

Report

	IDBA_UD	Ray	SOAPdenovo2	SPAdes
# contigs (>= 1000 bp)	226	331	1089	138
# contigs (>= 5000 bp)	123	164	39	89
# contigs (>= 10000 bp)	90	78	1	58
# contigs (>= 25000 bp)	31	15	0	29
# contigs (>= 50000 bp)	8	4	0	9
Total length (>= 1000 bp)	2750988	2697387	2198751	2197251
Total length (>= 5000 bp)	2514173	2273625	249489	2085591
Total length (>= 10000 bp)	2276905	1624684	12799	1874133
Total length (>= 25000 bp)	1347227	633673	0	1388753
Total length (>= 50000 bp)	568597	252019	0	699123
# contigs	272	393	2236	171
Largest contig	117419	88128	12799	162985
Total length	2784038	2739588	3001802	2221858
Reference length	5442925	5442925	5442925	5442925
GC (%)	42.89	42.51	42.53	42.74
Reference GC (%)	42.70	42.70	42.70	42.70
N50	23507	13277	1628	34196
NG50	1340	664	644	-
N75	12553	7054	963	16524
L50	33	57	537	19
LG50	201	362	1742	-
L75	74	129	1143	43
# misassemblies	41	39	5	32
# misassembled contigs	31	32	4	24
Misassembled contigs length	449034	441176	11169	1020099
# local misassemblies	19	228	164	20
# structural variations	0	0	0	0
# unaligned contigs	0 + 74 part	0 + 39 part	0 + 62 part	0 + 58 part
Unaligned length	308418	185142	54045	143288
Genome fraction (%)	43.090	43.504	53.578	33.927
Duplication ratio	1.056	1.079	1.011	1.126
# N's per 100 kbp	44.72	1302.68	336.76	73.18
# mismatches per 100 kbp	673.88	559.66	489.47	816.13
# indels per 100 kbp	30.70	19.22	12.62	31.46
Largest alignment	117419	40426	12799	114881
NA50	16210	9613	1545	17344
NGA50	-	-	595	-
NA75	4674	4476	911	5436
LA50	45	76	556	37
LGA50	-	-	1835	-
LA75	115	176	1192	92

