

Report

	IDBA_UD	Ray	SOAPdenovo2	SPAdes
# contigs (>= 1000 bp)	275	46	181	183
# contigs (>= 5000 bp)	47	16	9	41
# contigs (>= 10000 bp)	22	5	0	19
# contigs (>= 25000 bp)	8	1	0	10
# contigs (>= 50000 bp)	2	1	0	5
Total length (>= 1000 bp)	1170514	262762	375245	1217460
Total length (>= 5000 bp)	701730	212308	63195	937169
Total length (>= 10000 bp)	531683	134441	0	784924
Total length (>= 25000 bp)	340466	64174	0	646939
Total length (>= 50000 bp)	110238	64174	0	456015
# contigs	508	126	445	325
Largest contig	56613	64174	9065	162985
Total length	1343289	317179	556206	1314995
Reference length	5538248	5538248	5538248	5538248
GC (%)	42.08	42.00	41.24	41.94
Reference GC (%)	41.75	41.75	41.75	41.75
N50	5444	7907	1480	22352
N75	1758	1580	847	3745
L50	42	8	99	11
L75	155	26	226	53
# misassemblies	15	5	0	19
# misassembled contigs	10	4	0	8
Misassembled contigs length	225552	88518	0	533591
# local misassemblies	7	15	54	13
# structural variations	2	1	0	2
# unaligned contigs	0 + 20 part	0 + 14 part	0 + 17 part	0 + 25 part
Unaligned length	114723	41527	17769	95331
Genome fraction (%)	21.194	4.406	9.640	19.112
Duplication ratio	1.047	1.130	1.009	1.152
# N's per 100 kbp	89.04	1256.07	561.12	251.03
# mismatches per 100 kbp	1122.44	1935.17	927.55	1628.07
# indels per 100 kbp	43.96	42.62	19.67	59.90
Largest alignment	47708	26811	9065	43412
NA50	3112	1661	1339	5148
NGA50	-	-	-	-
NA75	981	546	790	851
LA50	85	22	106	46
LA75	282	114	243	219

