

Report

	IDBA_UD	Ray	SOAPdenovo2	SPAdes
# contigs (>= 1000 bp)	503	442	233	305
# contigs (>= 5000 bp)	71	101	40	106
# contigs (>= 10000 bp)	23	34	14	32
# contigs (>= 25000 bp)	5	4	4	5
# contigs (>= 50000 bp)	0	1	0	1
Total length (>= 1000 bp)	1669469	1828894	875648	1657997
Total length (>= 5000 bp)	740880	1052647	475858	1154911
Total length (>= 10000 bp)	402309	612298	276251	638442
Total length (>= 25000 bp)	145057	159140	136445	248232
Total length (>= 50000 bp)	0	69202	0	108978
# contigs	889	668	508	521
Largest contig	33515	69202	37314	108978
Total length	1944848	1987018	1060146	1808801
Reference length	1864179	1864179	1864179	1864179
GC (%)	56.66	56.95	55.79	56.58
Reference GC (%)	56.03	56.03	56.03	56.03
N50	3610	5200	4424	6946
NG50	3838	5647	767	6740
N75	1562	2464	1366	3645
NG75	1717	2937	-	3318
L50	127	90	52	65
LG50	116	79	298	69
L75	333	226	163	153
LG75	296	192	-	165
# misassemblies	5	6	2	12
# misassembled contigs	5	6	2	11
Misassembled contigs length	25779	46011	7396	83573
# local misassemblies	7	126	24	7
# structural variations	3	1	0	3
# unaligned contigs	0 + 141 part	0 + 127 part	0 + 208 part	0 + 106 part
Unaligned length	318110	438630	506368	390673
Genome fraction (%)	76.159	69.797	26.400	71.909
Duplication ratio	1.146	1.190	1.125	1.058
# N's per 100 kbp	0.00	1826.25	4792.08	464.56
# mismatches per 100 kbp	3179.65	3223.72	2687.60	3296.51
# indels per 100 kbp	36.06	31.05	49.17	50.06
Largest alignment	33515	27758	33570	38583
NA50	2205	2356	-	3963
NGA50	2418	2716	-	3748
NA75	754	-	-	562
NGA75	892	699	-	-
LA50	187	178	-	109
LGA50	169	154	-	116
LA75	582	-	-	423
LGA75	508	497	-	-

