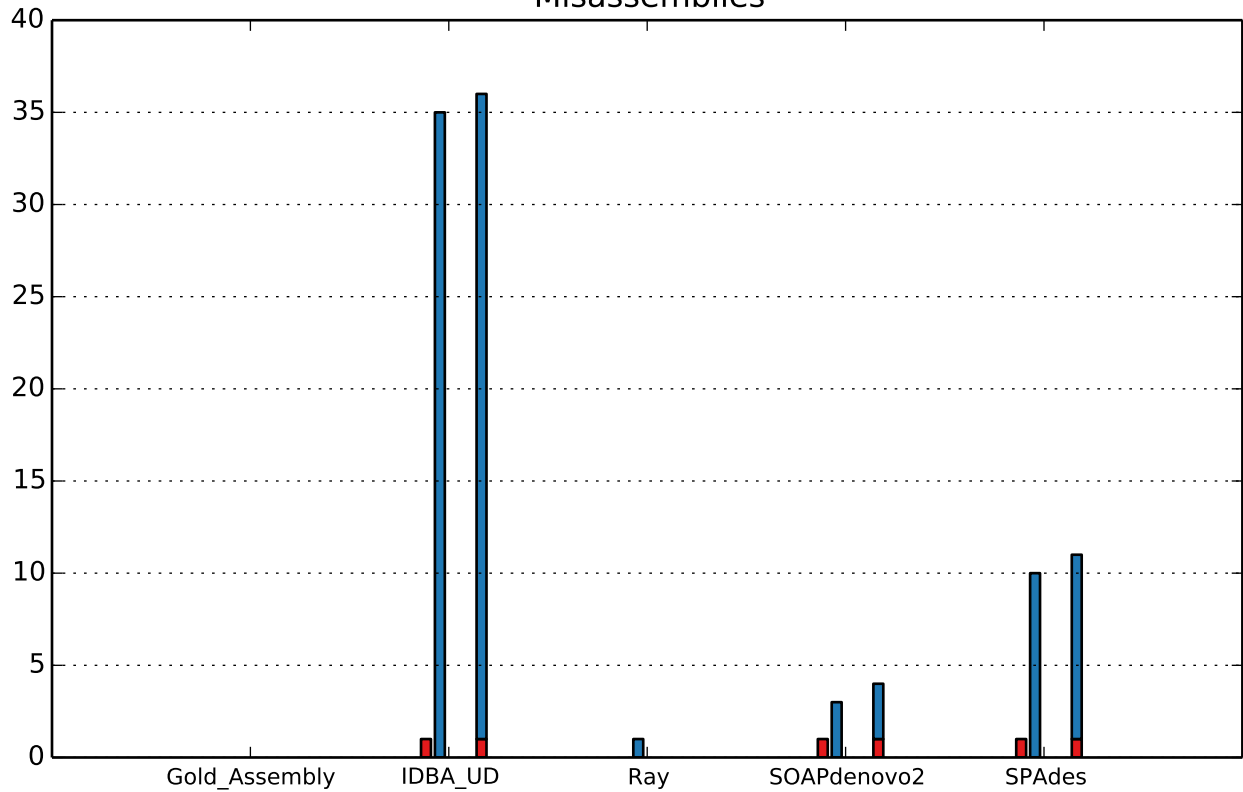




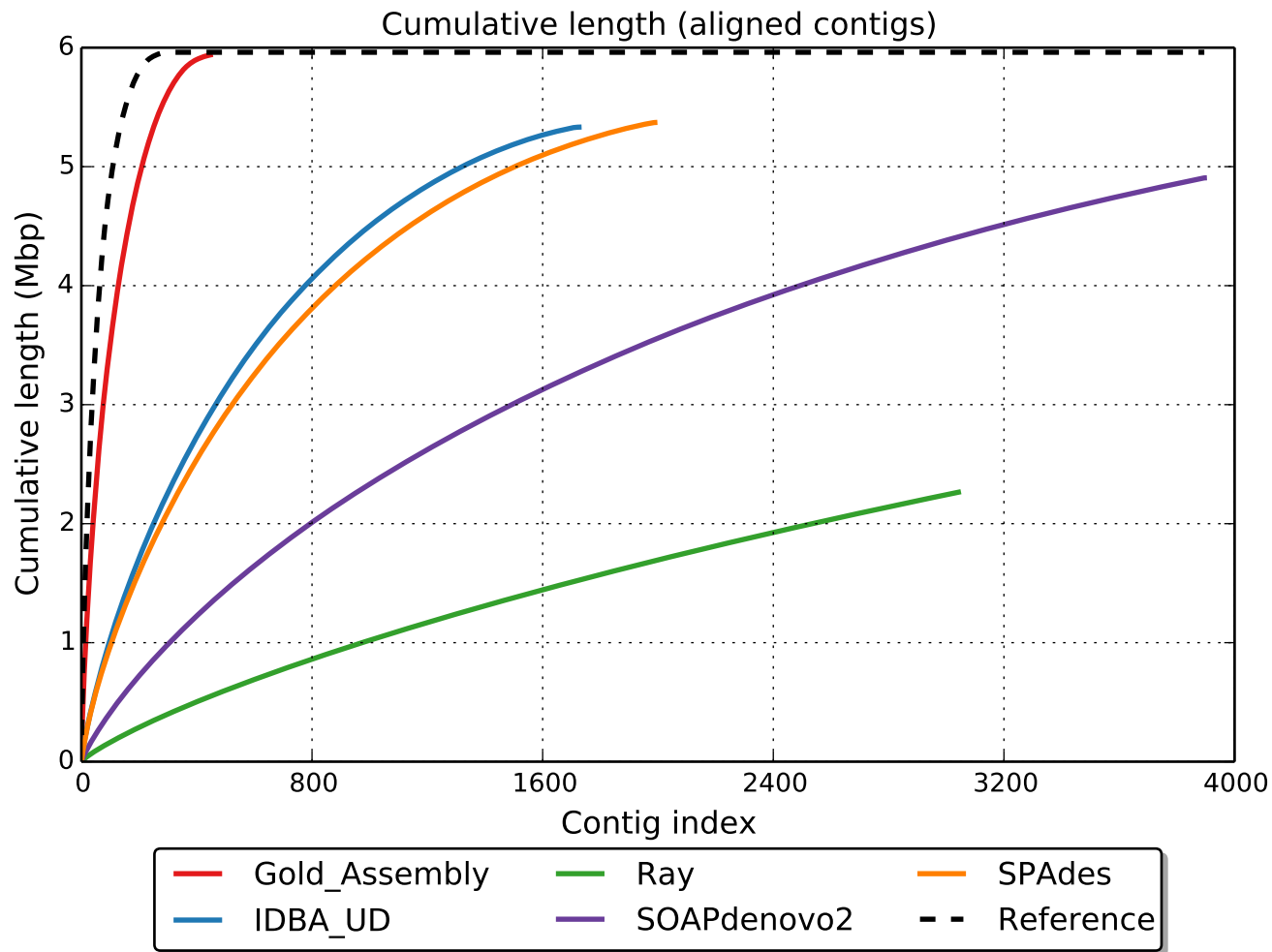
GC content



