

Report

	IDBA_UD	Ray	SOAPdenovo2	SPAdes
# contigs (>= 1000 bp)	604	8	77	418
# contigs (>= 5000 bp)	48	5	1	45
# contigs (>= 10000 bp)	7	2	0	7
# contigs (>= 25000 bp)	0	0	0	1
# contigs (>= 50000 bp)	0	0	0	0
Total length (>= 1000 bp)	1393596	54343	114523	1135357
Total length (>= 5000 bp)	363814	46769	5467	375138
Total length (>= 10000 bp)	97574	29772	0	117408
Total length (>= 25000 bp)	0	0	0	25191
Total length (>= 50000 bp)	0	0	0	0
# contigs	1038	24	411	730
Largest contig	22495	15570	5467	25191
Total length	1714464	64438	338323	1360204
Reference length	5976145	5976145	5976145	5976145
GC (%)	42.39	41.15	41.49	42.48
Reference GC (%)	41.89	41.89	41.89	41.89
N50	2018	6015	806	2517
N75	1147	4245	625	1316
L50	217	3	138	131
L75	503	6	260	317
# misassemblies	10	0	5	8
# misassembled contigs	9	0	5	7
Misassembled contigs length	25139	0	5724	22023
# local misassemblies	6	0	351	8
# structural variations	0	0	0	0
# unaligned contigs	0 + 89 part	0 + 6 part	0 + 73 part	0 + 122 part
Unaligned length	135305	31611	40568	252505
Genome fraction (%)	26.146	0.523	4.408	18.252
Duplication ratio	1.011	1.050	1.130	1.016
# N's per 100 kbp	158.53	585.06	7736.69	692.76
# mismatches per 100 kbp	1795.91	150.30	1450.51	2058.33
# indels per 100 kbp	48.70	3.20	20.12	52.99
Largest alignment	14202	14202	5467	17666
NA50	1643	354	579	1488
NGA50	-	-	-	-
NA75	915	-	173	621
LA50	271	22	185	225
LA75	624	-	383	578

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

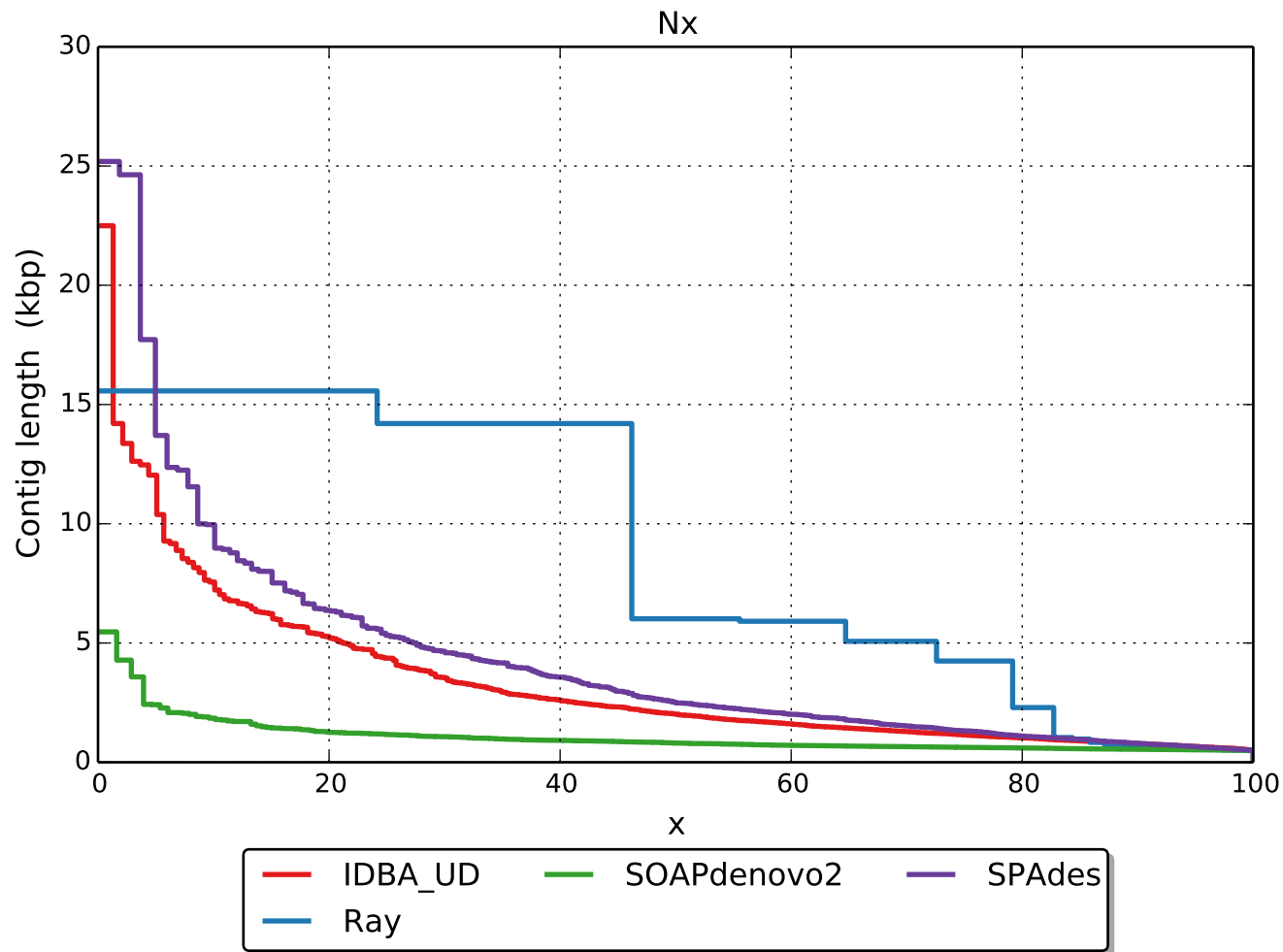
	IDBA_UD	Ray	SOAPdenovo2	SPAdes
# misassemblies	10	0	5	8
# relocations	10	0	5	7
# translocations	0	0	0	0
# inversions	0	0	0	1
# possibly misassembled contigs	29	2	7	55
# misassembled contigs	9	0	5	7
Misassembled contigs length	25139	0	5724	22023
# local misassemblies	6	0	351	8
# structural variations	0	0	0	0
# mismatches	28061	47	3821	22451
# indels	761	1	53	578
# short indels	675	1	48	471
# long indels	86	0	5	107
Indels length	2116	1	91	1973

