

Report

	Gold_Assembly	IDBA_UD	Ray	SOAPdenovo2	SPAdes
# contigs (>= 1000 bp)	47	44	44	344	47
# contigs (>= 5000 bp)	32	31	32	35	30
# contigs (>= 10000 bp)	28	26	30	3	25
# contigs (>= 25000 bp)	22	20	22	0	19
# contigs (>= 50000 bp)	13	13	13	0	12
Total length (>= 1000 bp)	1606951	1611413	2016433	927281	1620062
Total length (>= 5000 bp)	1572683	1581071	1991032	230381	1581450
Total length (>= 10000 bp)	1542954	1545257	1974224	38960	1542377
Total length (>= 25000 bp)	1450703	1453028	1845971	0	1450602
Total length (>= 50000 bp)	1105604	1185450	1510536	0	1181921
# contigs	67	61	60	488	65
Largest contig	154049	154002	266465	14975	168892
Total length	1619610	1622594	2026629	1035413	1631808
Reference length	1761763	1761763	1761763	1761763	1761763
GC (%)	37.49	37.48	37.49	37.82	37.50
Reference GC (%)	37.35	37.35	37.35	37.35	37.35
N50	63907	70462	99633	2829	80163
NG50	63337	67838	111746	1191	72347
N75	41295	49729	49728	1709	49732
NG75	37911	40545	70460	-	35539
L50	9	8	7	112	7
LG50	10	9	6	302	8
L75	16	14	14	229	13
LG75	18	16	11	-	16
# misassemblies	40	37	32	14	25
# misassembled contigs	16	14	14	13	12
Misassembled contigs length	981069	941173	976169	43008	856190
# local misassemblies	5	5	9	0	5
# structural variations	7	7	8	1	7
# unaligned contigs	0 + 12 part	0 + 12 part	0 + 12 part	0 + 38 part	0 + 19 part
Unaligned length	310542	317084	510069	35205	396523
Genome fraction (%)	63.565	63.551	64.277	56.368	63.608
Duplication ratio	1.169	1.166	1.339	1.007	1.102
# N's per 100 kbp	0.00	0.00	0.94	0.00	28.13
# mismatches per 100 kbp	2751.86	2755.30	2803.13	2198.42	2758.02
# indels per 100 kbp	39.47	39.57	39.38	22.46	39.89
Largest alignment	69847	121441	94744	14975	121441
NA50	15186	15551	20376	2615	15551
NGA50	12802	12802	25462	963	13208
NA75	-	-	-	1451	-
NGA75	-	-	2810	-	-
LA50	23	21	23	120	20
LGA50	28	26	18	339	24
LA75	-	-	-	252	-
LGA75	-	-	60	-	-