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

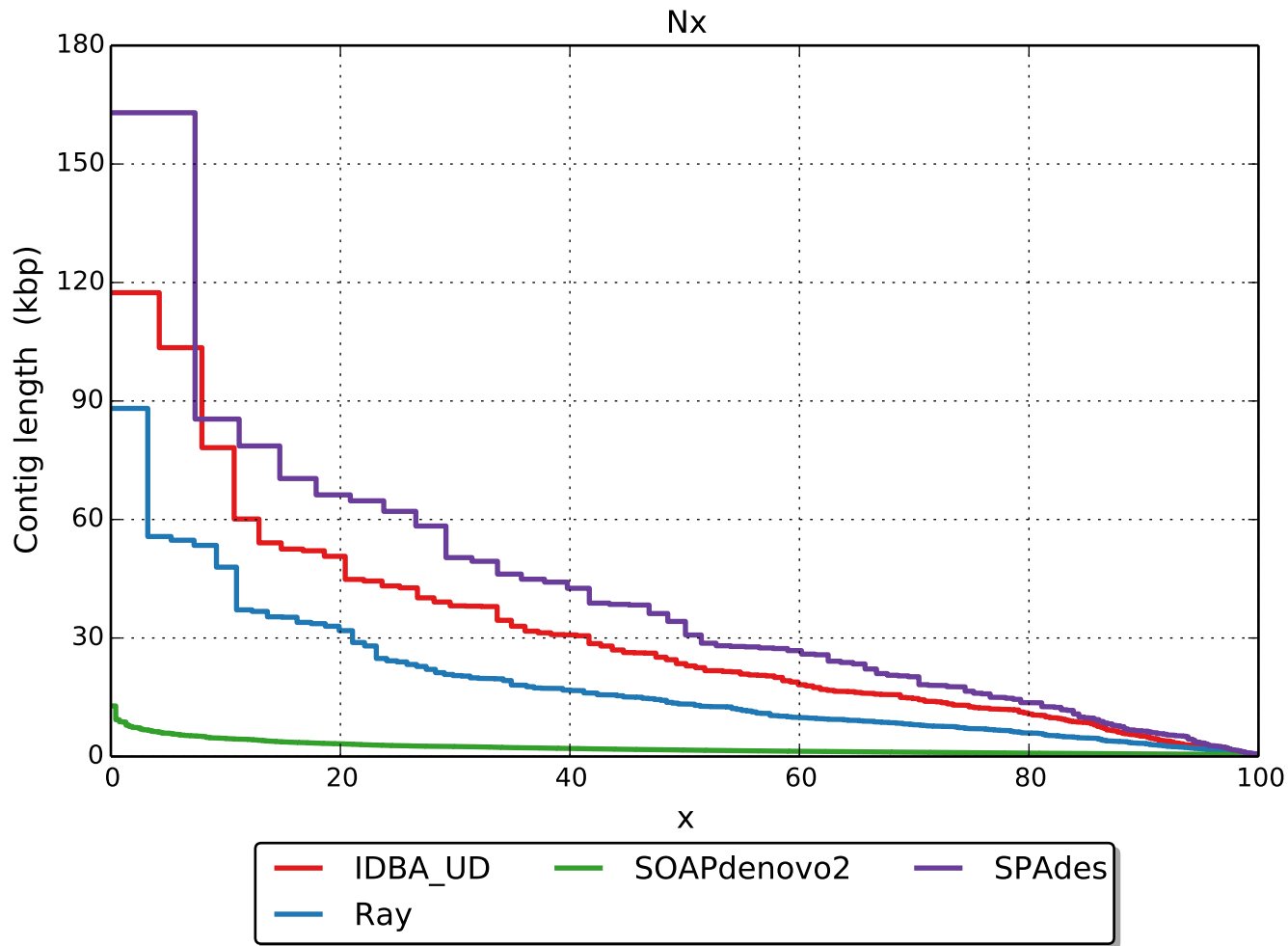
	IDBA_UD	Ray	SOAPdenovo2	SPAdes
# misassemblies	41	39	5	32
# relocations	19	14	2	18
# translocations	19	24	1	12
# inversions	3	1	2	2
# possibly misassembled contigs	39	48	11	43
# misassembled contigs	31	32	4	24
Misassembled contigs length	449034	441176	11169	1020099
# local misassemblies	19	228	164	20
# structural variations	0	0	0	0
# mismatches	15805	13252	14274	15071
# indels	720	455	368	581
# short indels	645	410	351	536
# long indels	75	45	17	45
Indels length	2028	1373	670	1491

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).