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

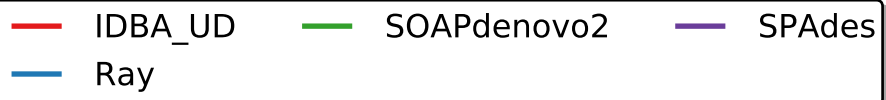
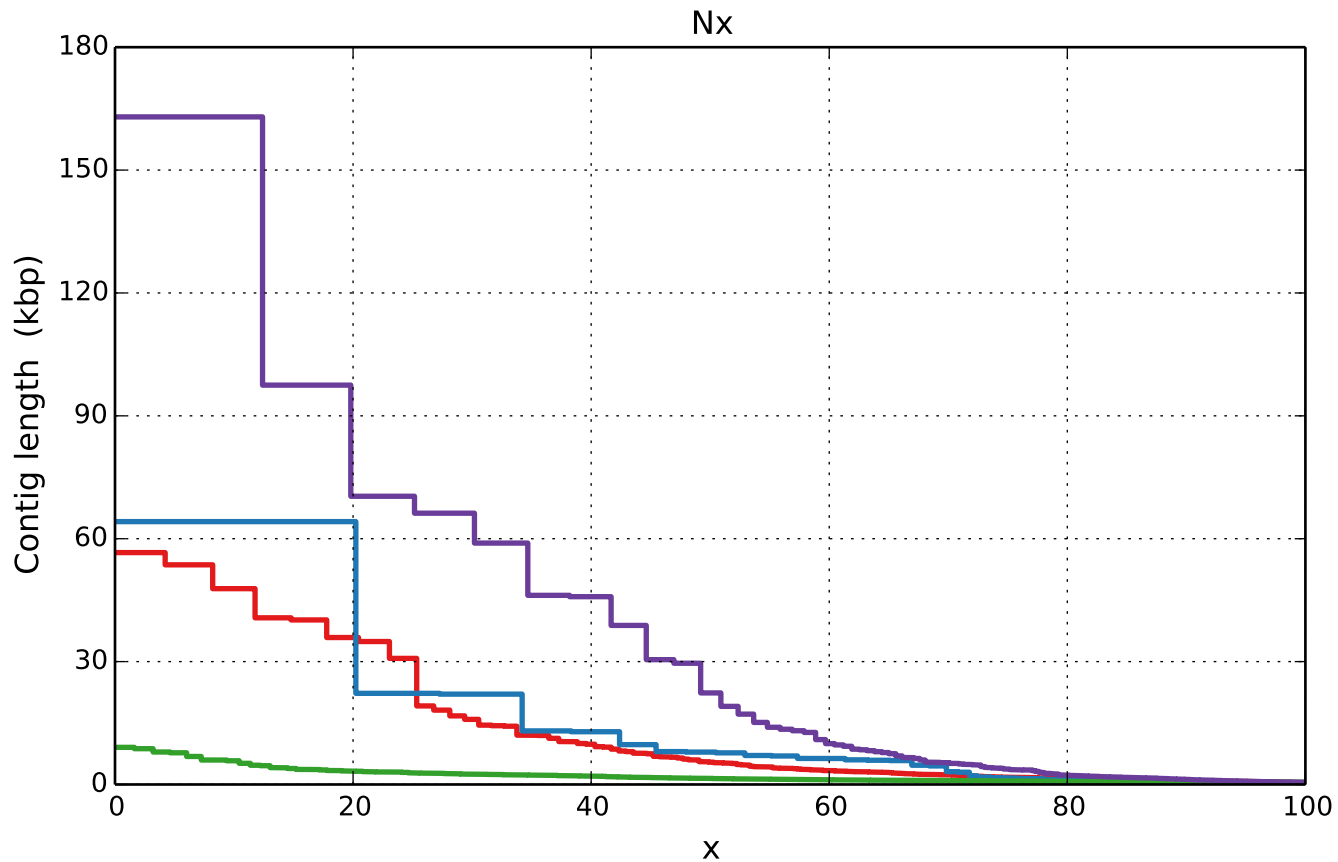
	IDBA_UD	Ray	SOAPdenovo2	SPAdes
# misassemblies	15	5	0	19
# relocations	8	4	0	13
# translocations	7	1	0	5
# inversions	0	0	0	1
# possibly misassembled contigs	14	10	3	17
# misassembled contigs	10	4	0	8
Misassembled contigs length	225552	88518	0	533591
# local misassemblies	7	15	54	13
# structural variations	2	1	0	2
# mismatches	13175	4722	4952	17233
# indels	516	104	105	634
# short indels	461	95	97	529
# long indels	55	9	8	105
Indels length	1369	273	205	1937

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).