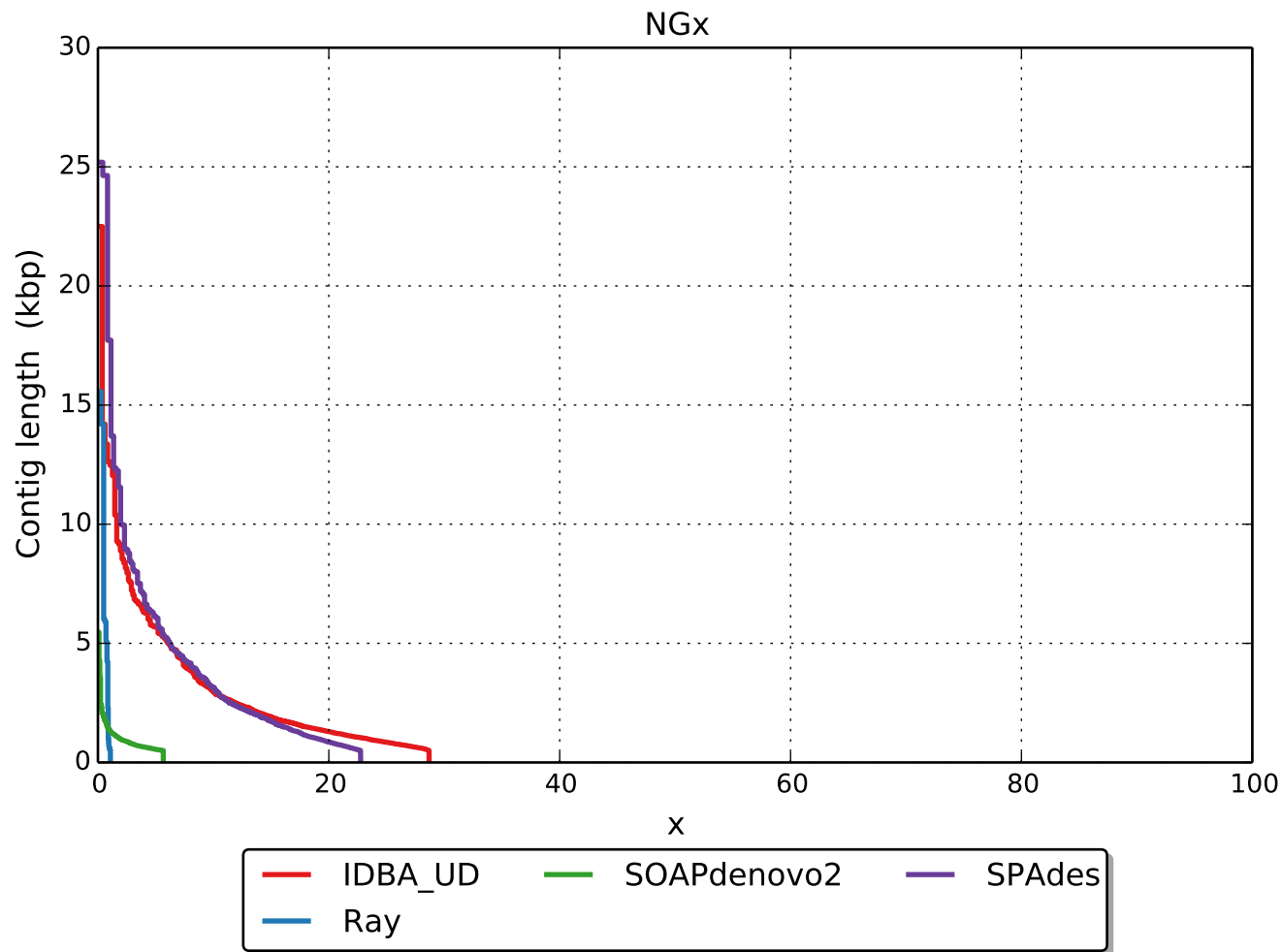
All statistics are based on contigs of size ≥ 500 bp, unless otherwise noted (e.g., "# contigs (≥ 0 bp)" and "Total length (≥ 0 bp)" include all contigs).