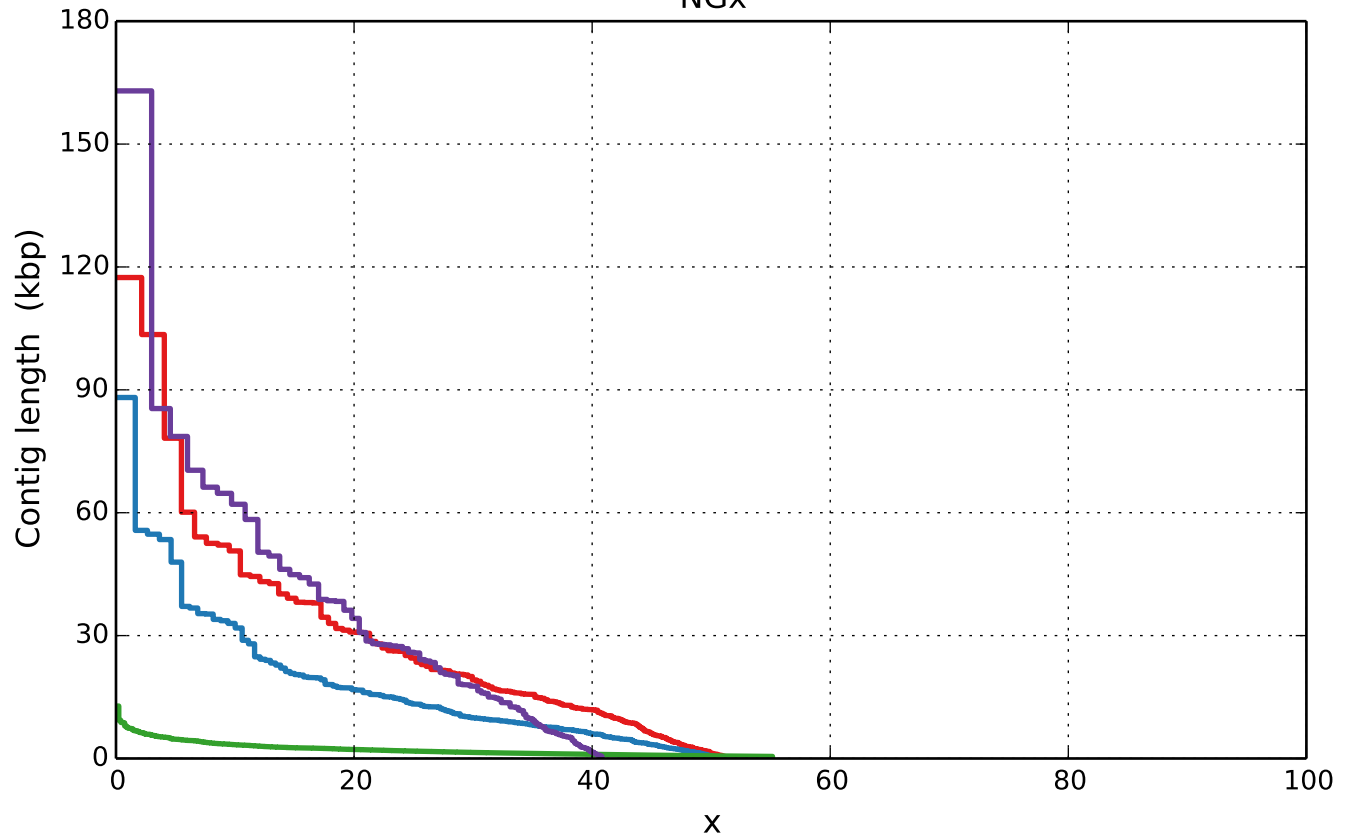
Unaligned report

	IDBA_UD	Ray	SOAPdenovo2	SPAdes
# fully unaligned contigs	0	0	0	0
Fully unaligned length	0	0	0	0
# partially unaligned contigs	74	39	62	58
# with misassembly	12	7	7	5
# both parts are significant	23	14	8	21
Partially unaligned length	308418	185142	54045	143288
# N's	1245	35688	10109	1626

