

Report

	IDBA_UD	Ray	SOAPdenovo2	SPAdes
# contigs (>= 1000 bp)	151	587	1034	338
# contigs (>= 5000 bp)	111	18	49	204
# contigs (>= 10000 bp)	92	4	8	135
# contigs (>= 25000 bp)	47	0	0	44
# contigs (>= 50000 bp)	24	0	0	12
Total length (>= 1000 bp)	4005160	1198955	2195856	4213224
Total length (>= 5000 bp)	3906806	136236	336359	3858270
Total length (>= 10000 bp)	3769097	51212	86811	3369913
Total length (>= 25000 bp)	2945621	0	0	1927581
Total length (>= 50000 bp)	2090627	0	0	849821
# contigs	173	1295	1928	380
Largest contig	179824	15047	12231	126159
Total length	4021472	1690334	2833439	4244326
Reference length	4611535	4611535	4611535	4611535
GC (%)	44.83	42.95	44.69	44.86
Reference GC (%)	44.71	44.71	44.71	44.71
N50	51456	1571	1785	21952
NG50	45430	-	907	20846
N75	24854	900	1054	11902
NG75	16816	-	-	9084
L50	23	310	448	53
LG50	29	-	1150	61
L75	50	660	965	118
LG75	70	-	-	145
# misassemblies	53	11	20	46
# misassembled contigs	33	9	19	36
Misassembled contigs length	1788741	28132	64687	738668
# local misassemblies	27	388	1142	21
# structural variations	6	0	4	6
# unaligned contigs	0 + 58 part	0 + 67 part	0 + 158 part	0 + 132 part
Unaligned length	521788	54302	113094	940290
Genome fraction (%)	70.516	32.495	56.920	68.387
Duplication ratio	1.076	1.092	1.036	1.048
# N's per 100 kbp	42.52	3837.64	1992.31	195.41
# mismatches per 100 kbp	721.24	725.57	849.80	797.10
# indels per 100 kbp	31.40	18.15	19.09	29.93
Largest alignment	179515	14202	12231	68909
NA50	24829	1329	1591	8856
NGA50	20660	-	715	7591
NA75	7154	734	871	-
LA50	42	381	503	111
LGA50	55	-	1341	133
LA75	113	812	1110	-