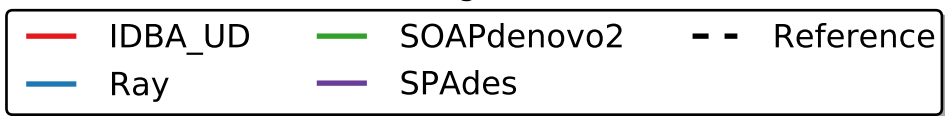
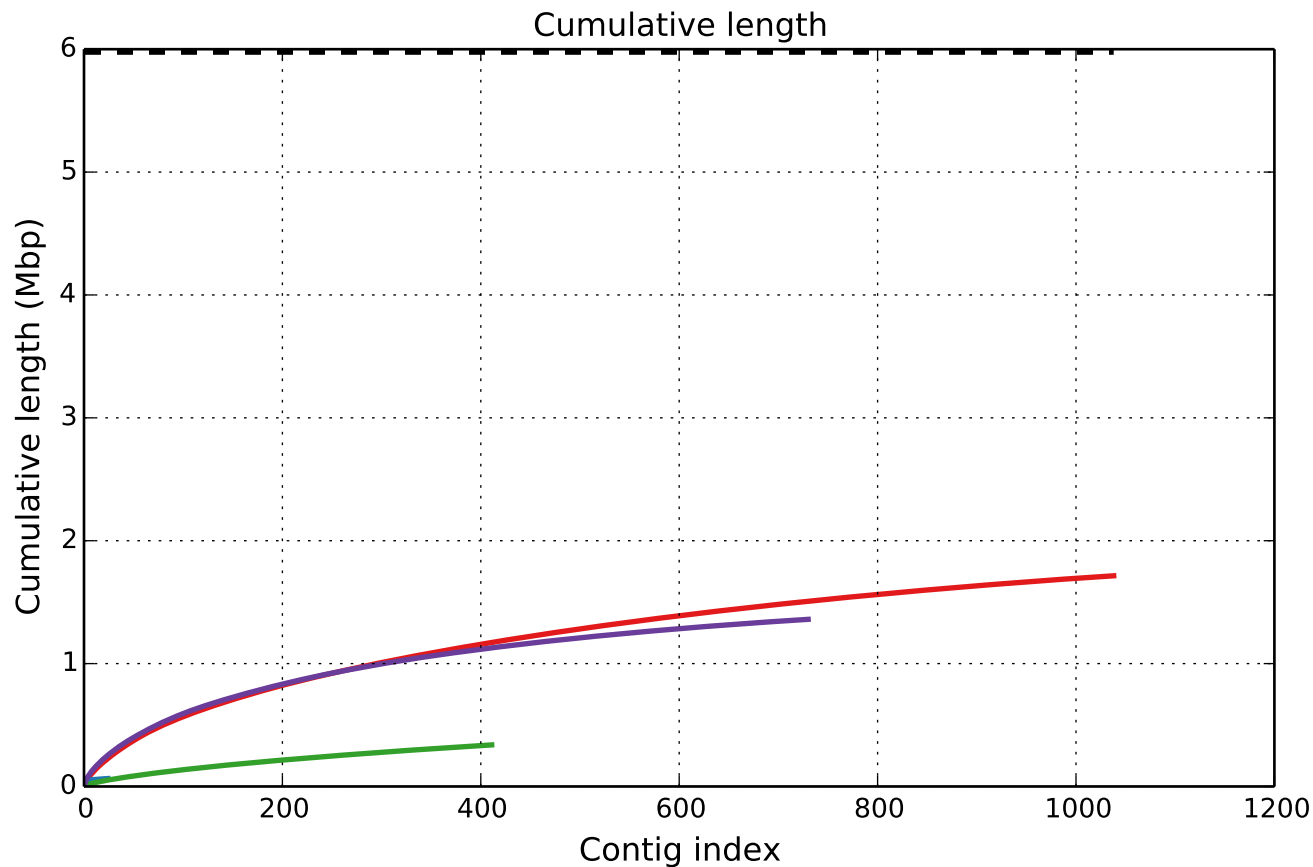
Unaligned report