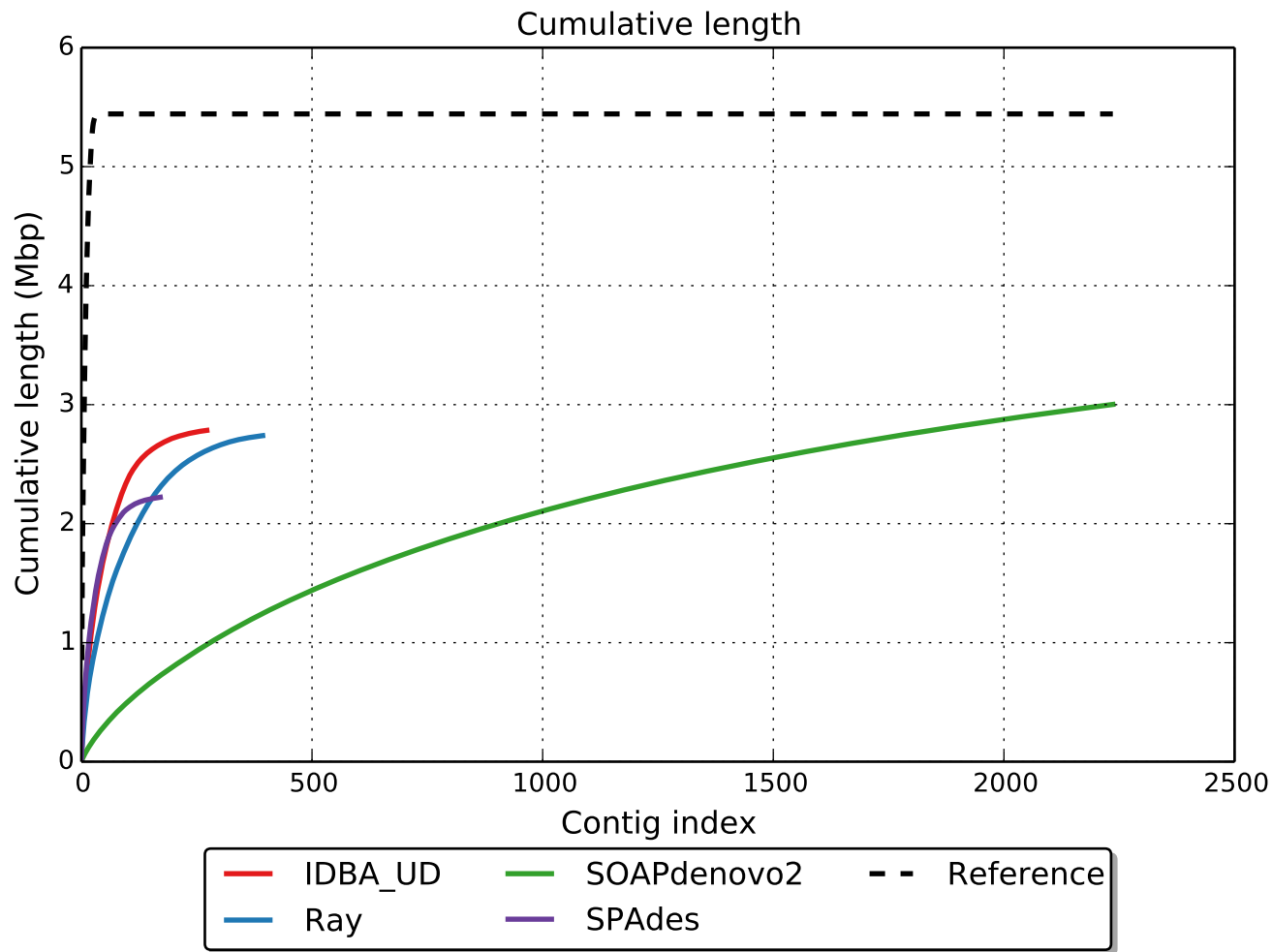
All statistics are based on contigs of size ≥ 500 bp, unless otherwise noted (e.g., "# contigs (≥ 0 bp)" and "Total length (≥ 0 bp)" include all contigs).