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

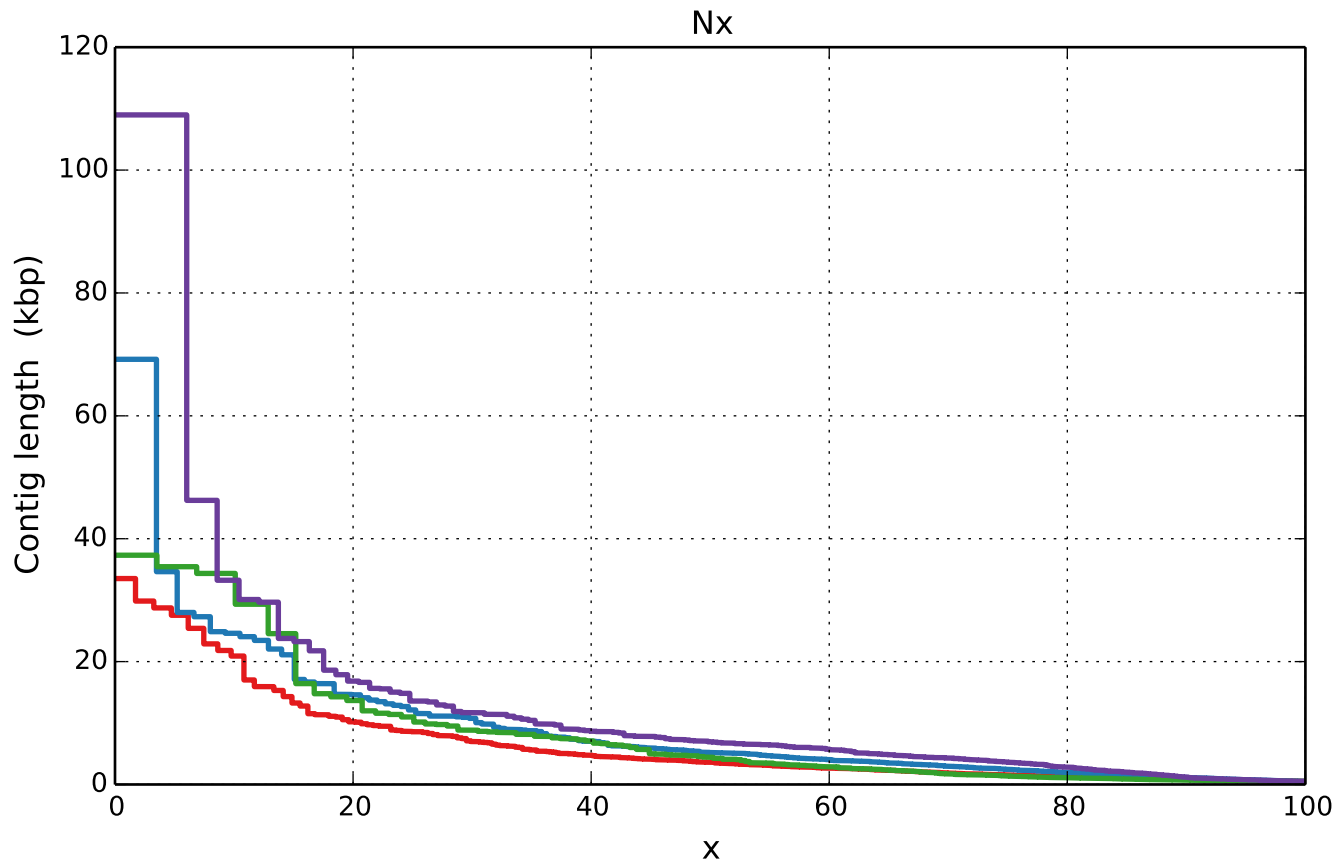
	IDBA_UD	Ray	SOAPdenovo2	SPAdes
# misassemblies	5	6	2	12
# relocations	4	4	2	8
# translocations	1	2	0	4
# inversions	0	0	0	0
# possibly misassembled contigs	31	77	79	45
# misassembled contigs	5	6	2	11
Misassembled contigs length	25779	46011	7396	83573
# local misassemblies	7	126	24	7
# structural variations	3	1	0	3
# mismatches	45143	41945	13227	44190
# indels	512	404	242	671
# short indels	469	381	136	584
# long indels	43	23	106	87
Indels length	1379	762	2529	2888