	IDBA_UD	Ray	SOAPdenovo2	SPAdes
# fully unaligned contigs	0	0	0	0
Fully unaligned length	0	0	0	0
# partially unaligned contigs	89	6	73	122
# with misassembly	1	0	39	2
# both parts are significant	27	2	3	46
Partially unaligned length	135305	31611	40568	252505
# N's	2718	377	26175	9423

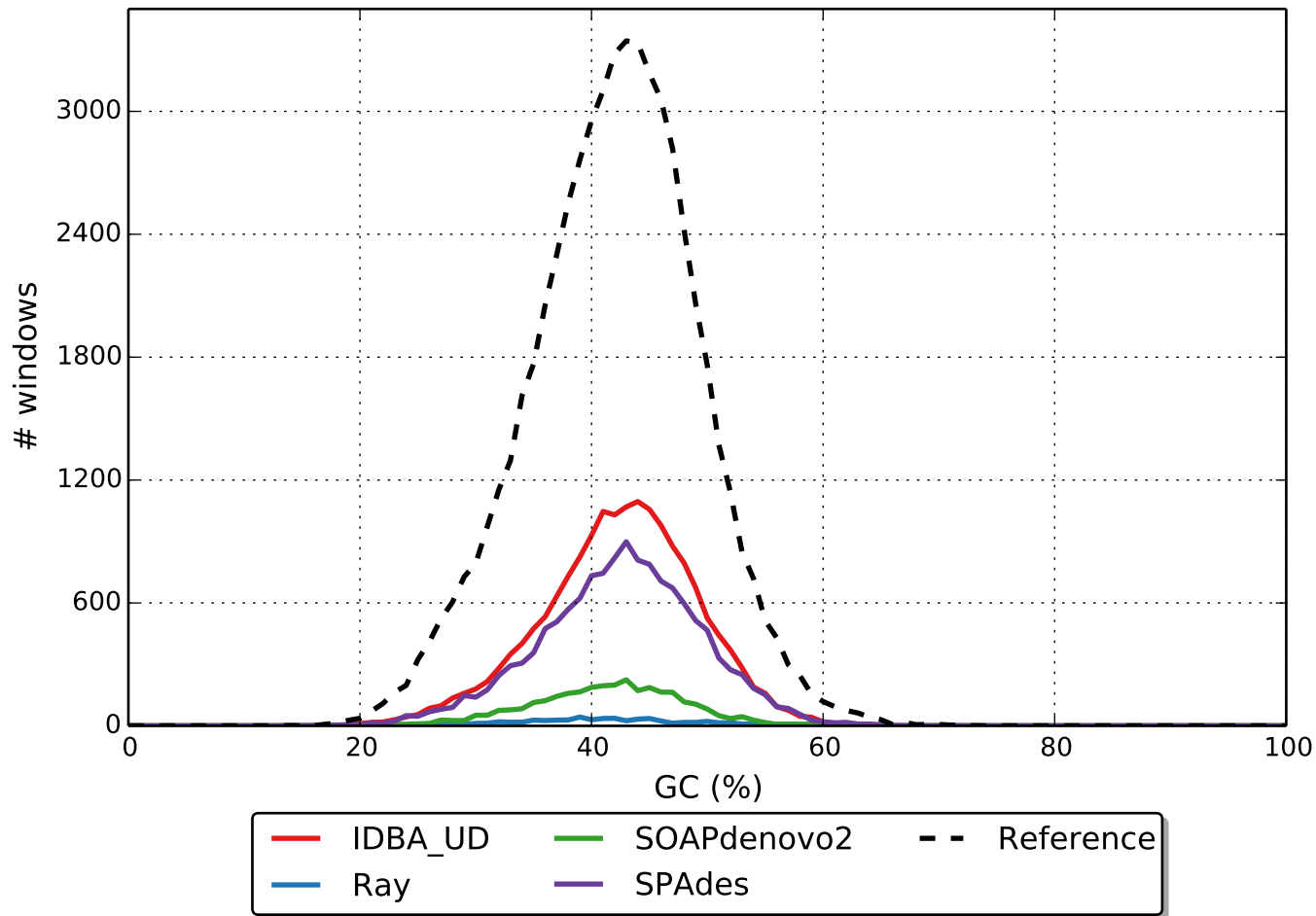
All statistics are based on contigs of size ≥ 500 bp, unless otherwise noted (e.g., "# contigs (≥ 0 bp)" and "Total length (≥ 0 bp)" include all contigs).



