

Report

	IDBA_UD	Ray	SOAPdenovo2	SPAdes
# contigs (>= 1000 bp)	53	314	161	48
# contigs (>= 5000 bp)	39	141	99	44
# contigs (>= 10000 bp)	33	68	67	42
# contigs (>= 25000 bp)	31	13	29	29
# contigs (>= 50000 bp)	20	4	12	21
Total length (>= 1000 bp)	3245364	2327119	2597378	3223375
Total length (>= 5000 bp)	3215643	1861700	2439247	3214291
Total length (>= 10000 bp)	3173496	1339801	2186344	3200082
Total length (>= 25000 bp)	3131546	496437	1562314	2968768
Total length (>= 50000 bp)	2776117	237370	961645	2631763
# contigs	66	345	186	59
Largest contig	509970	67804	139242	335888
Total length	3254892	2349386	2614391	3231313
Reference length	2650108	2650108	2650108	2650108
GC (%)	39.46	38.44	38.55	39.96
Reference GC (%)	38.36	38.36	38.36	38.36
N50	152061	12357	33764	114420
NG50	155329	10038	33764	157394
N75	77406	5764	15496	54856
NG75	108833	3982	15235	84046
L50	7	54	21	8
LG50	6	67	21	6
L75	15	123	50	18
LG75	10	169	51	12
# misassemblies	38	23	25	35
# misassembled contigs	19	19	18	19
Misassembled contigs length	2081286	376775	897858	1784864
# local misassemblies	21	51	21	19
# structural variations	15	13	10	15
# unaligned contigs	0 + 30 part	0 + 61 part	0 + 46 part	0 + 25 part
Unaligned length	801949	181045	356963	777438
Genome fraction (%)	87.610	77.384	80.752	87.497
Duplication ratio	1.057	1.057	1.055	1.058
# N's per 100 kbp	0.00	422.28	476.29	1.92
# mismatches per 100 kbp	2921.53	2778.11	2806.71	2924.08
# indels per 100 kbp	69.73	63.64	73.50	70.04
Largest alignment	161472	63339	93432	138395
NA50	61610	8675	18279	53133
NGA50	70330	7257	17366	66712
NA75	-	3655	5190	-
NGA75	27176	1610	4657	28961
LA50	18	70	37	19
LGA50	13	89	38	15
LA75	-	171	104	-
LGA75	27	261	110	29

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	38	23	25	35
# relocations	31	17	21	27
# translocations	7	6	4	8
# inversions	0	0	0	0
# possibly misassembled contigs	23	46	39	28
# misassembled contigs	19	19	18	19
Misassembled contigs length	2081286	376775	897858	1784864
# local misassemblies	21	51	21	19
# structural variations	15	13	10	15
# mismatches	67831	56972	60064	67803
# indels	1619	1305	1573	1624
# short indels	1559	1262	1328	1562
# long indels	60	43	245	62
Indels length	2827	2183	6612	2881