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

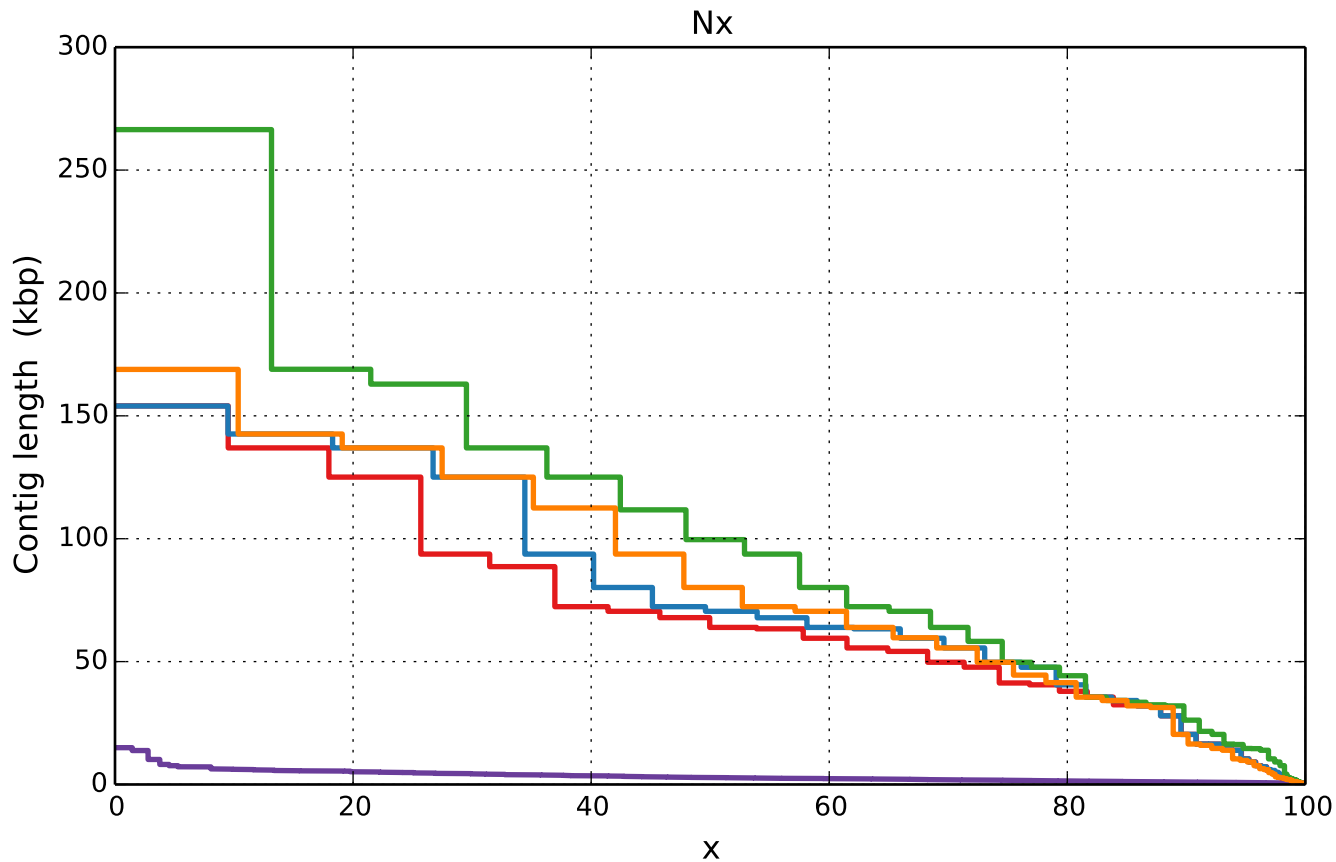
	Gold_Assembly	IDBA_UD	Ray	SOAPdenovo2	SPAdes
# misassemblies	40	37	32	14	25
# relocations	13	12	11	2	7
# translocations	25	25	20	12	18
# inversions	2	0	1	0	0
# possibly misassembled contigs	25	24	25	18	26
# misassembled contigs	16	14	14	13	12
Misassembled contigs length	981069	941173	976169	43008	856190
# local misassemblies	5	5	9	0	5
# structural variations	7	7	8	1	7
# mismatches	30817	30849	31743	21832	30907
# indels	442	443	446	223	447
# short indels	423	427	431	219	428
# long indels	19	16	15	4	19
Indels length	732	691	754	316	738

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).