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

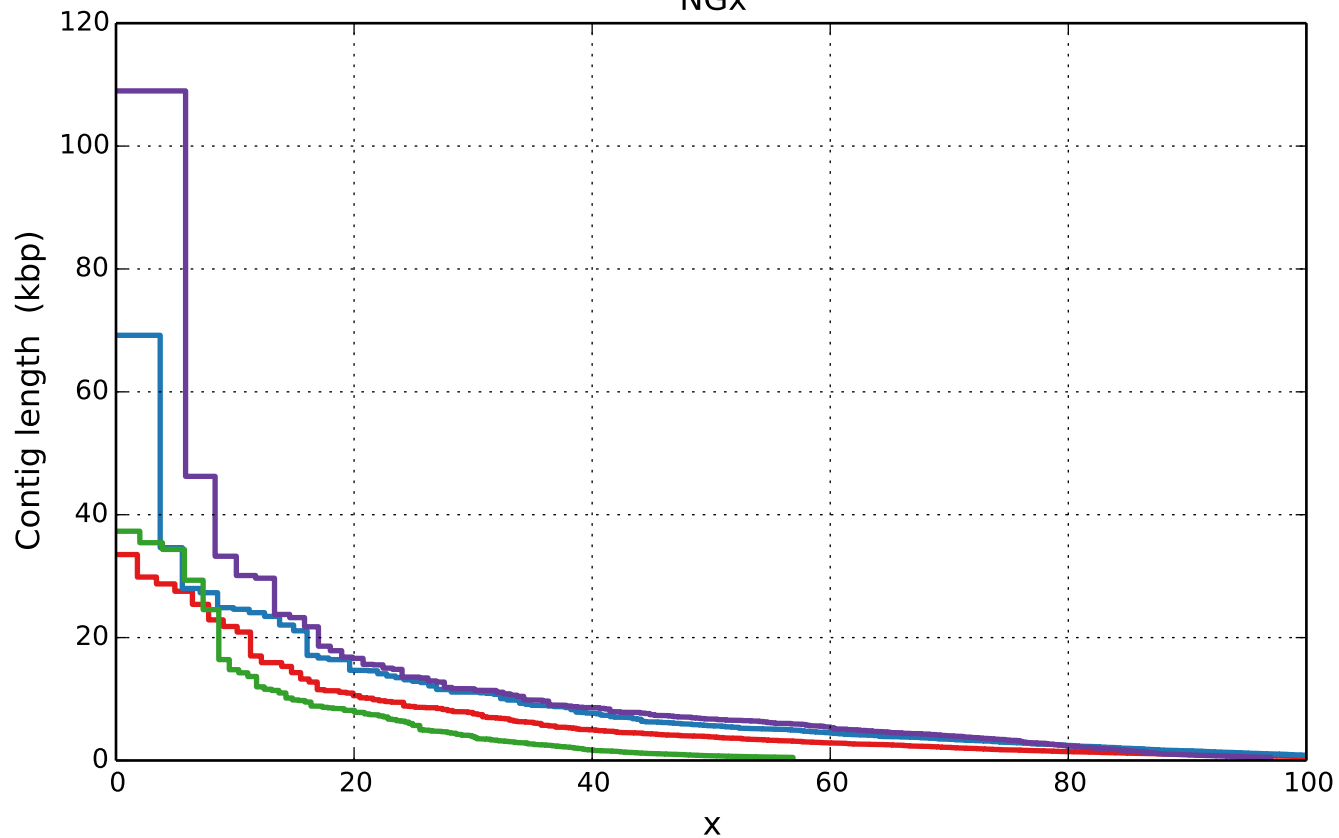
	IDBA_UD	Ray	SOAPdenovo2	SPAdes
# fully unaligned contigs	0	0	0	0
Fully unaligned length	0	0	0	0
# partially unaligned contigs	141	127	208	106
# with misassembly	6	8	24	5
# both parts are significant	27	52	68	36
Partially unaligned length	318110	438630	506368	390673
# N's	0	36288	50803	8403

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).