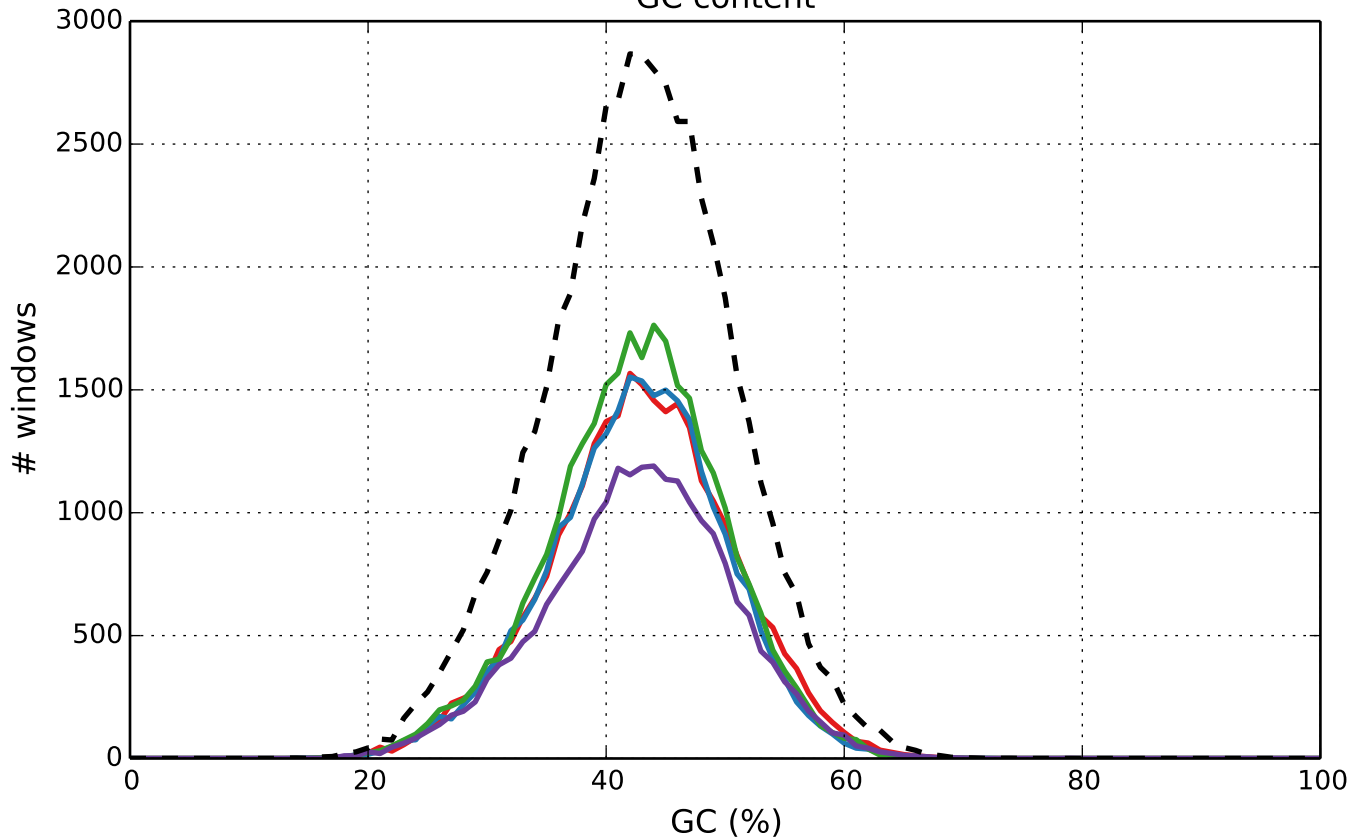
NGx



— IDBA_UD — SOAPdenovo2 — SPAdes
— Ray



GC content



IDBA_UD

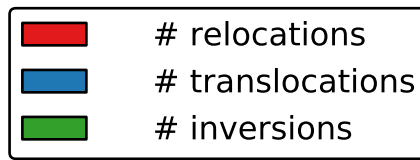
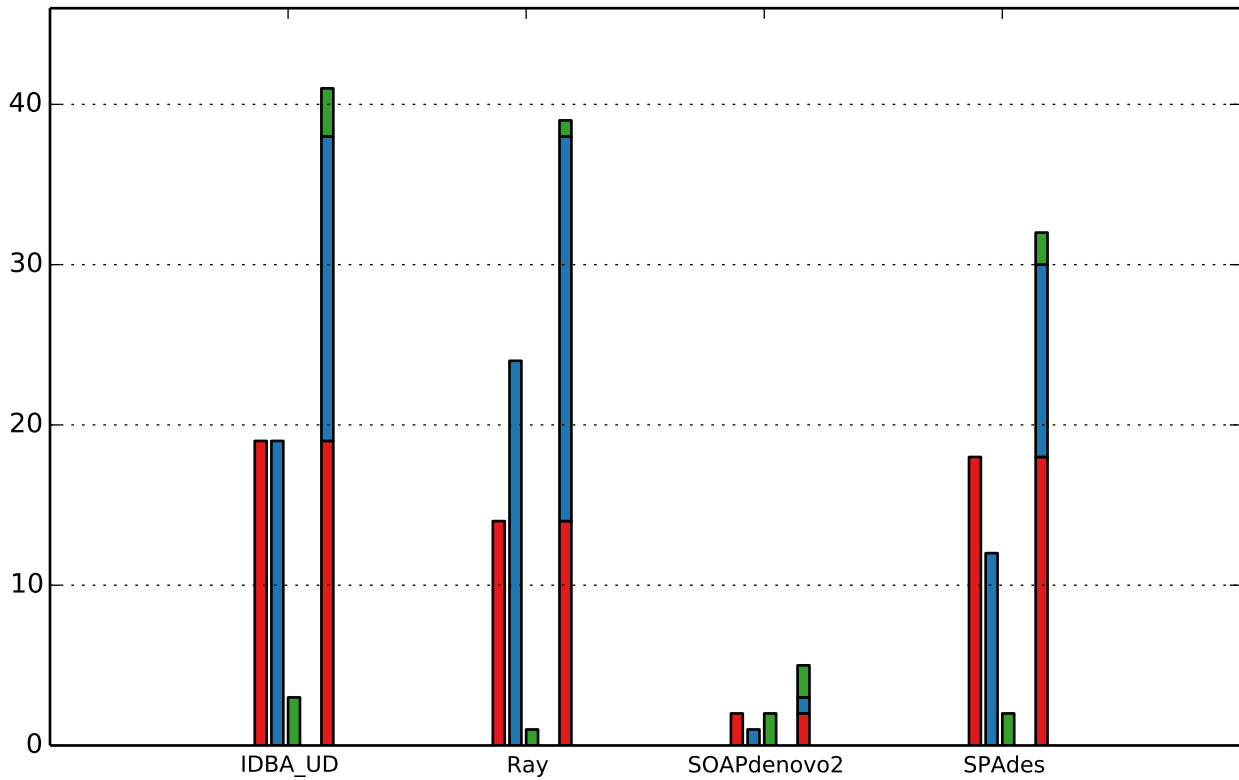
SOAPdenovo2