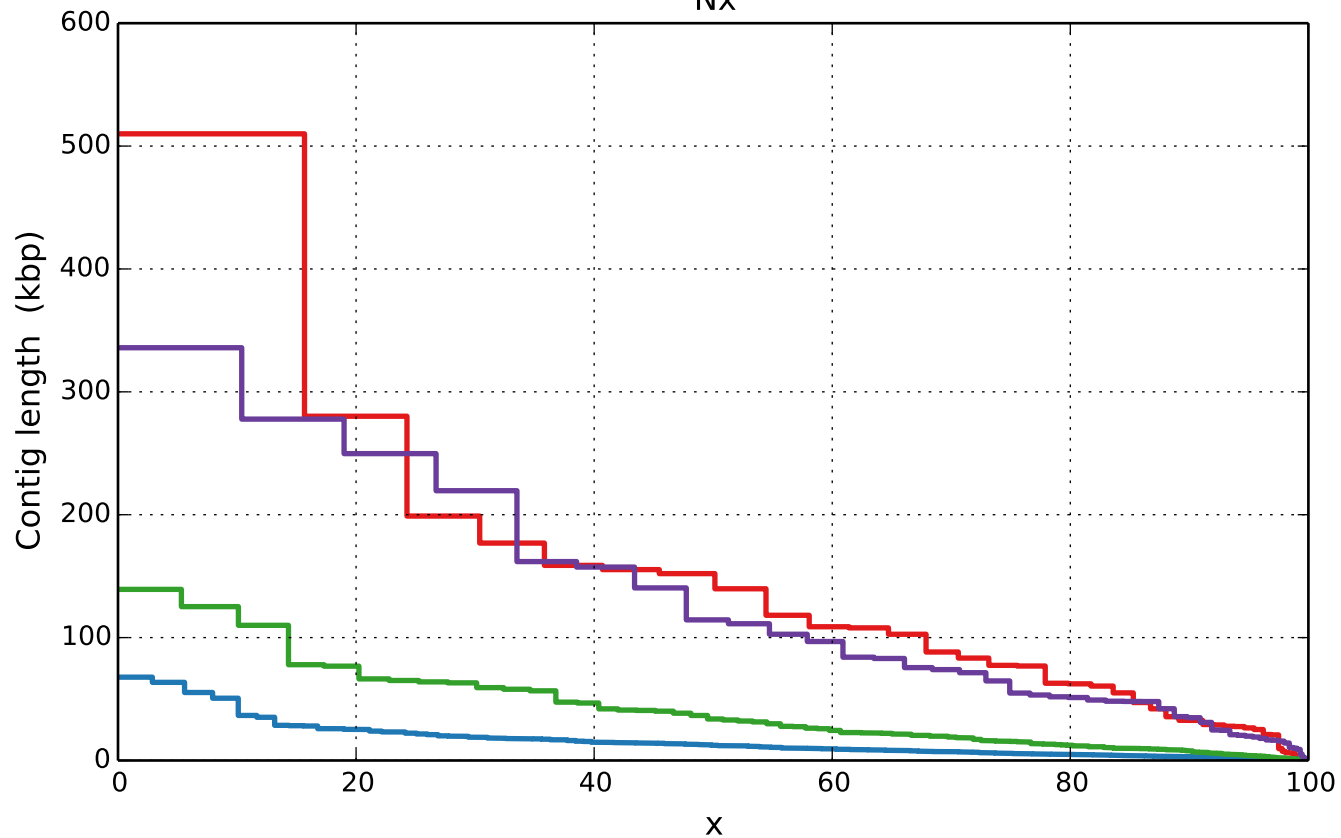
All statistics are based on contigs of size ≥ 500 bp, unless otherwise noted (e.g., "# contigs (≥ 0 bp)" and "Total length (≥ 0 bp)" include all contigs).

Unaligned report

	IDBA_UD	Ray	SOAPdenovo2	SPAdes
# fully unaligned contigs	0	0	0	0
Fully unaligned length	0	0	0	0
# partially unaligned contigs	30	61	46	25
# with misassembly	5	4	4	5
# both parts are significant	8	24	22	10
Partially unaligned length	801949	181045	356963	777438
# N's	0	9921	12452	62