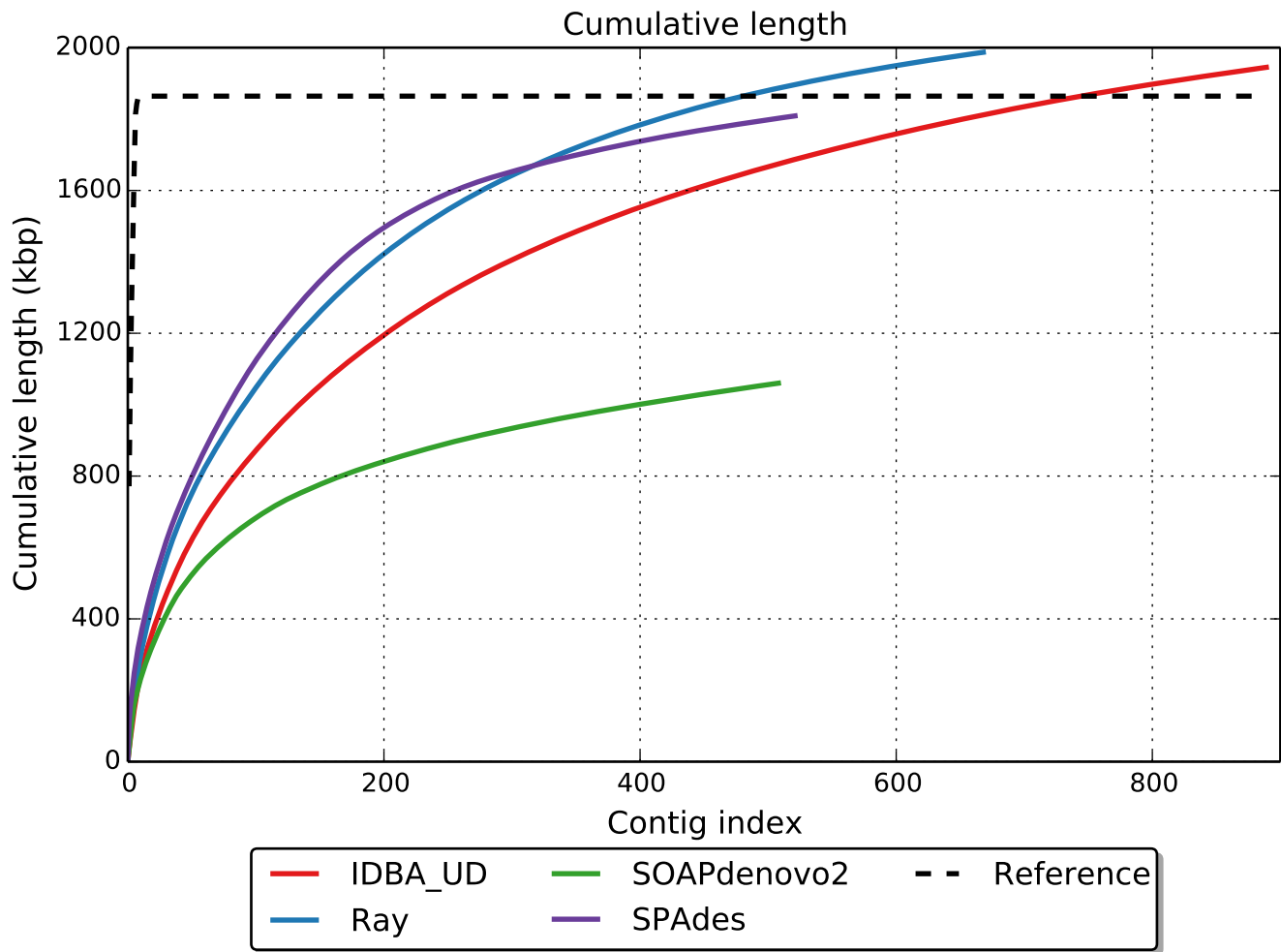


— IDBA_UD — SOAPdenovo2 — SPAdes
— Ray

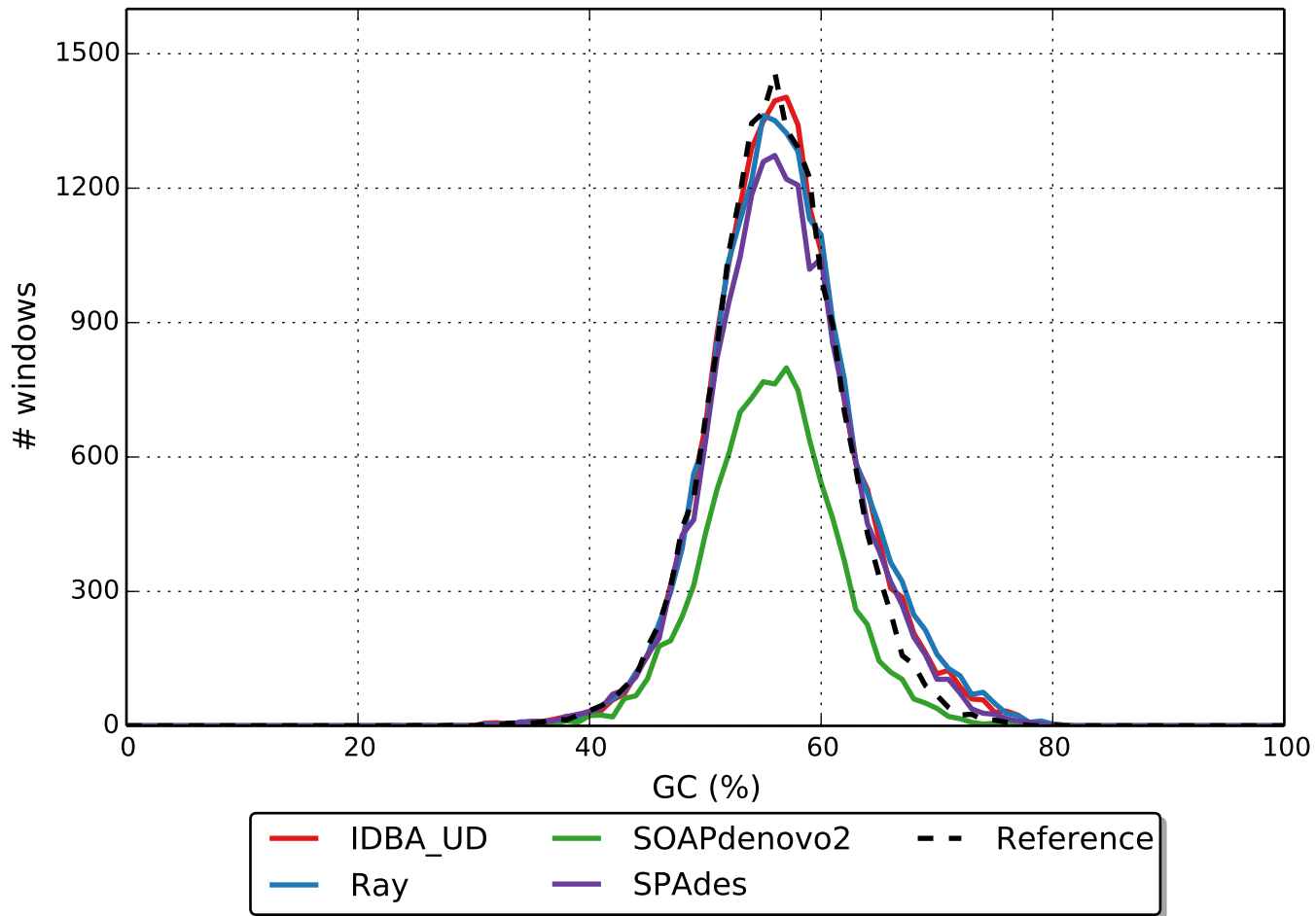