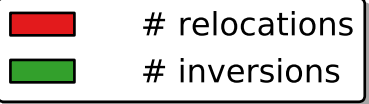
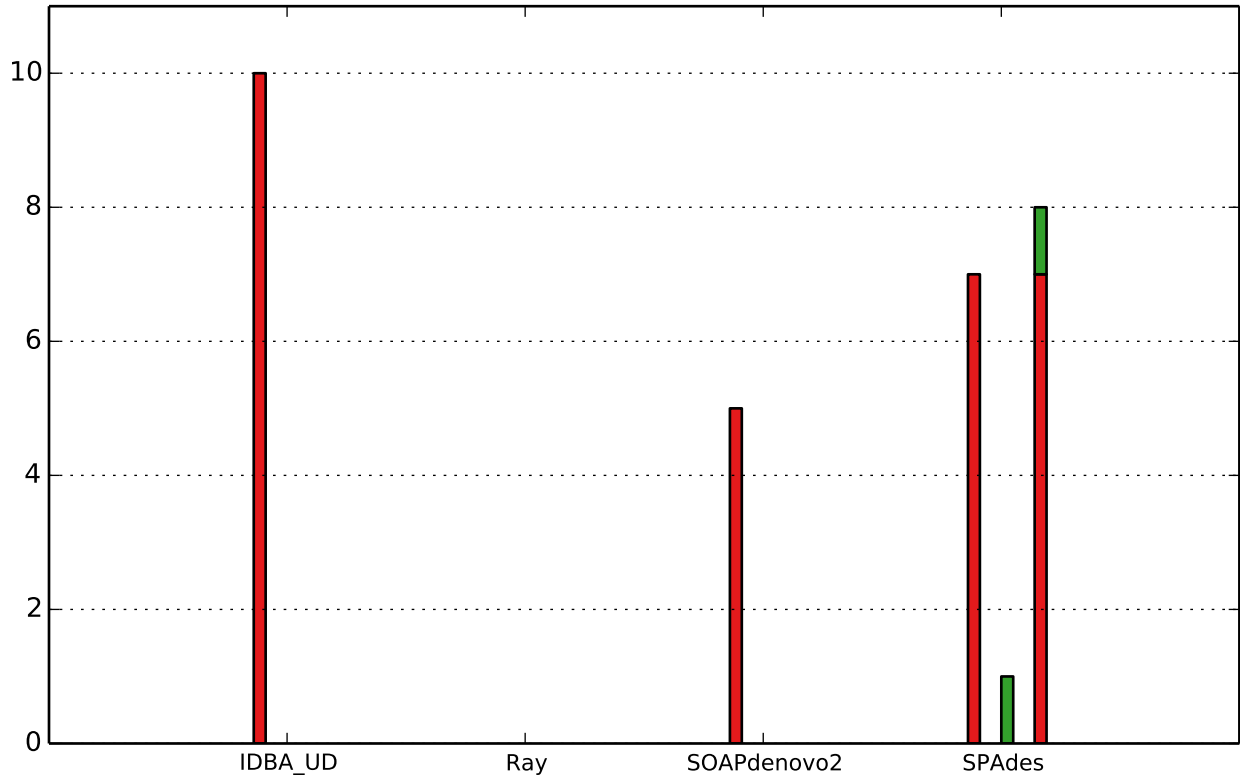