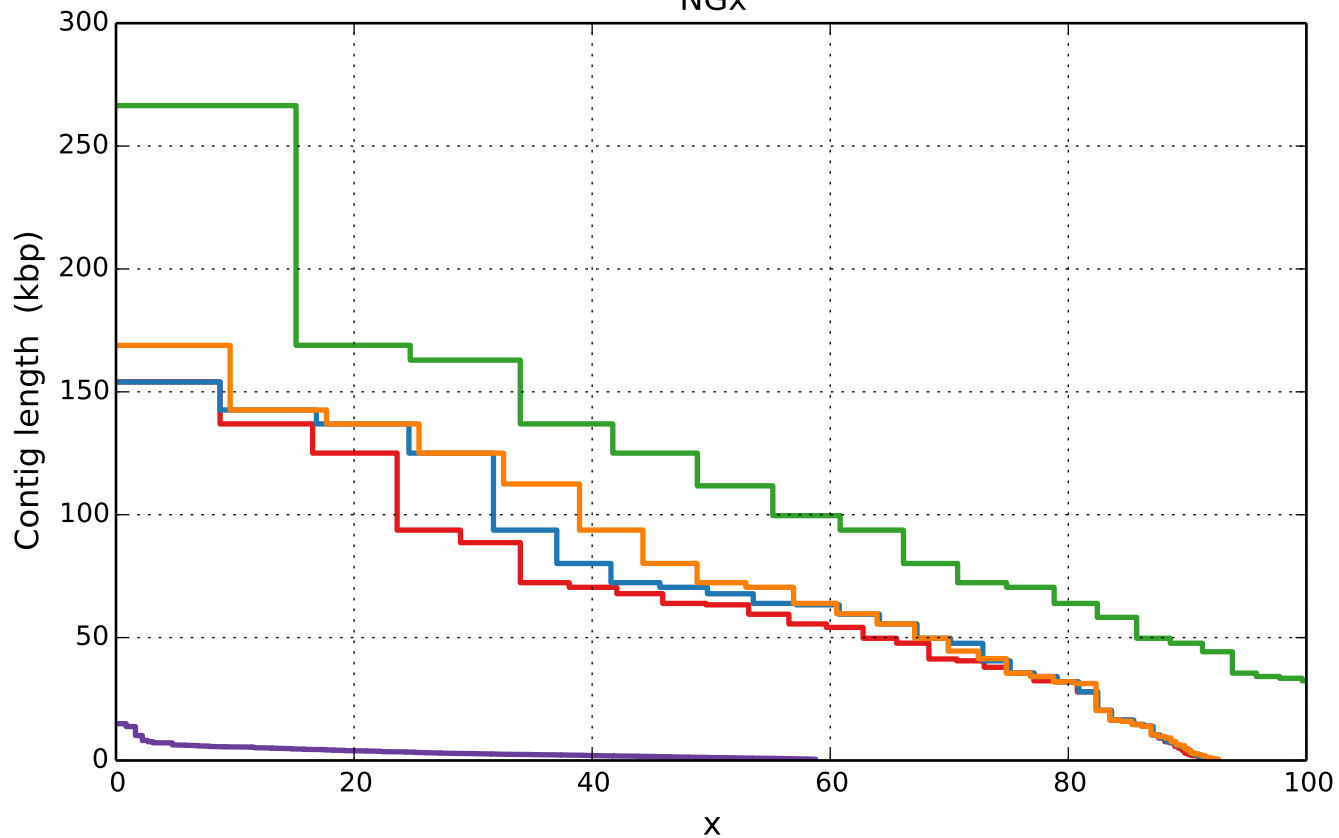
Unaligned report

	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	12	12	12	38	19
# with misassembly	3	3	4	0	4
# both parts are significant	10	11	11	14	13
Partially unaligned length	310542	317084	510069	35205	396523
# N's	0	0	19	0	459