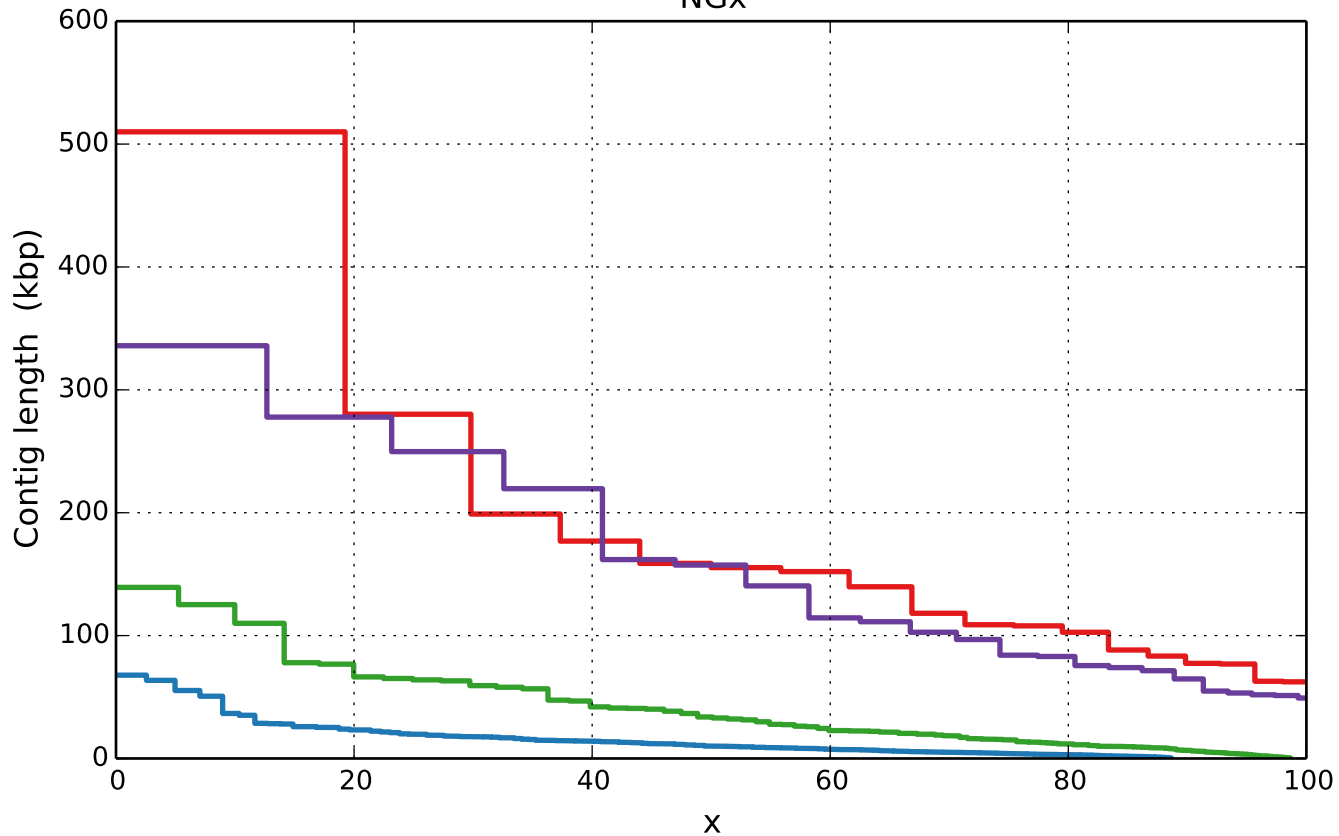
All statistics are based on contigs of size ≥ 500 bp, unless otherwise noted (e.g., "# contigs (≥ 0 bp)" and "Total length (≥ 0 bp)" include all contigs).