NGx

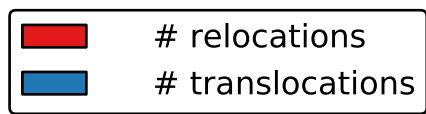
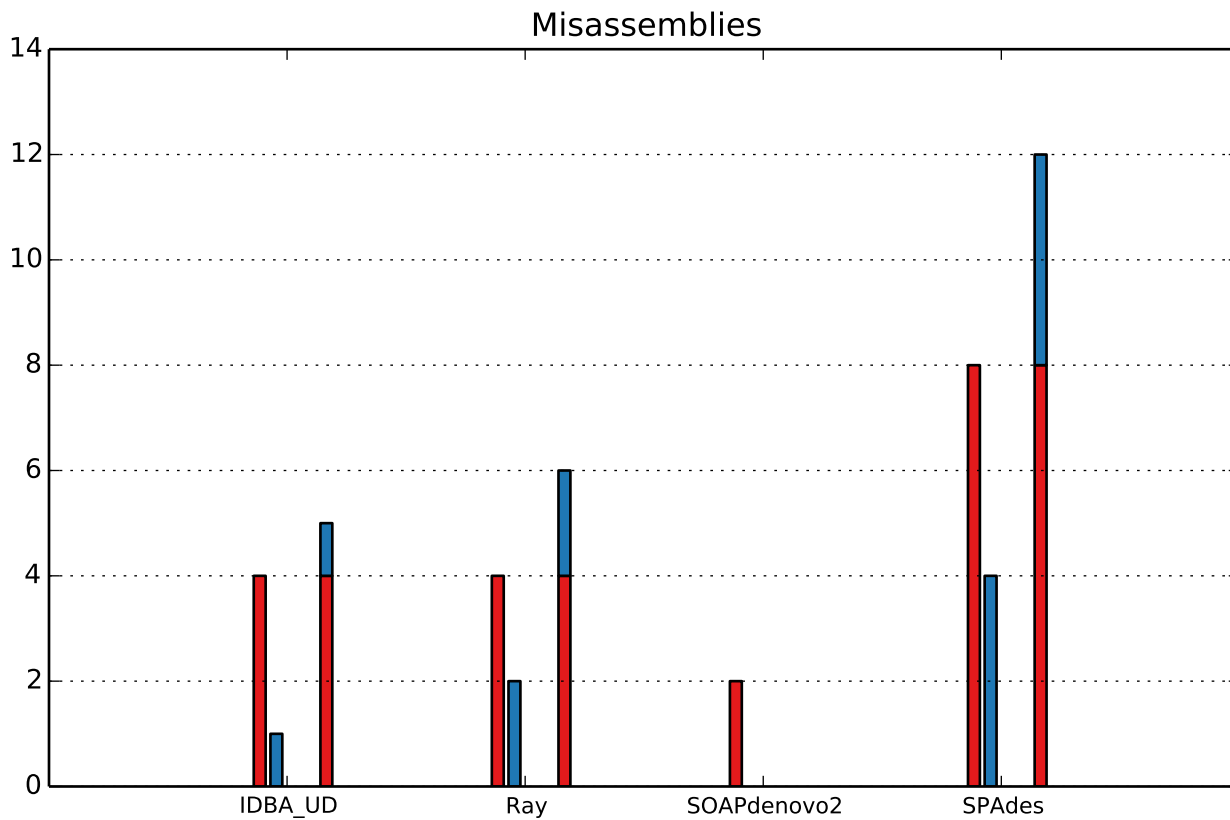