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

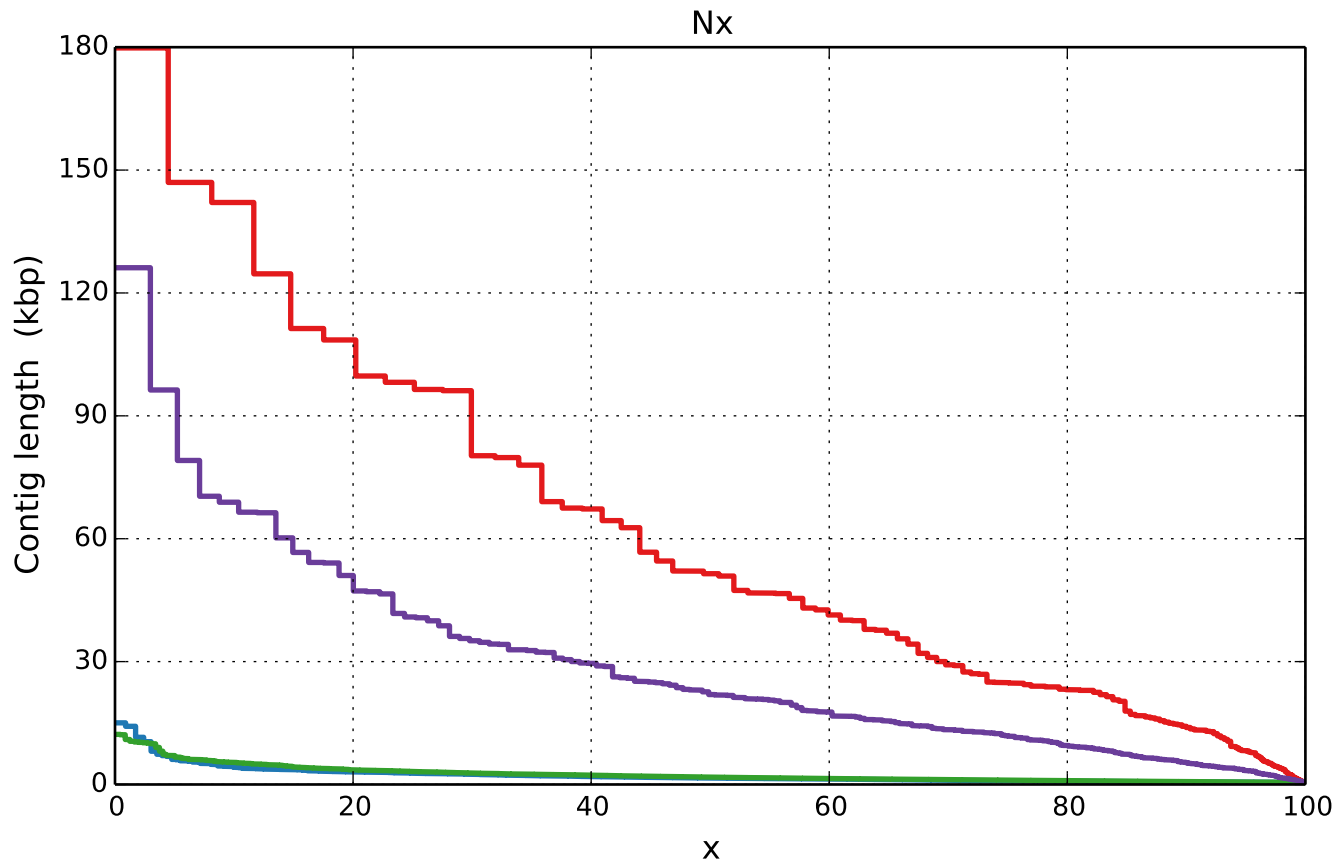
	IDBA_UD	Ray	SOAPdenovo2	SPAdes
# misassemblies	53	11	20	46
# relocations	36	4	14	25
# translocations	15	7	6	20
# inversions	2	0	0	1
# possibly misassembled contigs	71	39	44	111
# misassembled contigs	33	9	19	36
Misassembled contigs length	1788741	28132	64687	738668
# local misassemblies	27	388	1142	21
# structural variations	6	0	4	6
# mismatches	23454	10873	22306	25138
# indels	1021	272	501	944
# short indels	883	242	444	808
# long indels	138	30	57	136
Indels length	3392	766	1854	3142

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).