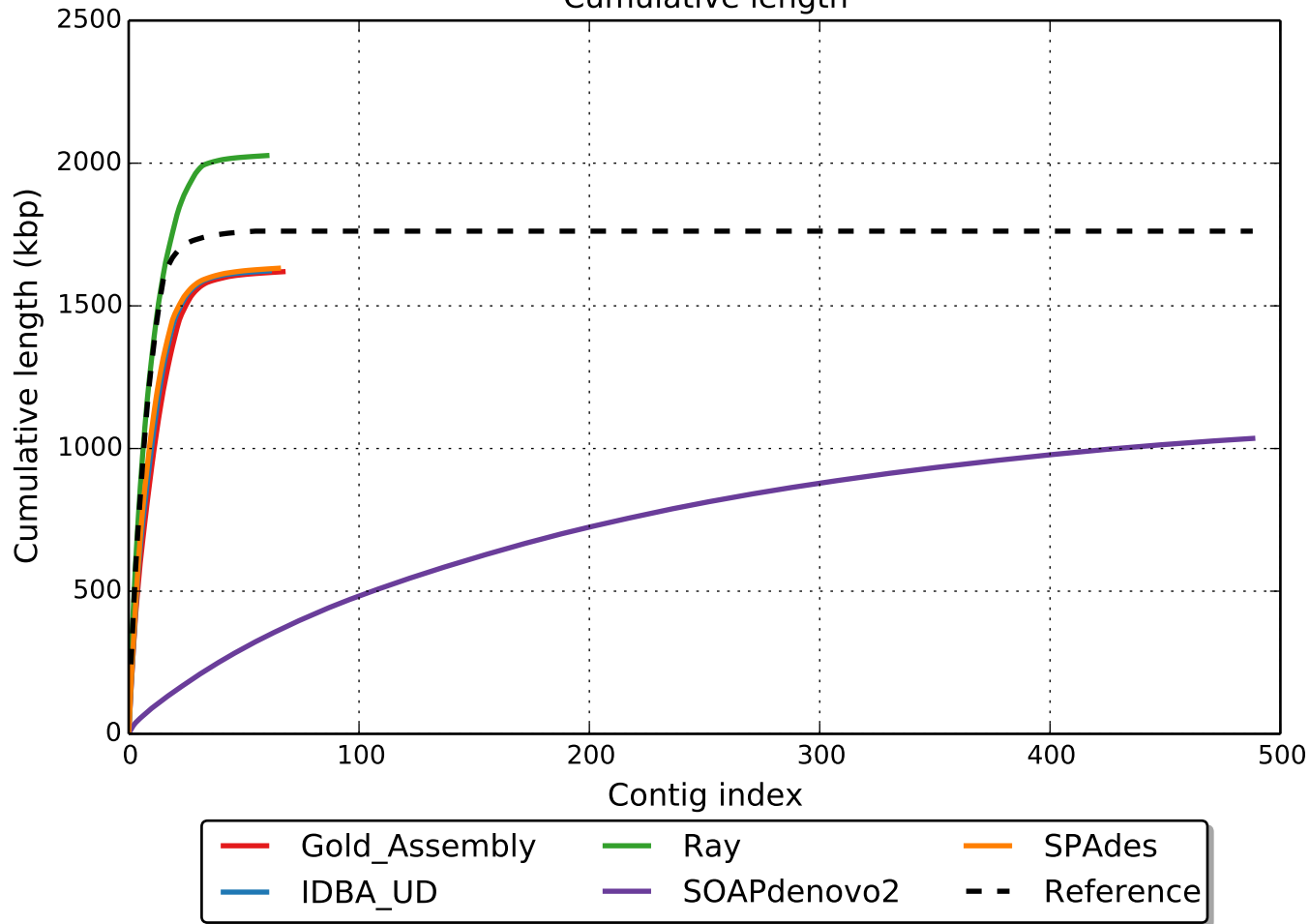
All statistics are based on contigs of size ≥ 500 bp, unless otherwise noted (e.g., "# contigs (≥ 0 