— IDBA_UD — SOAPdenovo2 — SPAdes
— Ray

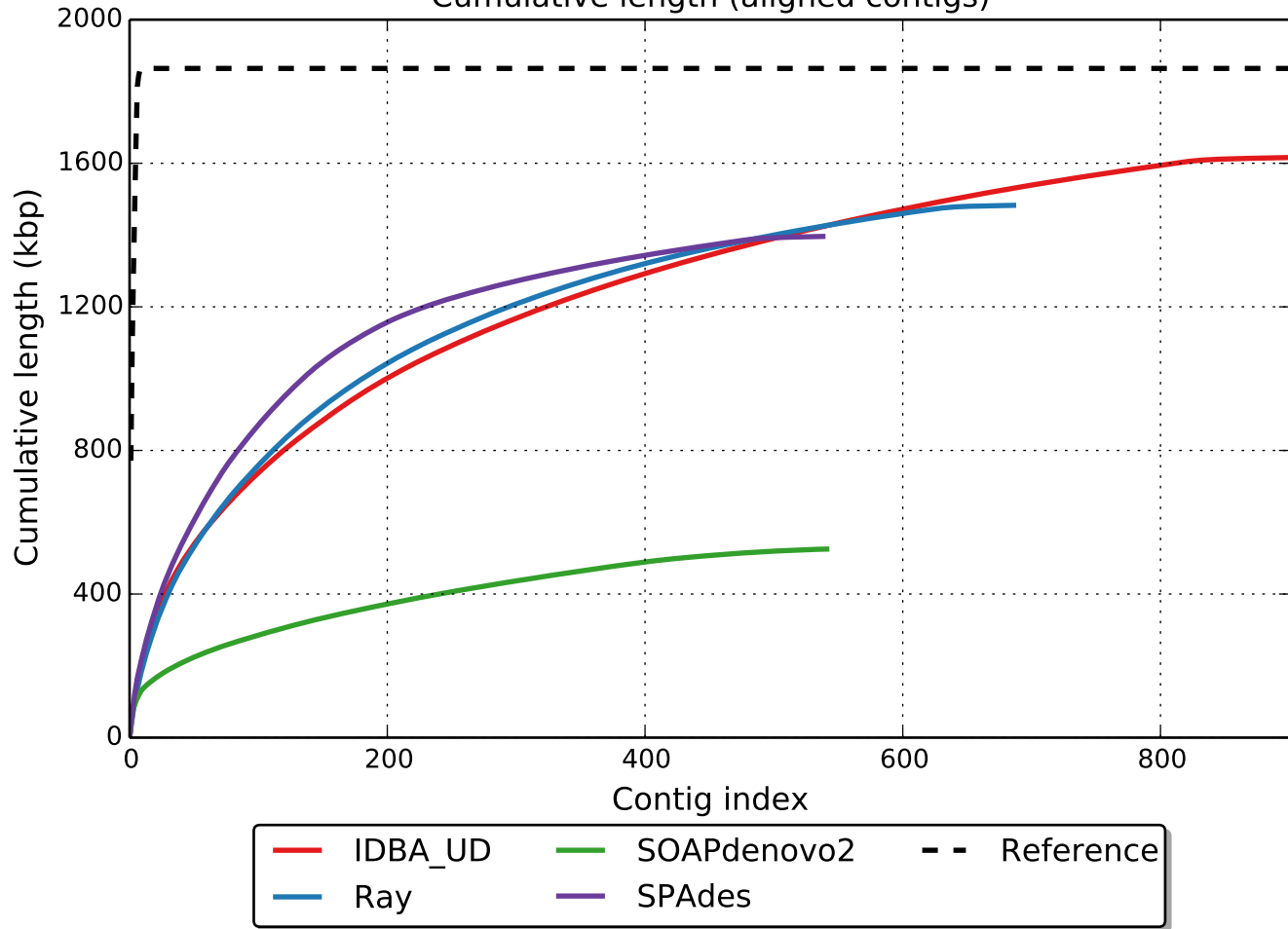