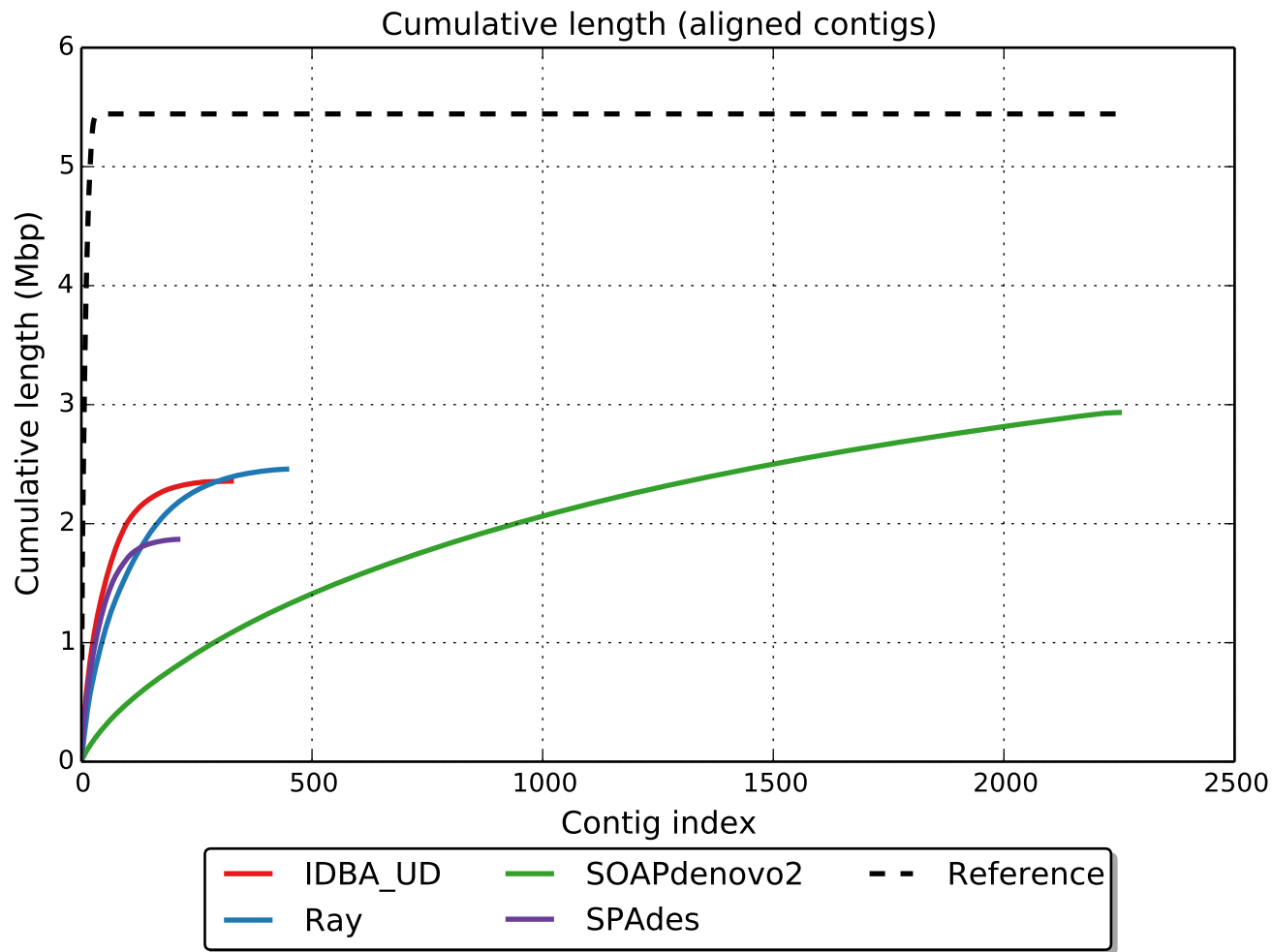
Reference

Ray