Nx

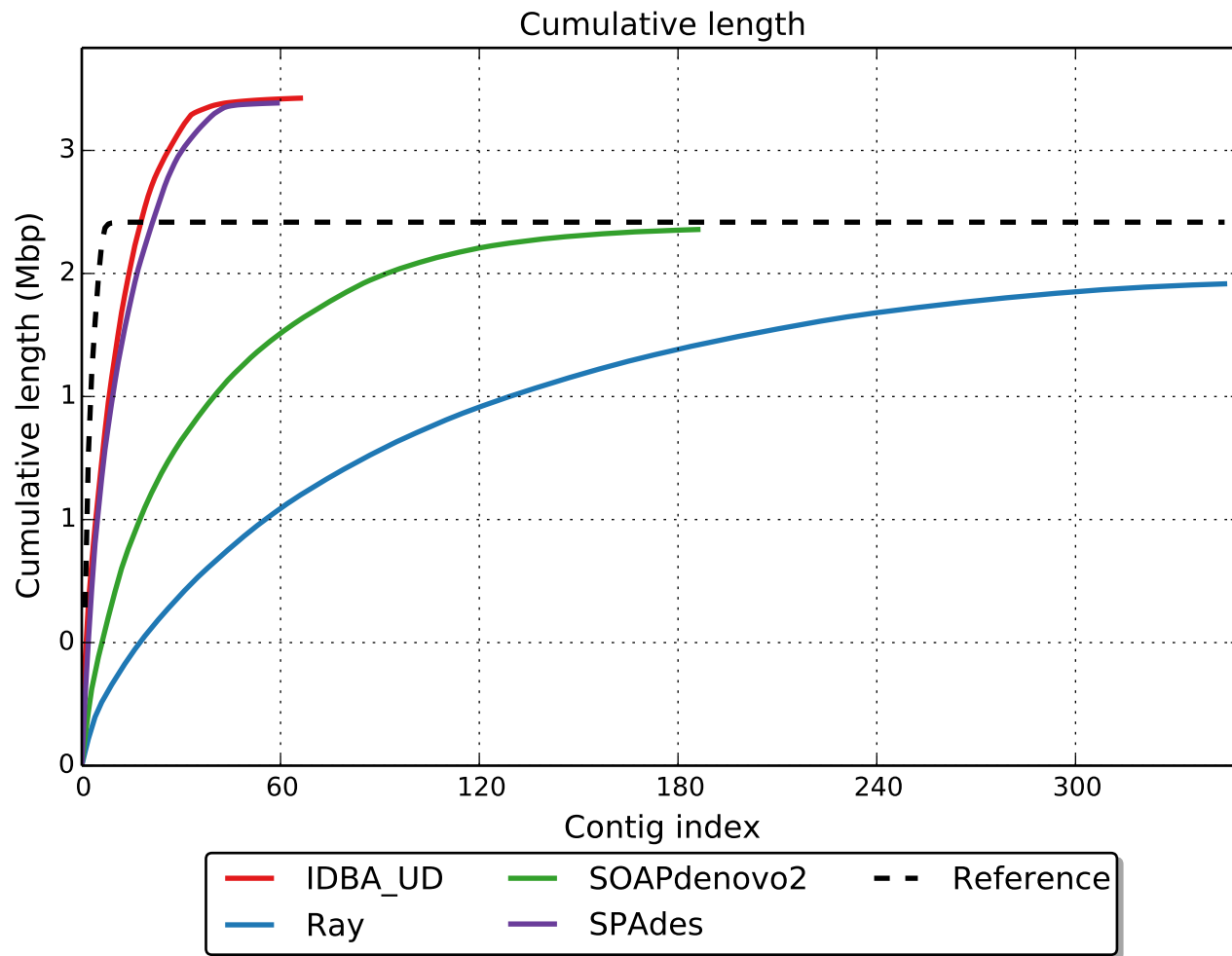


— IDBA_UD — SOAPdenovo2 — SPAdes
— Ray

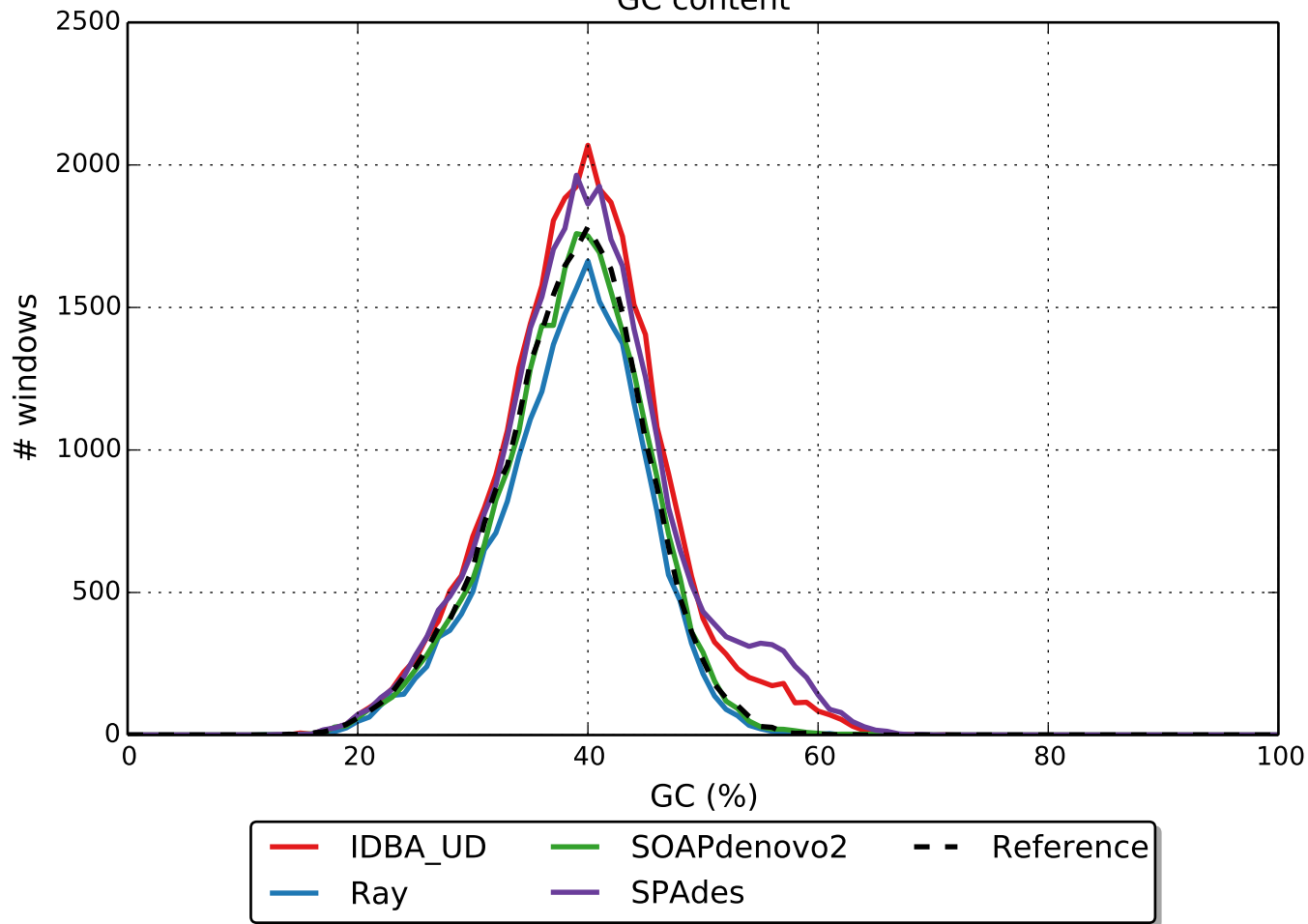