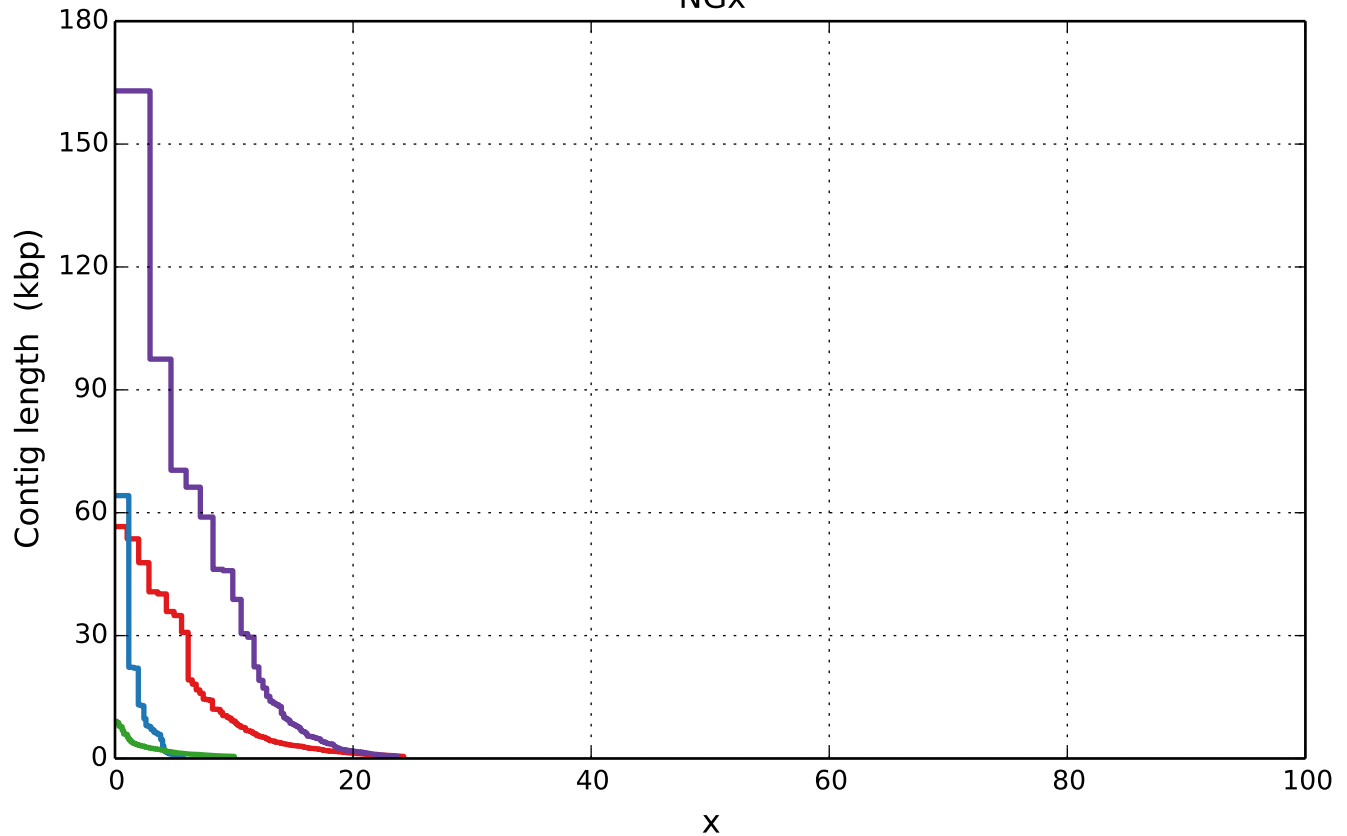
Unaligned report

	IDBA_UD	Ray	SOAPdenovo2	SPAdes
# fully unaligned contigs	0	0	0	0
Fully unaligned length	0	0	0	0
# partially unaligned contigs	20	14	17	25
# with misassembly	4	4	3	4
# both parts are significant	7	6	2	9
Partially