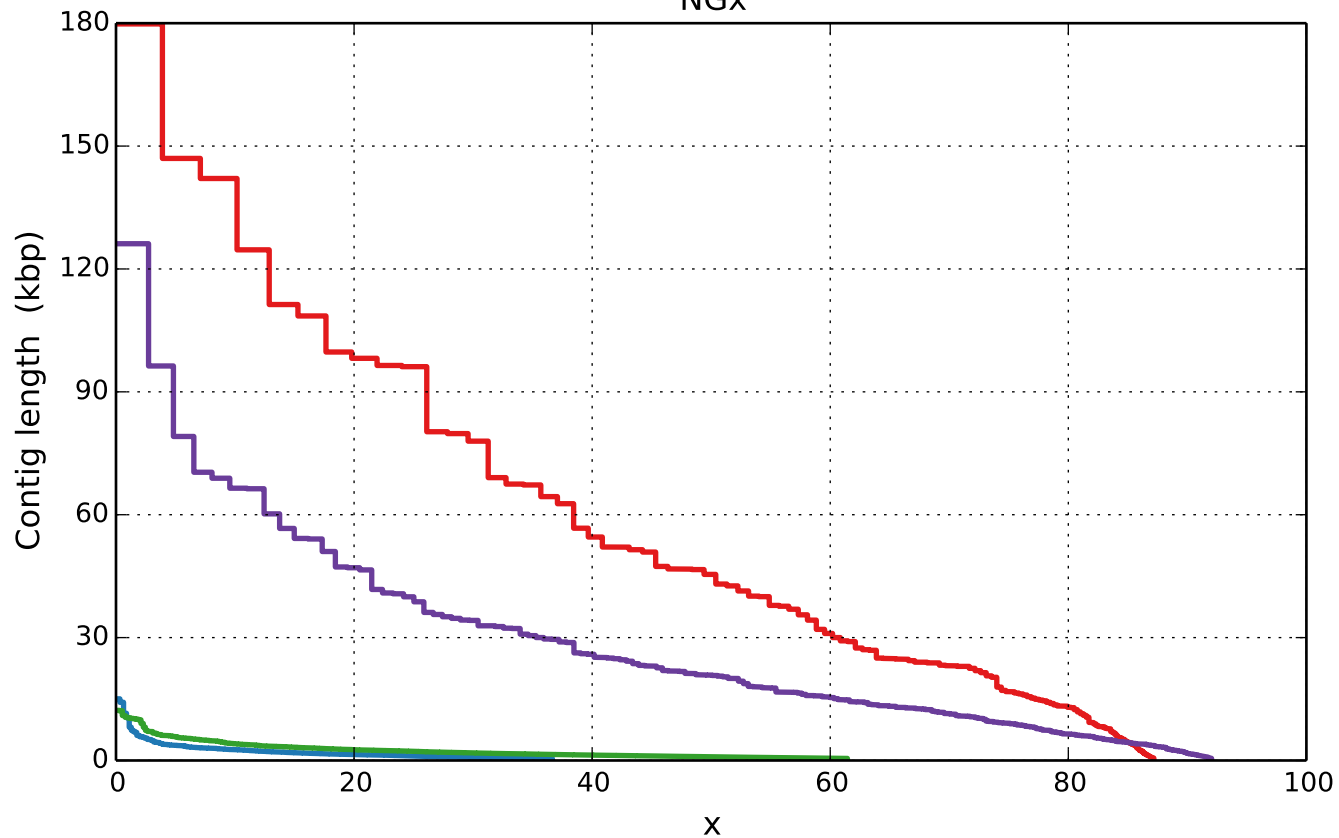
Unaligned report

	IDBA_UD	Ray	SOAPdenovo2	SPAdes
# fully unaligned contigs	0	0	0	0
Fully unaligned length	0	0	0	0
# partially unaligned contigs	58	67	158	132
# with misassembly	3	6	16	9
# both parts are significant	37	17	30	77
Partially