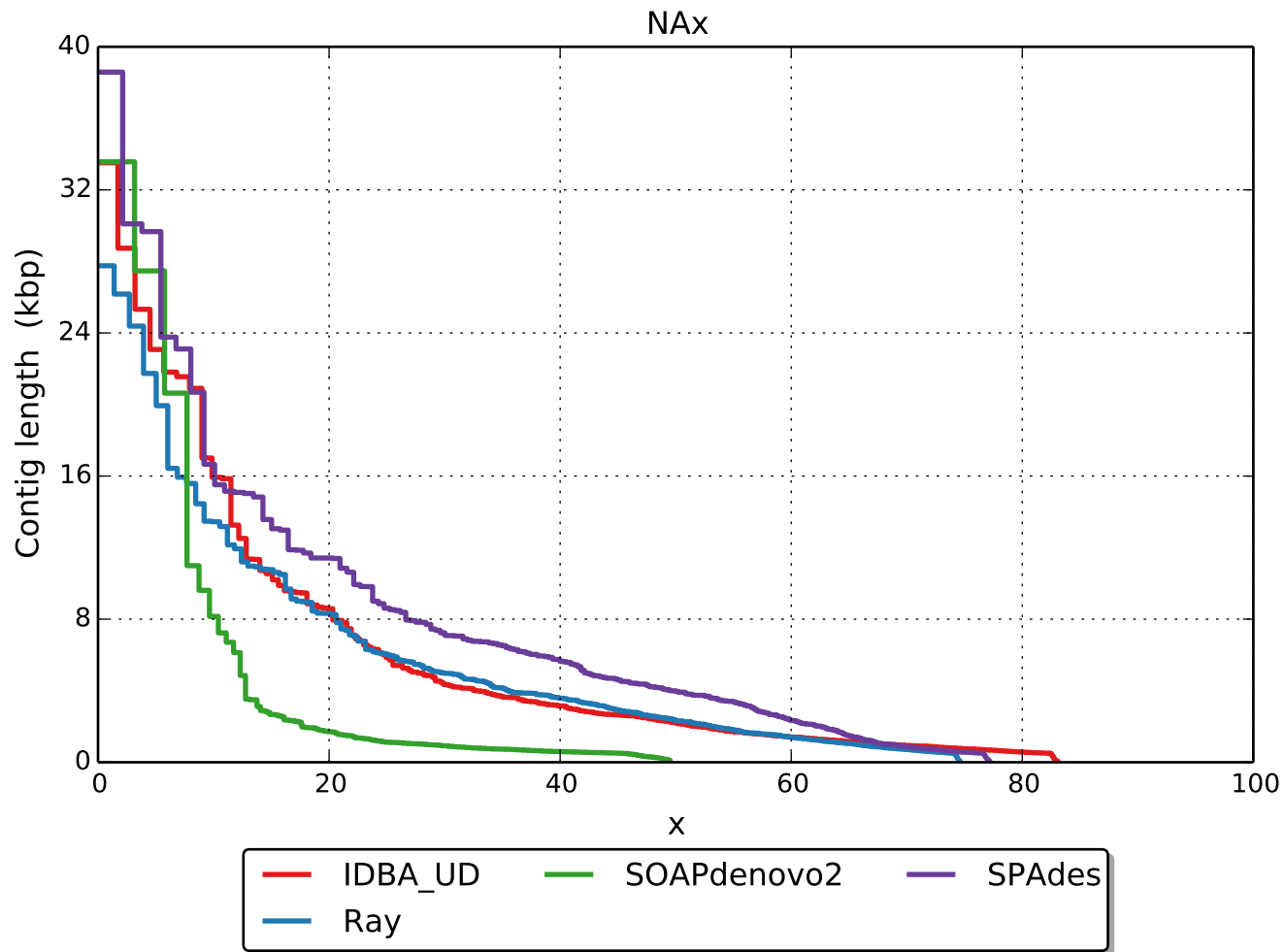
GC content





Cumulative length (aligned contigs)





NGAx