unaligned length	114723	41527	17769	95331
# N's	1196	3984	3121	3301

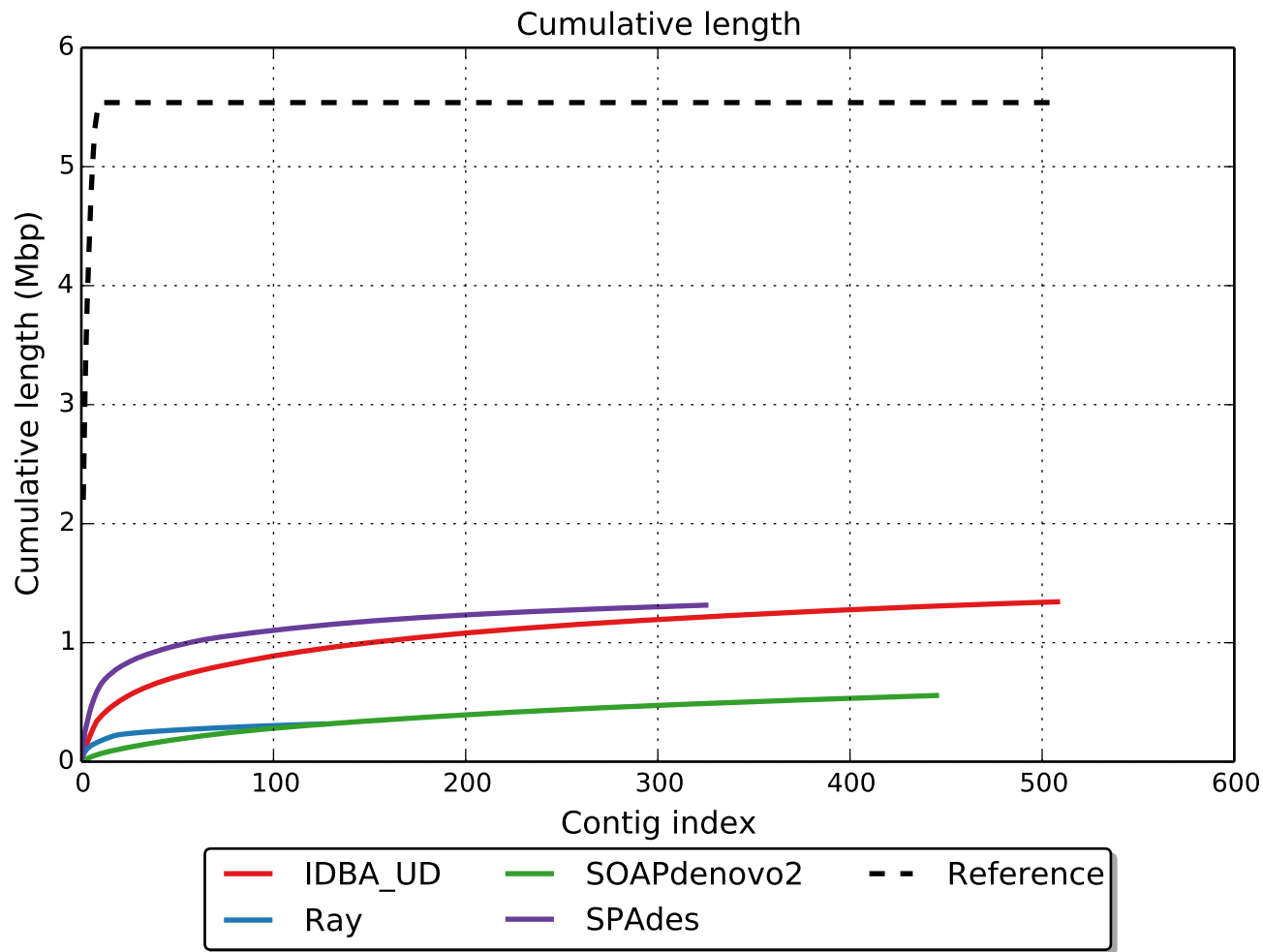
All statistics are based on contigs of size ≥ 500 bp, unless otherwise noted (e.g., "# contigs (≥ 0 bp)" and "Total length (≥ 0 bp)" include all contigs).