NGx



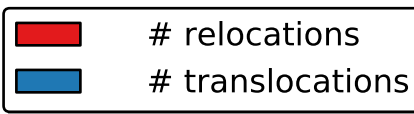
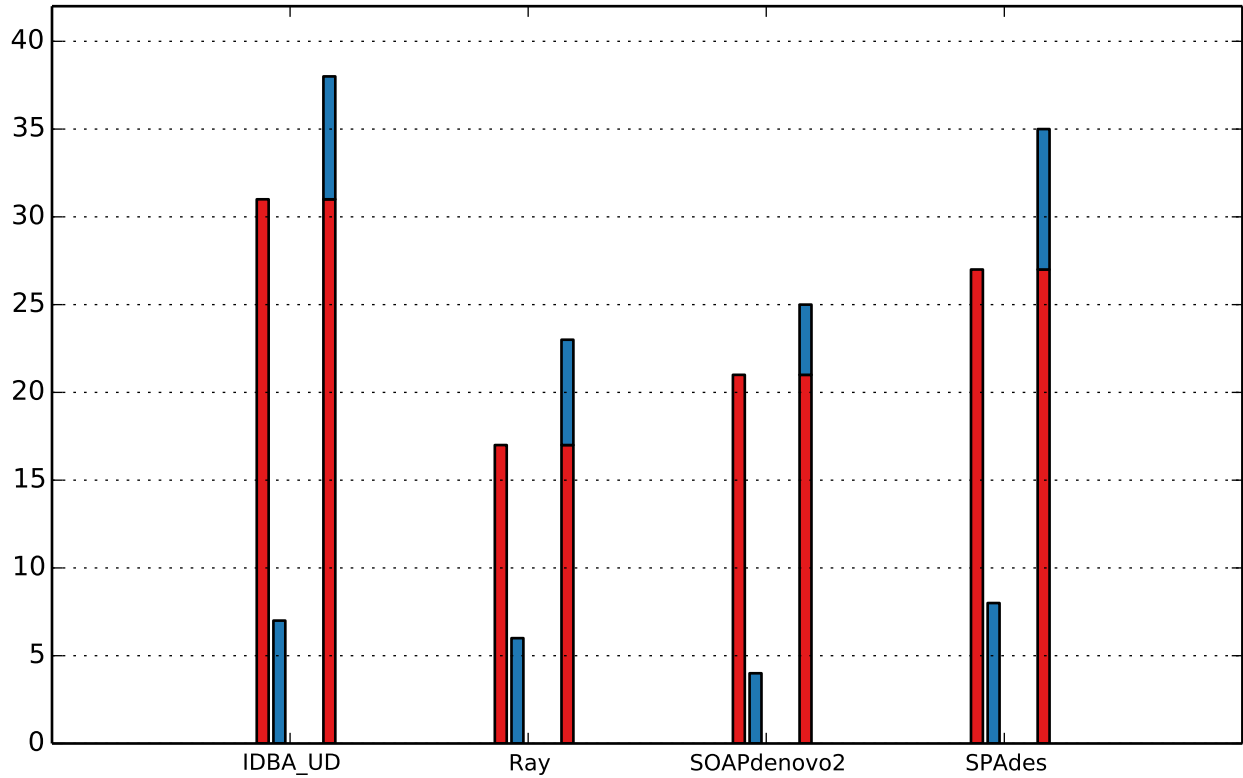
— IDBA_UD — SOAPdenovo2 — SPAdes
— Ray