bp)" and "Total length (≥ 0 bp)" include all contigs).



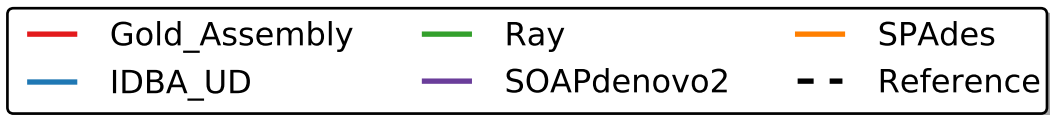
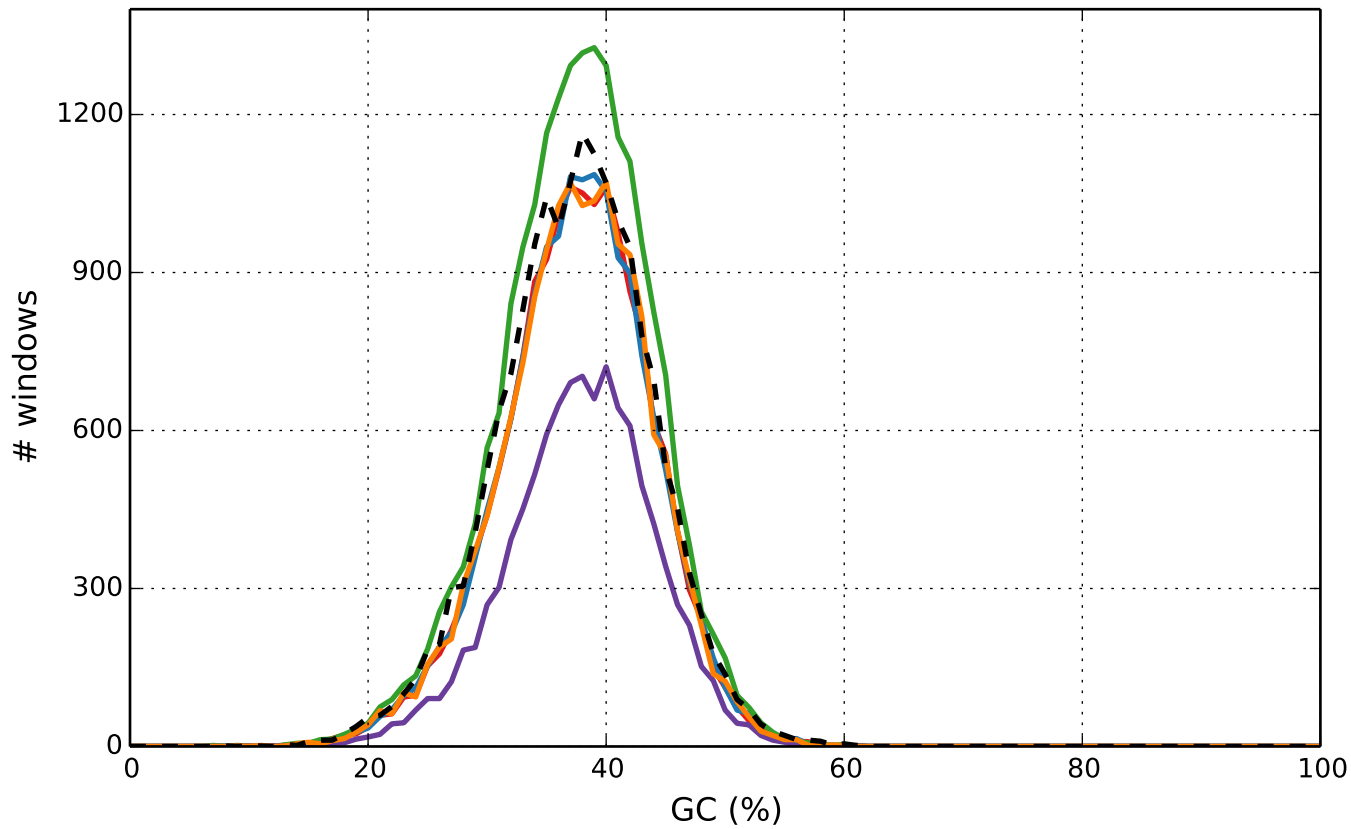
NGx