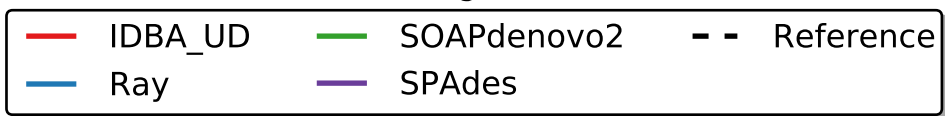
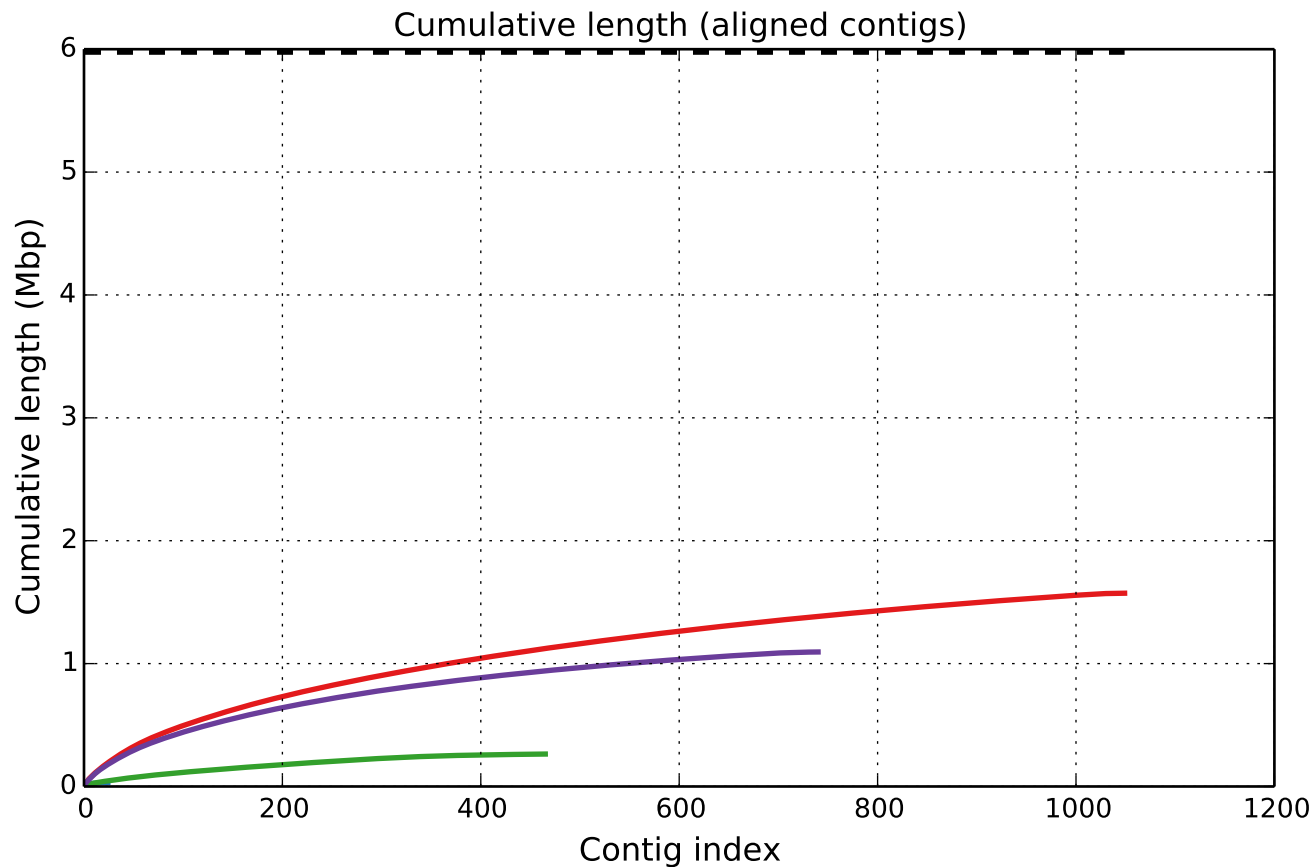