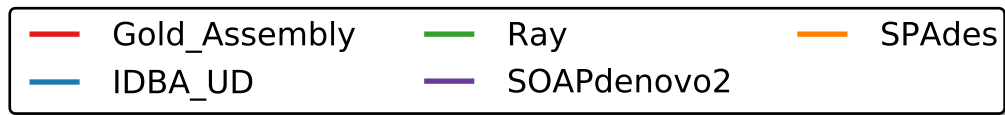
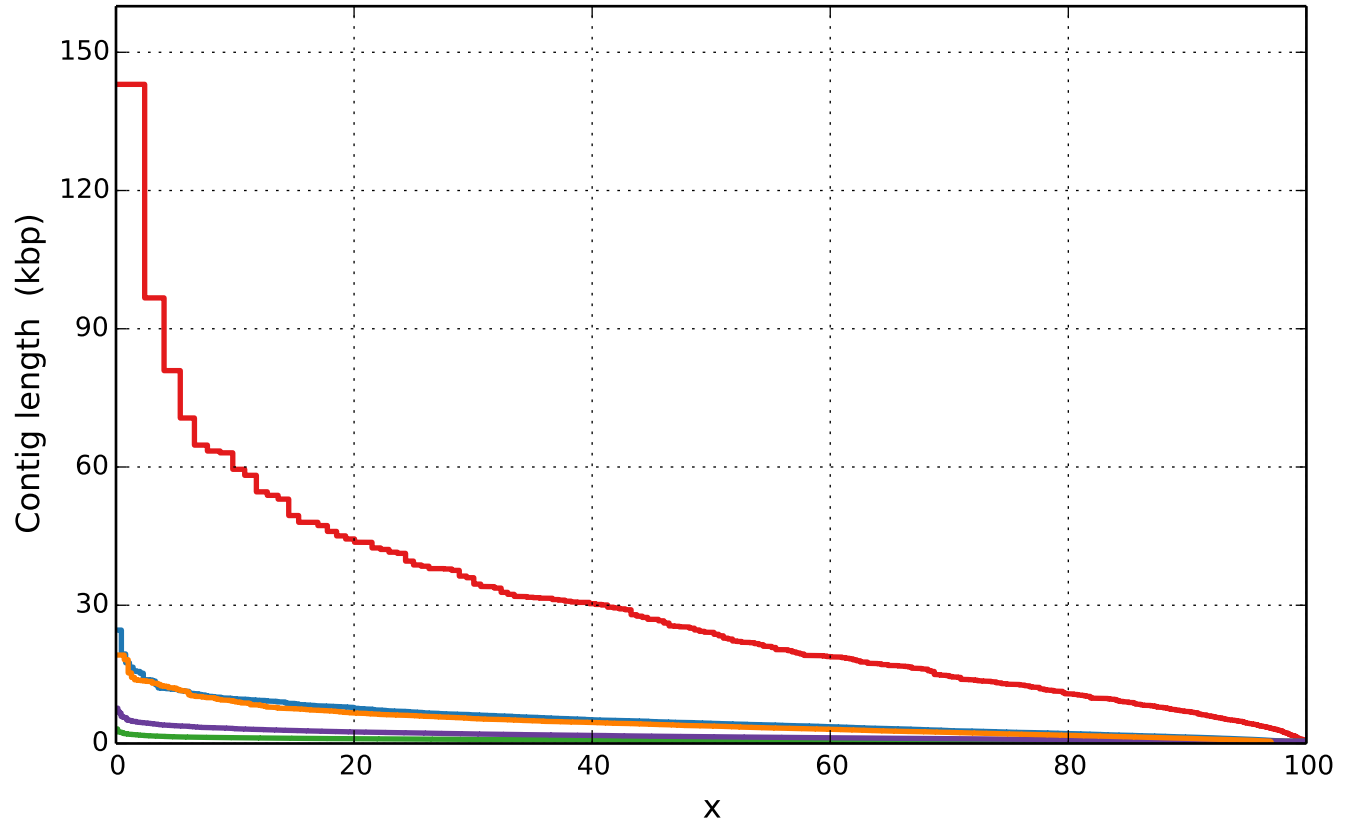
# Misassemblies







NAx



# NGAx