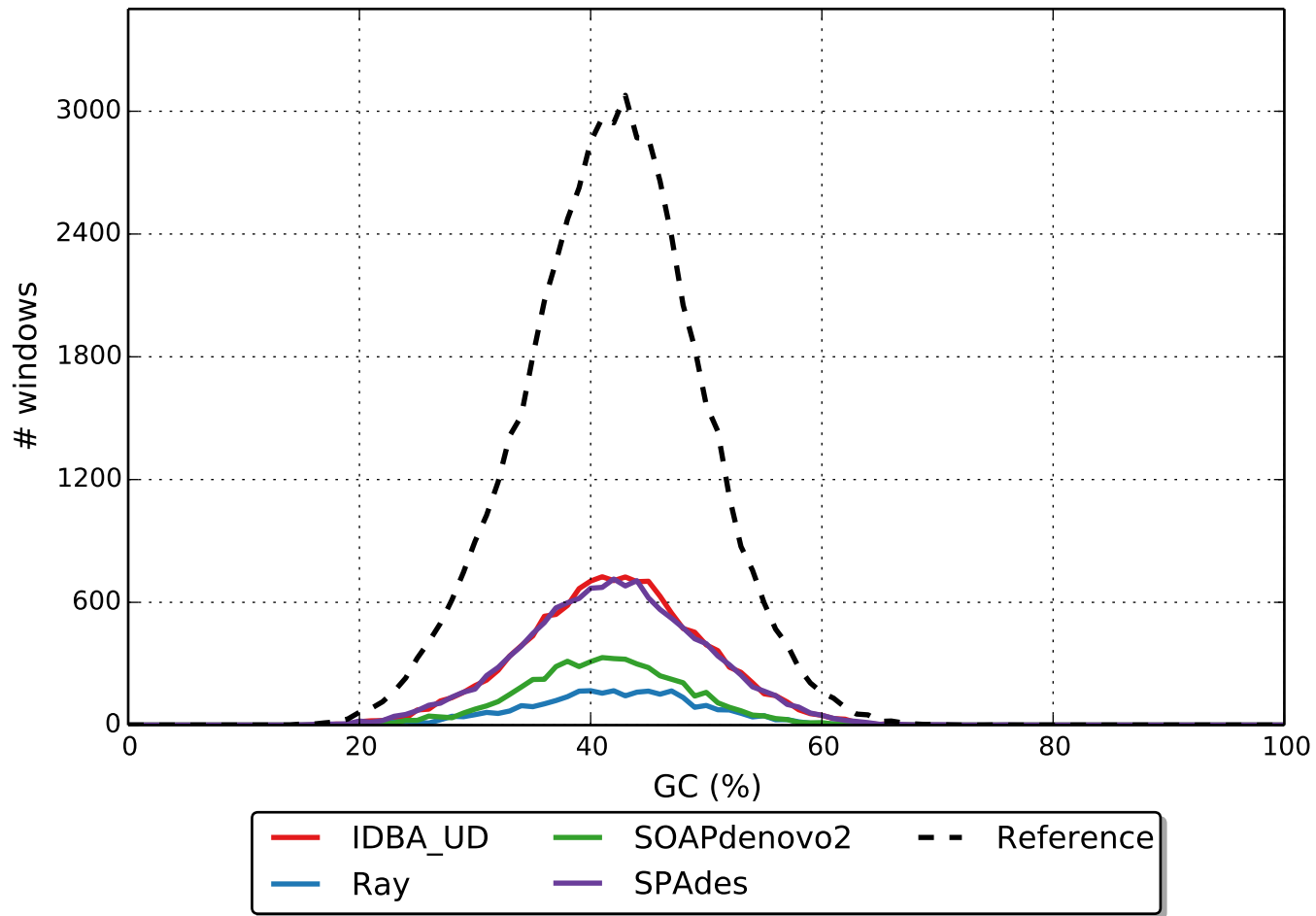
NGx



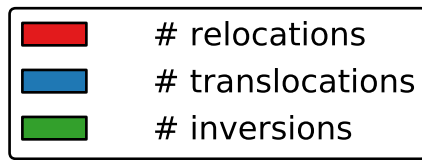
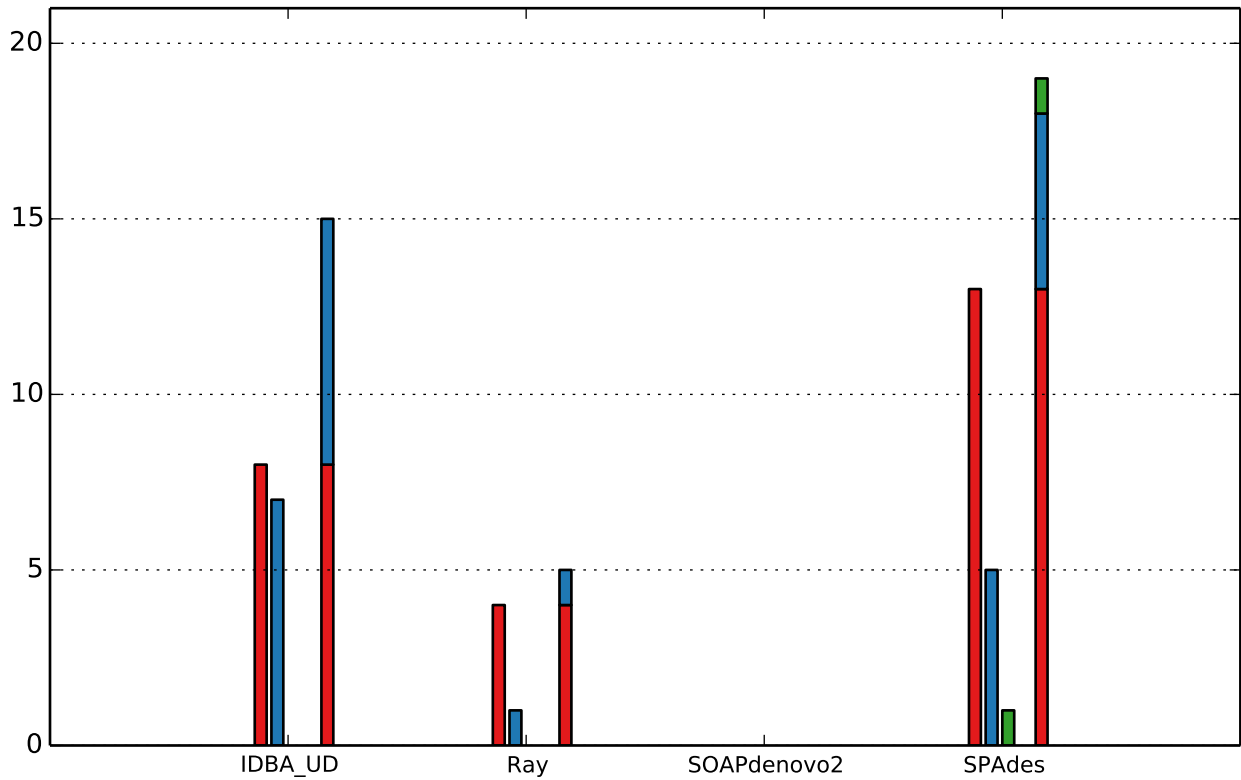
— IDBA_UD — SOAPdenovo2 — SPAdes
— Ray