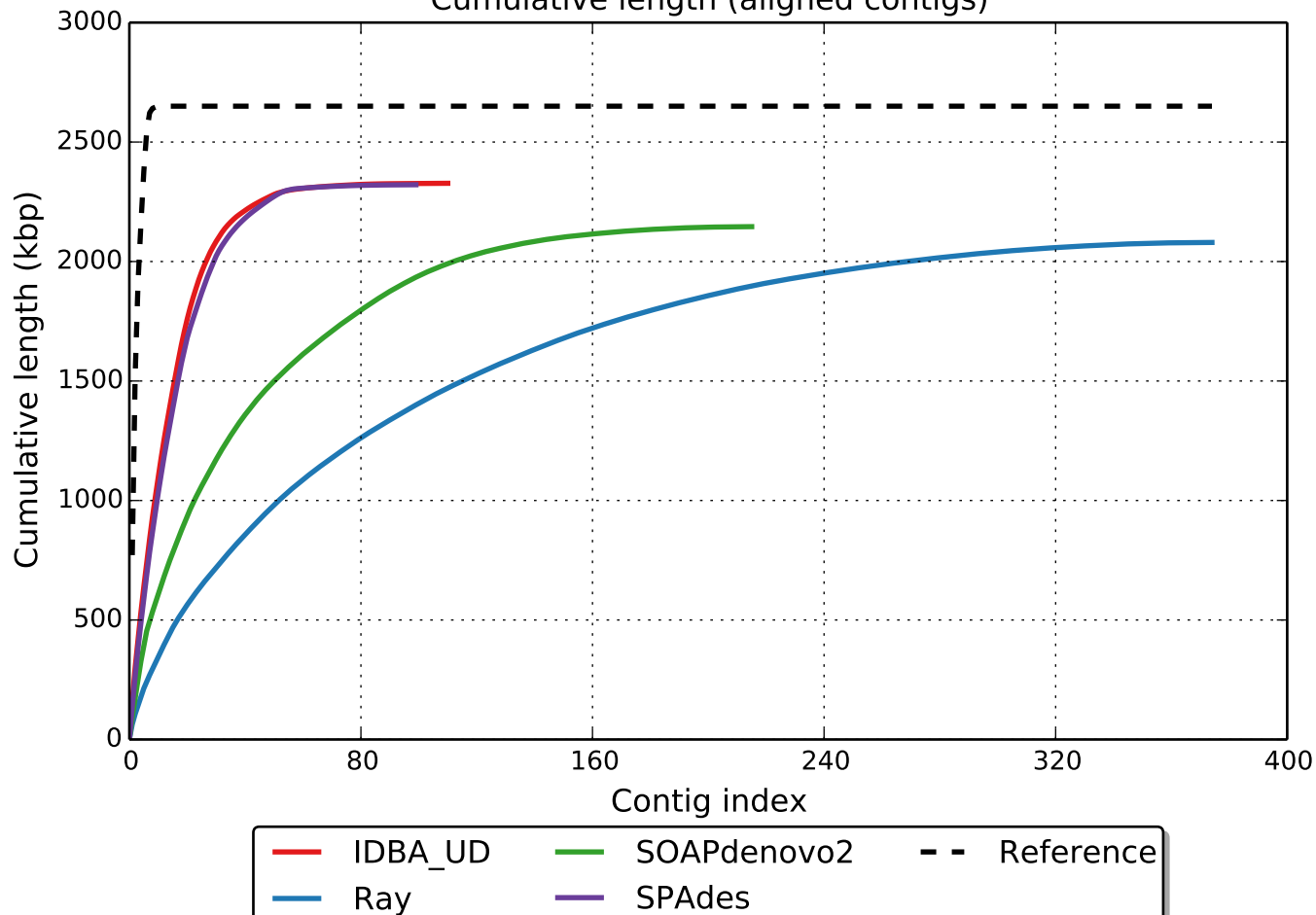
GC content