unaligned length	521788	54302	113094	940290
# N's	1710	64869	56451	8294

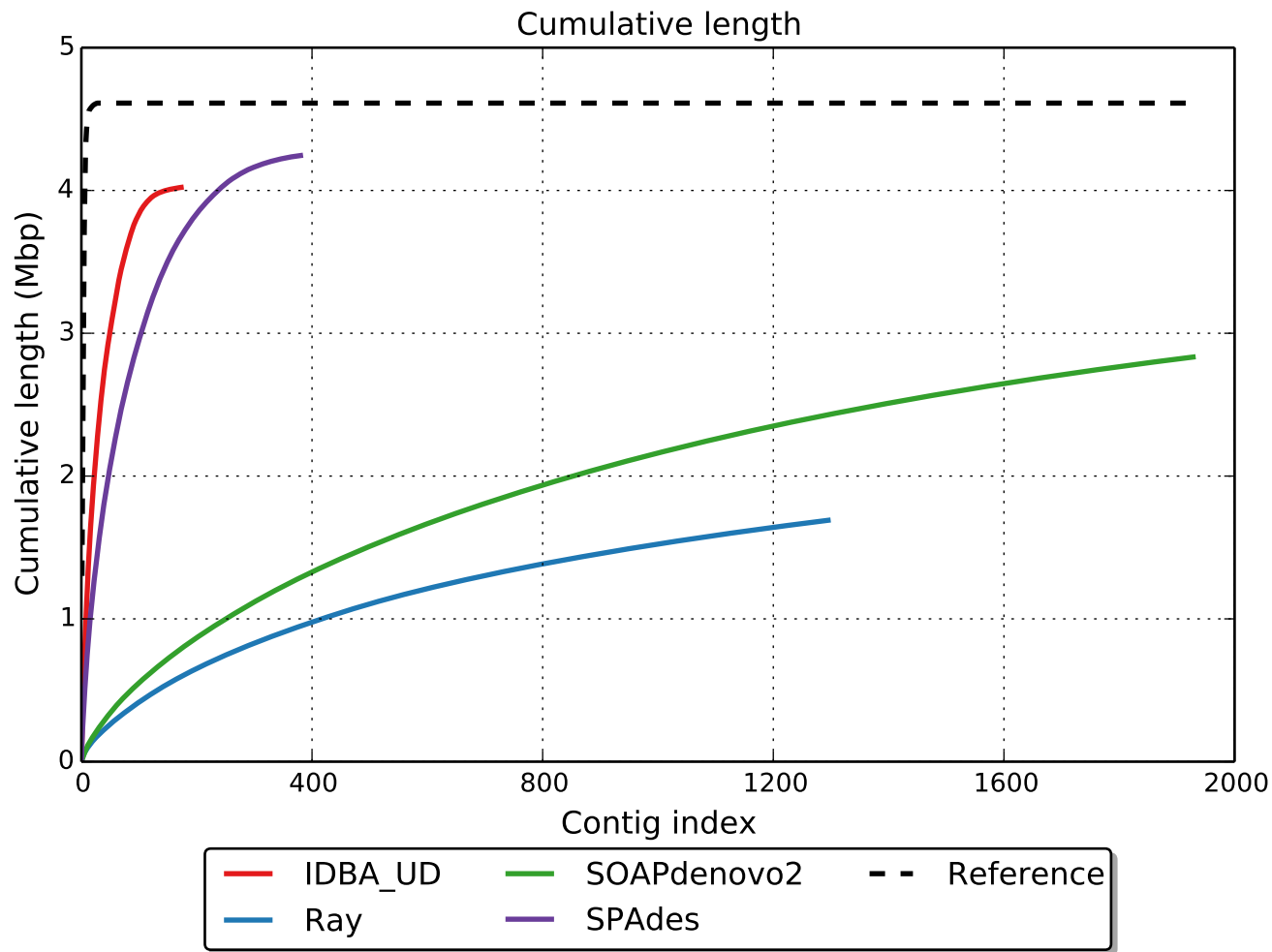
All statistics are based on contigs of size ≥ 500 bp, unless otherwise noted (e.g., "# contigs (≥ 0 bp)" and "Total length (≥ 0 bp)" include all contigs).