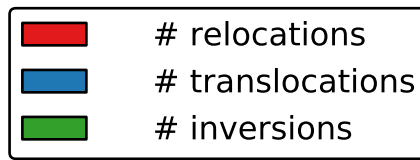
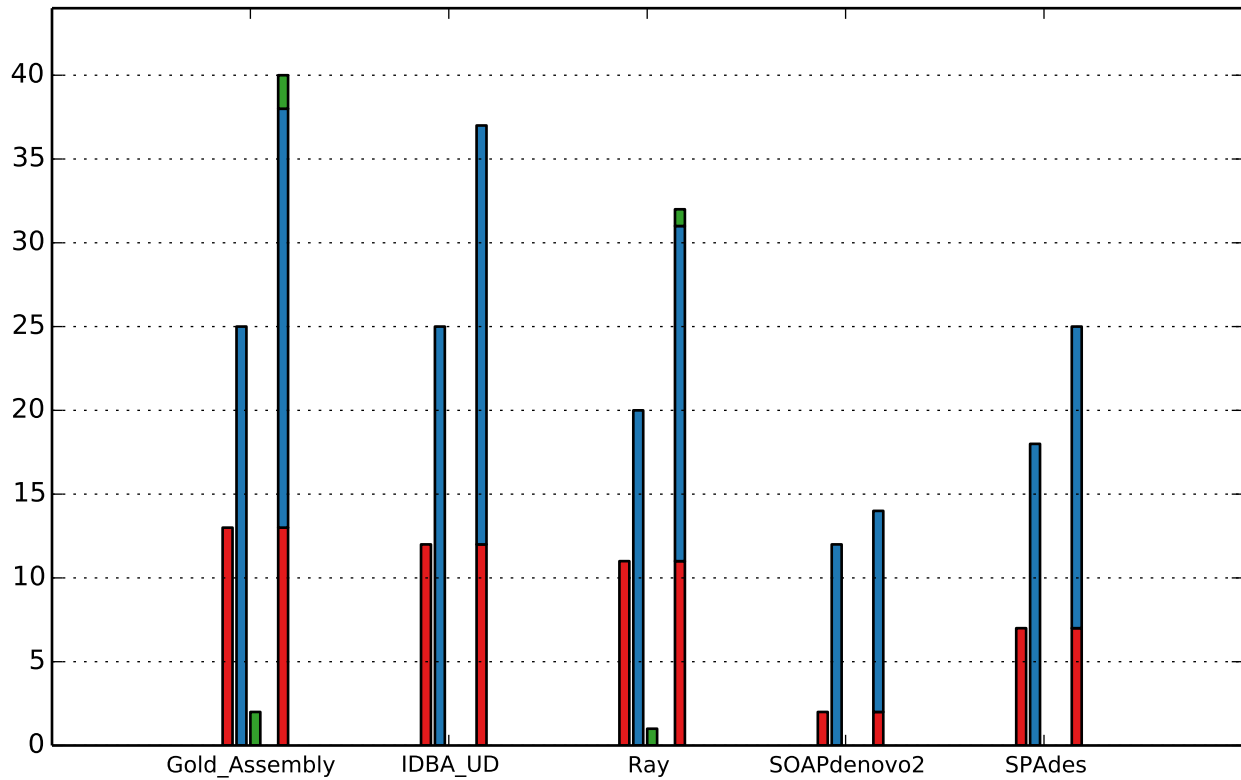
Cumulative length