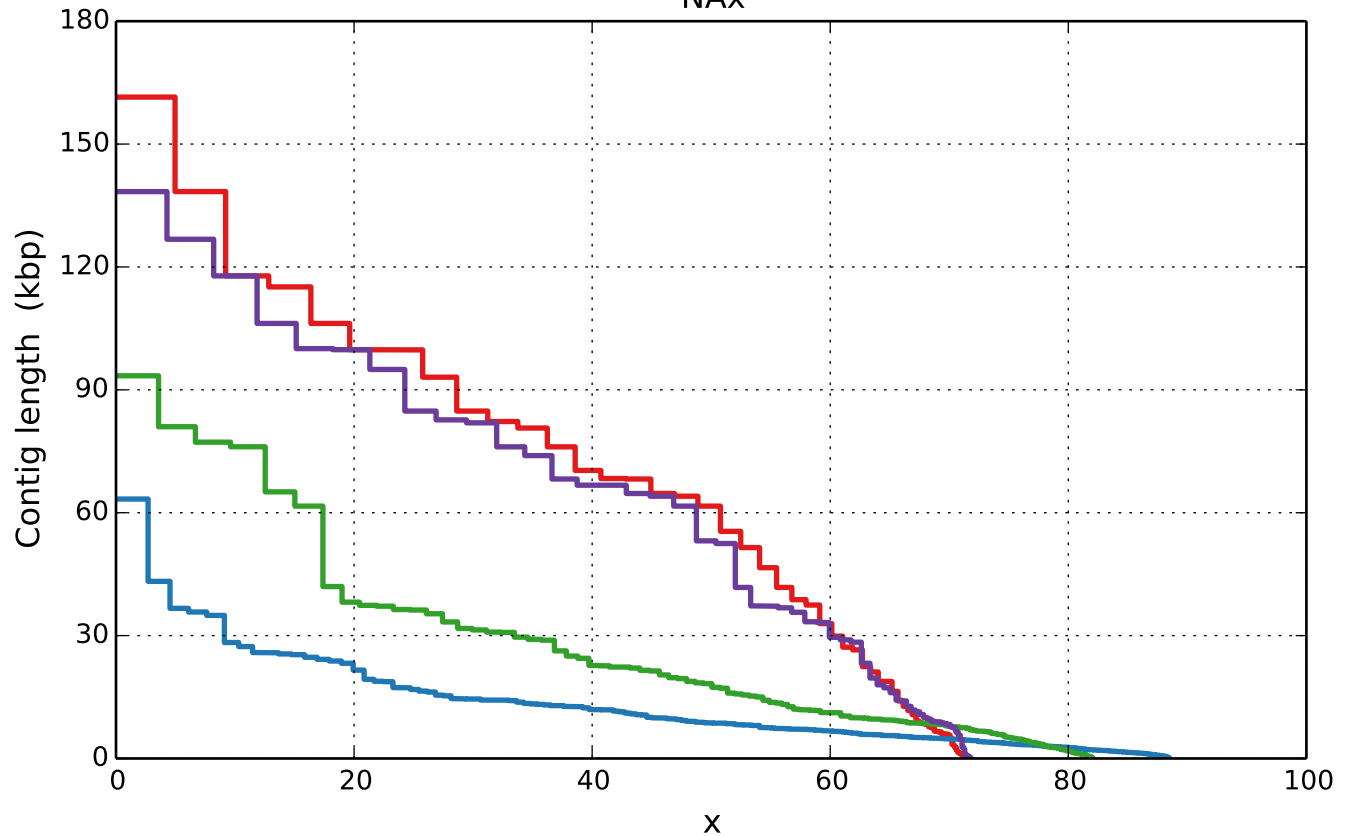
Misassemblies



Cumulative length (aligned contigs)