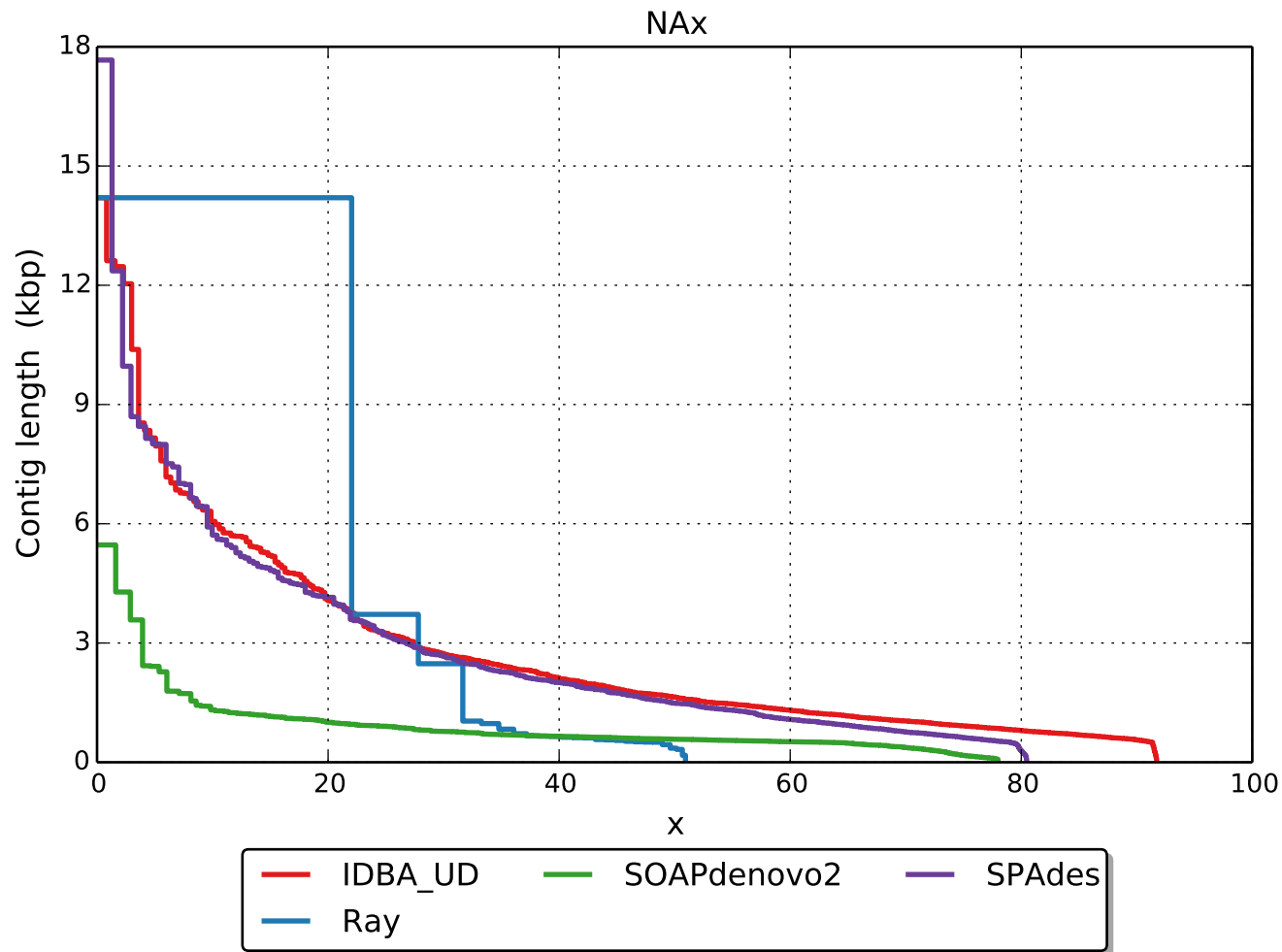
GC content



Misassemblies







NGAx