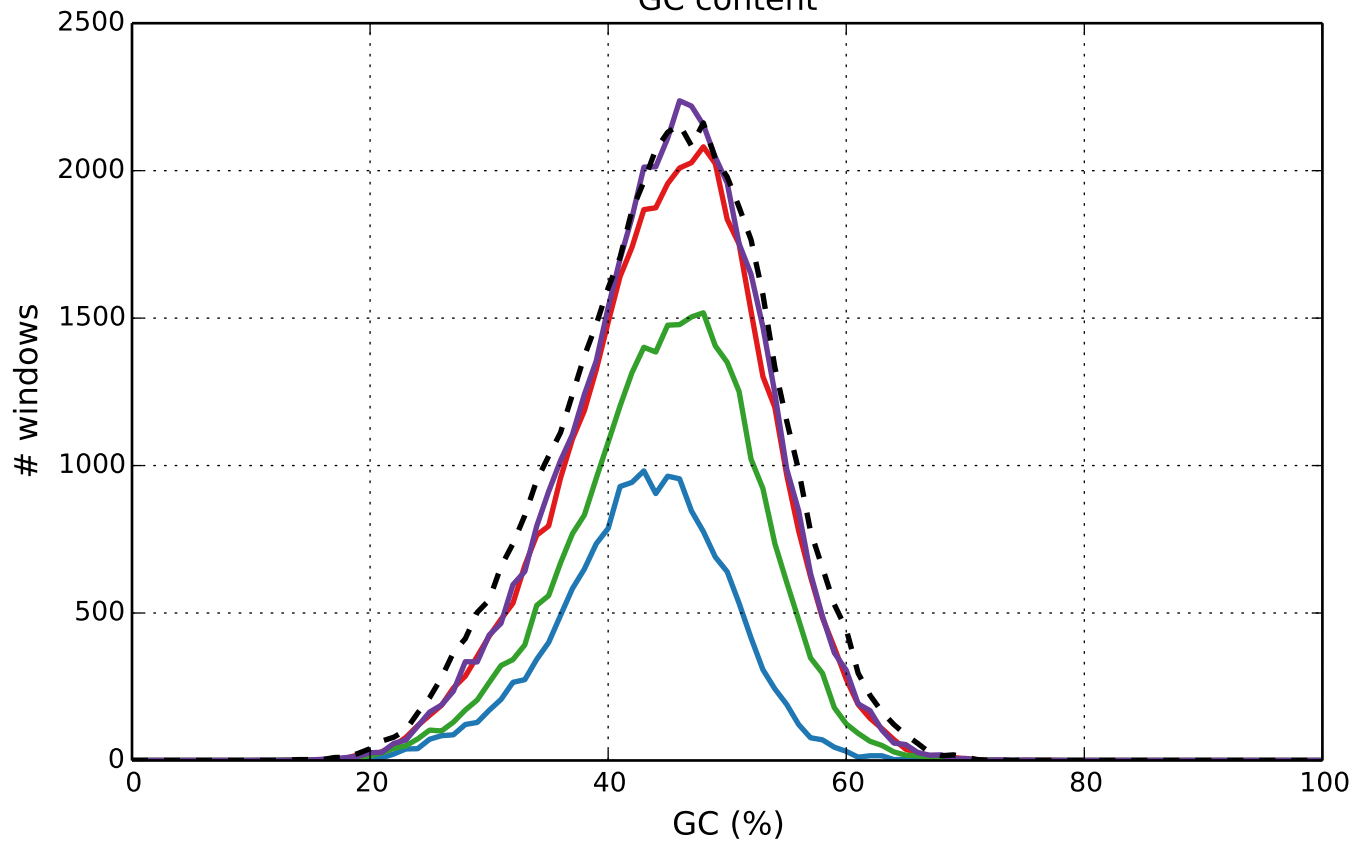
NGx



— IDBA_UD — SOAPdenovo2 — SPAdes
— Ray



GC content



— IDBA_UD

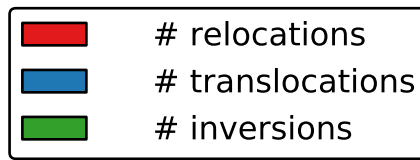
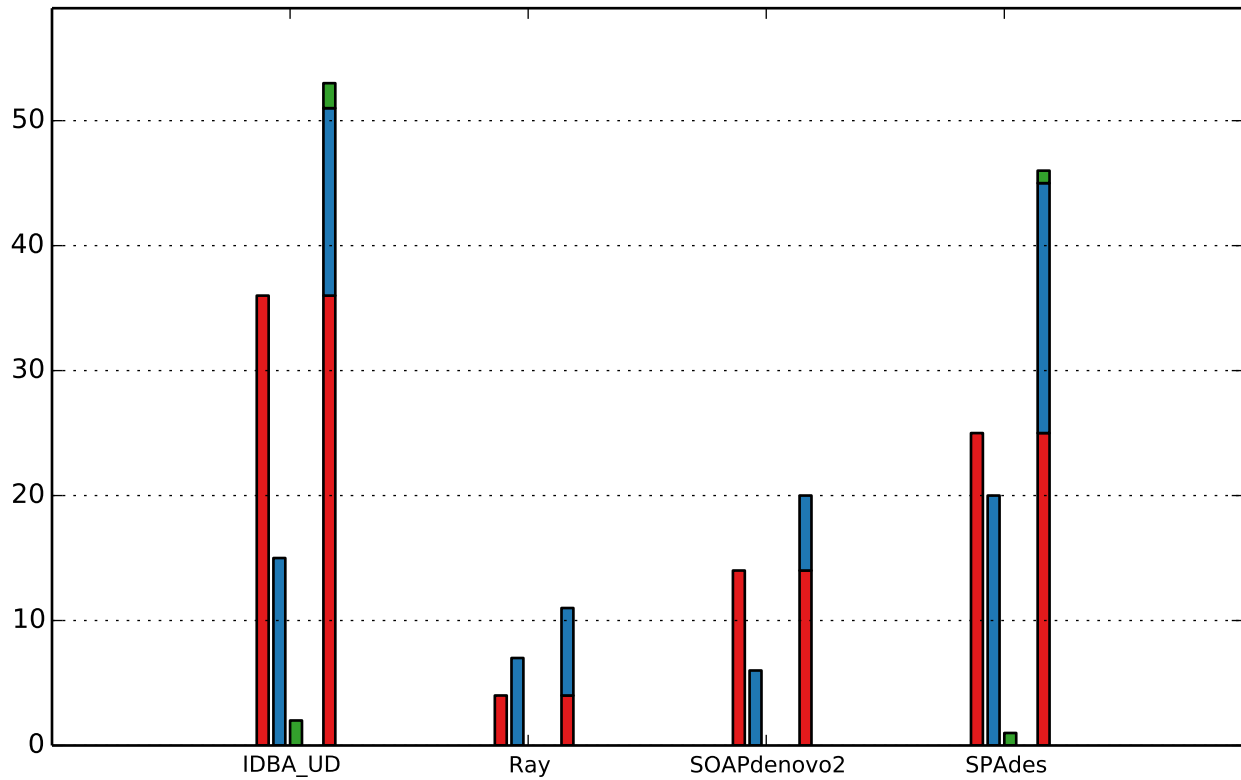
— SOAPdenovo2