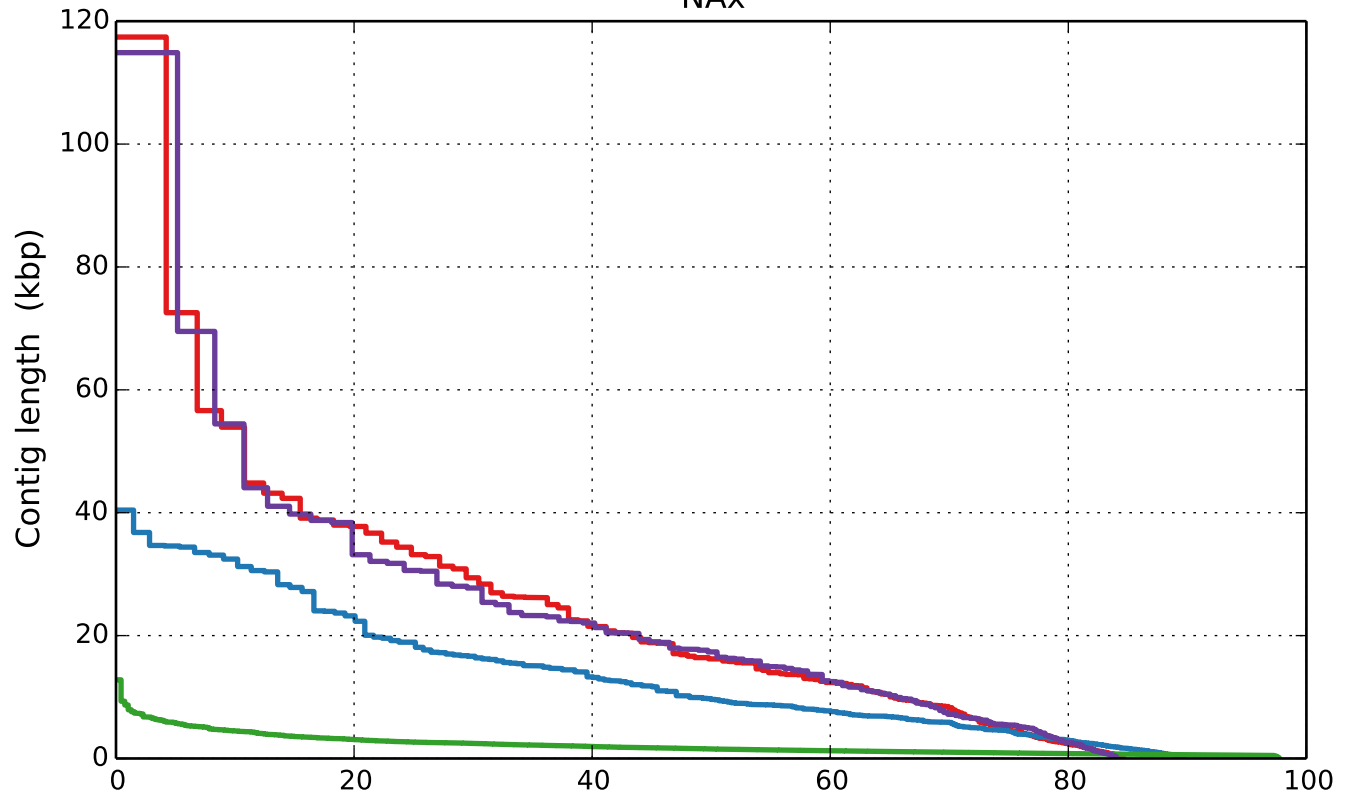
SPAdes

Misassemblies





NAx



NGAx