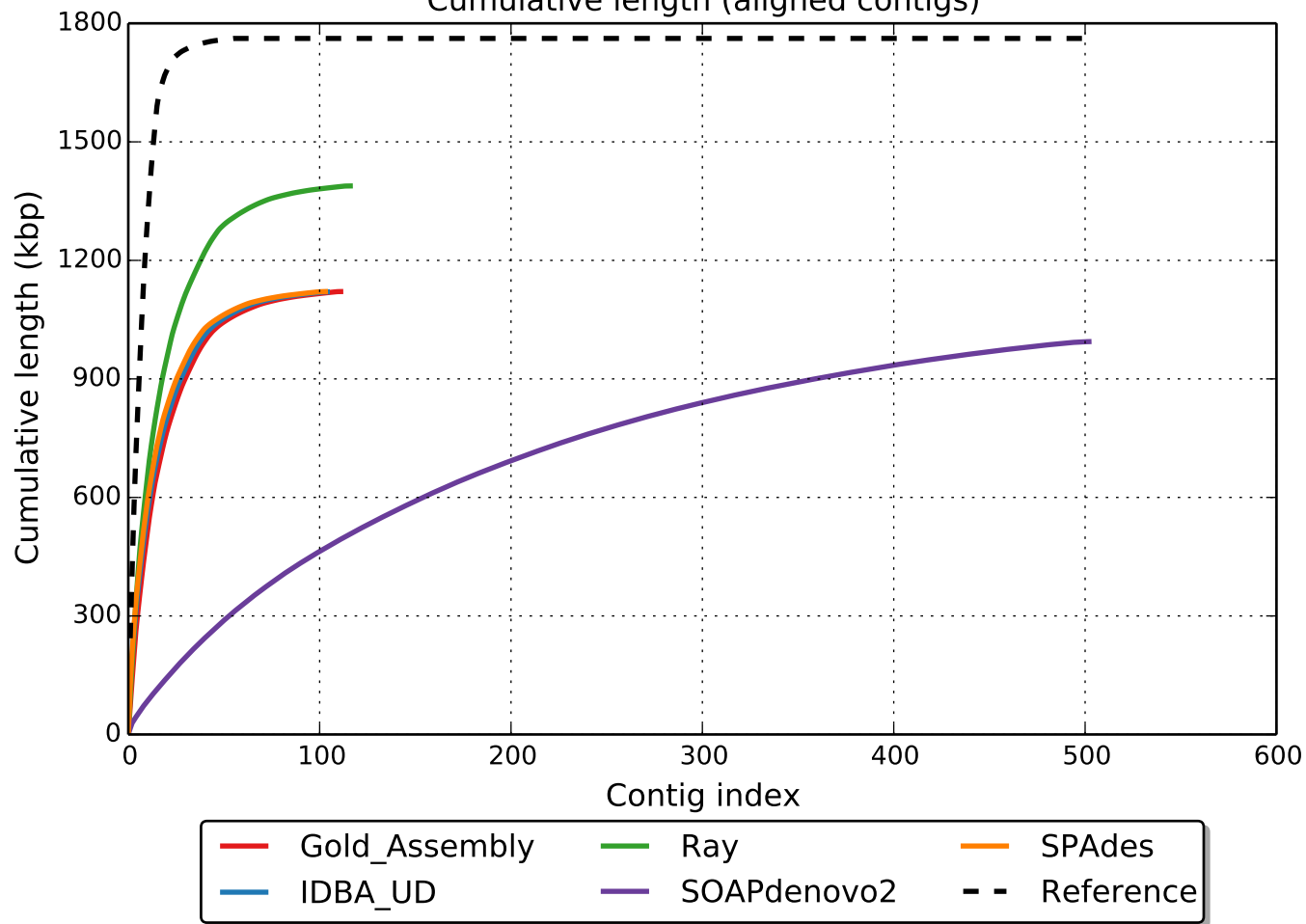
GC content



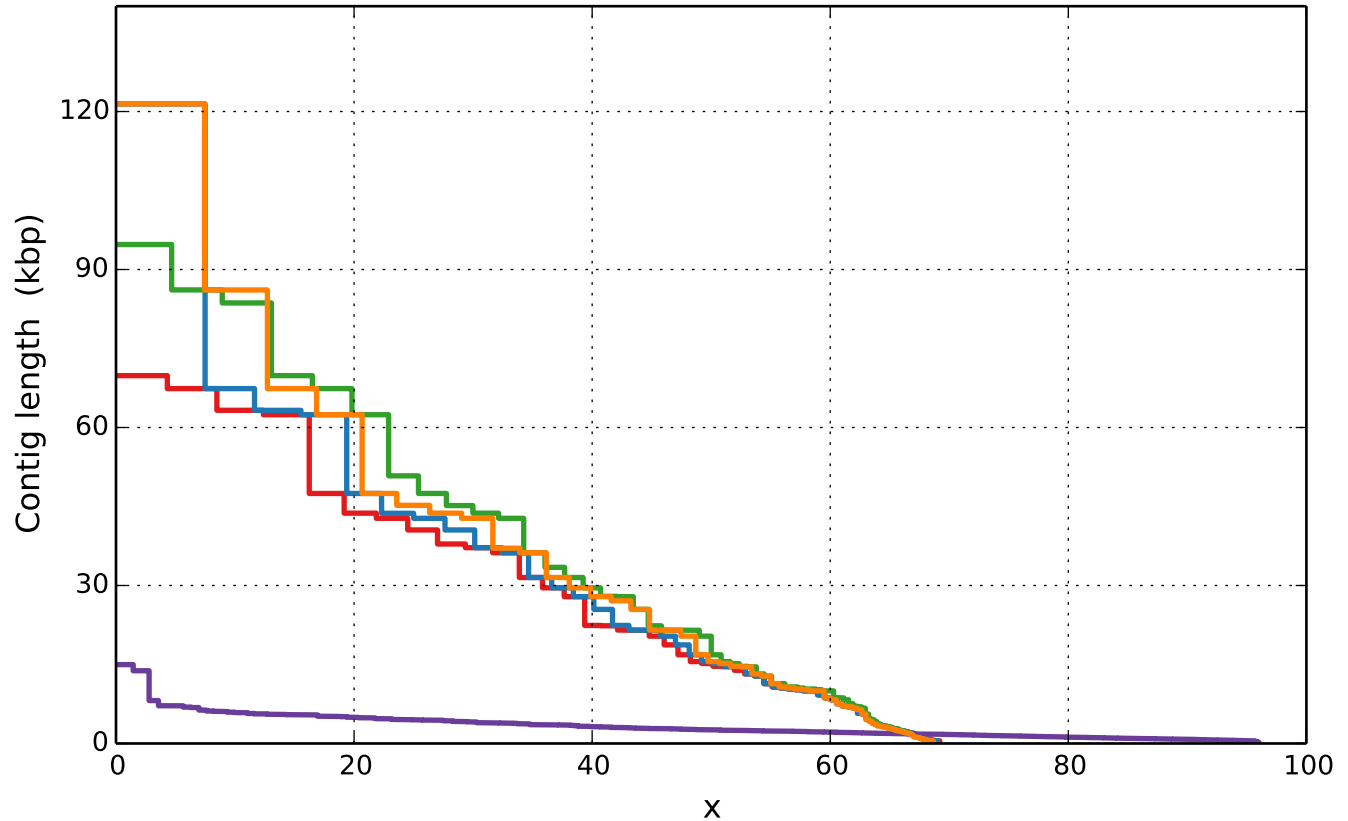
Misassemblies



Cumulative length (aligned contigs)



NAx



NGAx