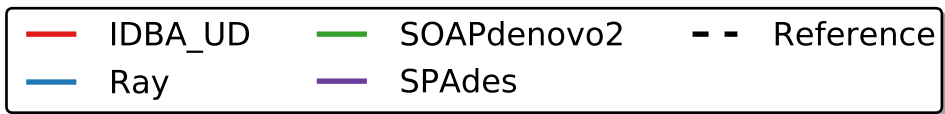
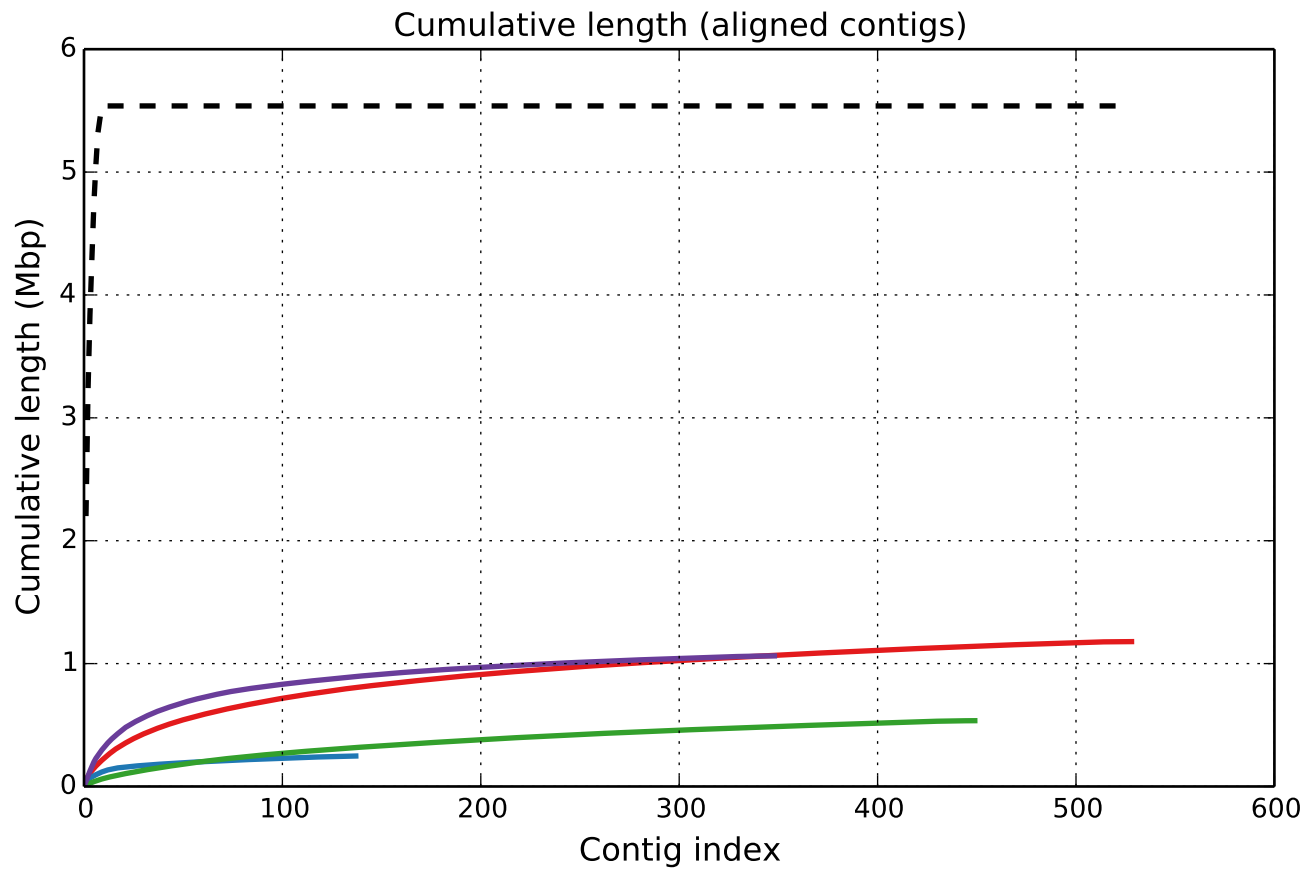