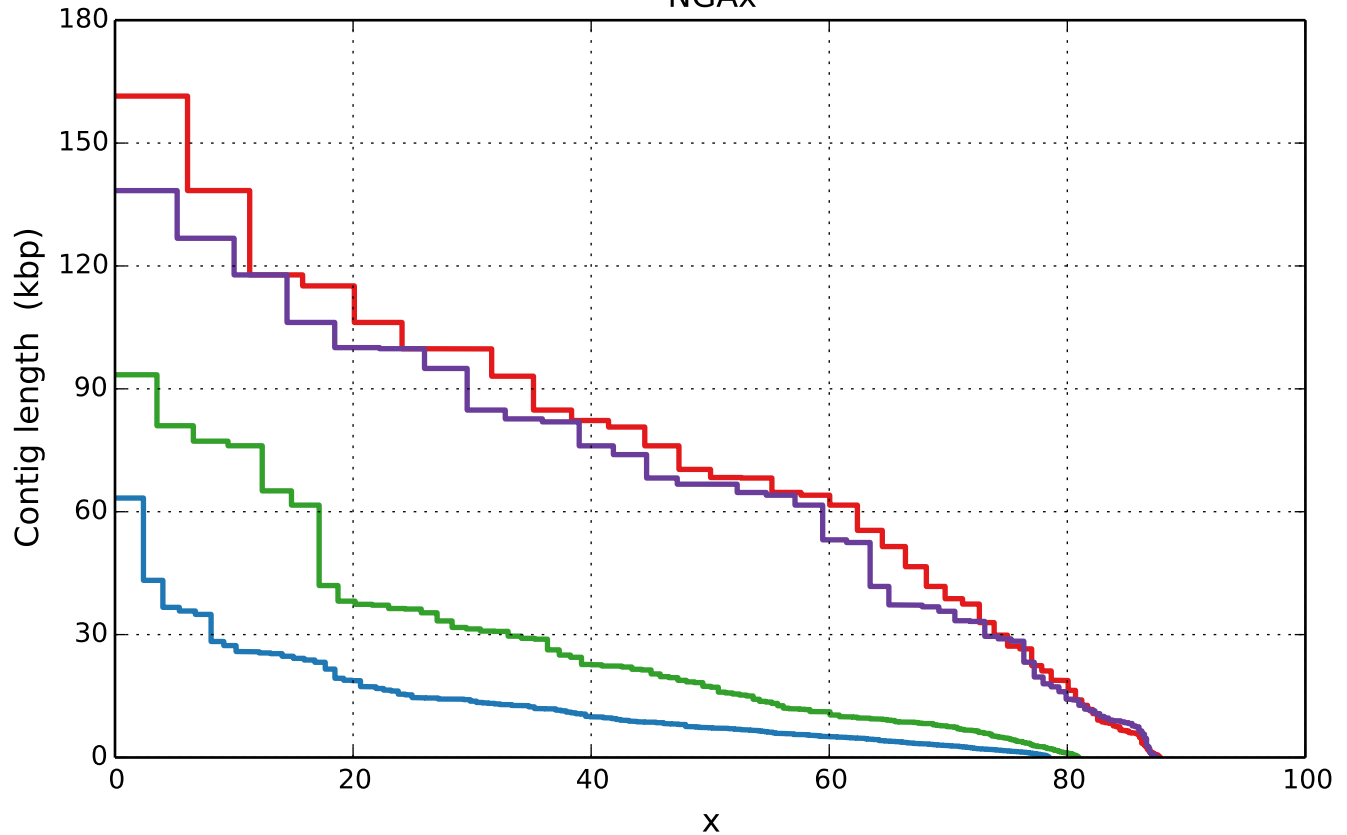


NAx



— IDBA_UD — SOAPdenovo2 — SPAdes
— Ray

NGAx



- IDBA_UD
- SOAPdenovo2
- SPAdes
- Ray