GC content

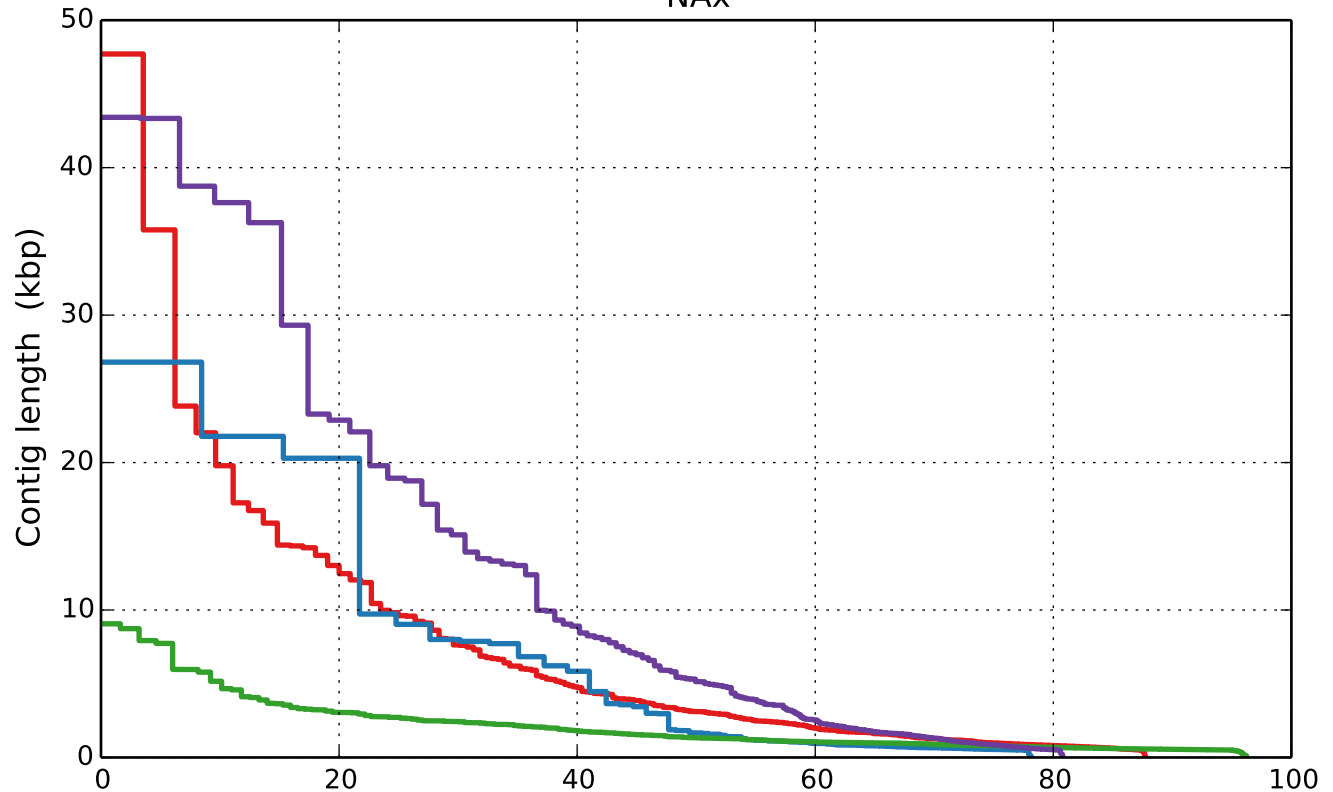


Misassemblies





NAx



— IDBA_UD — SOAPdenovo2 — SPAdes
— Ray

NGAx