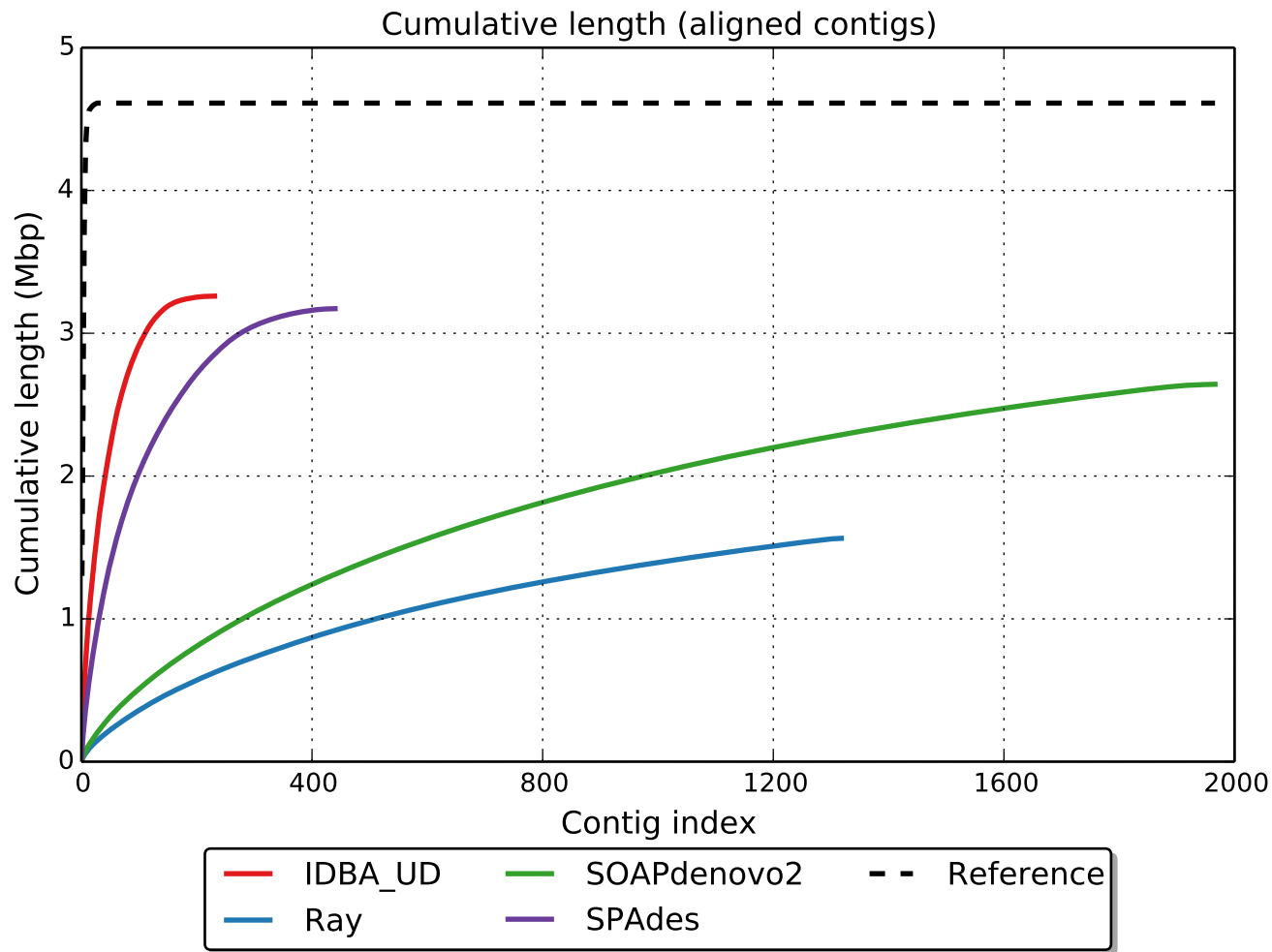
- - Reference

— Ray

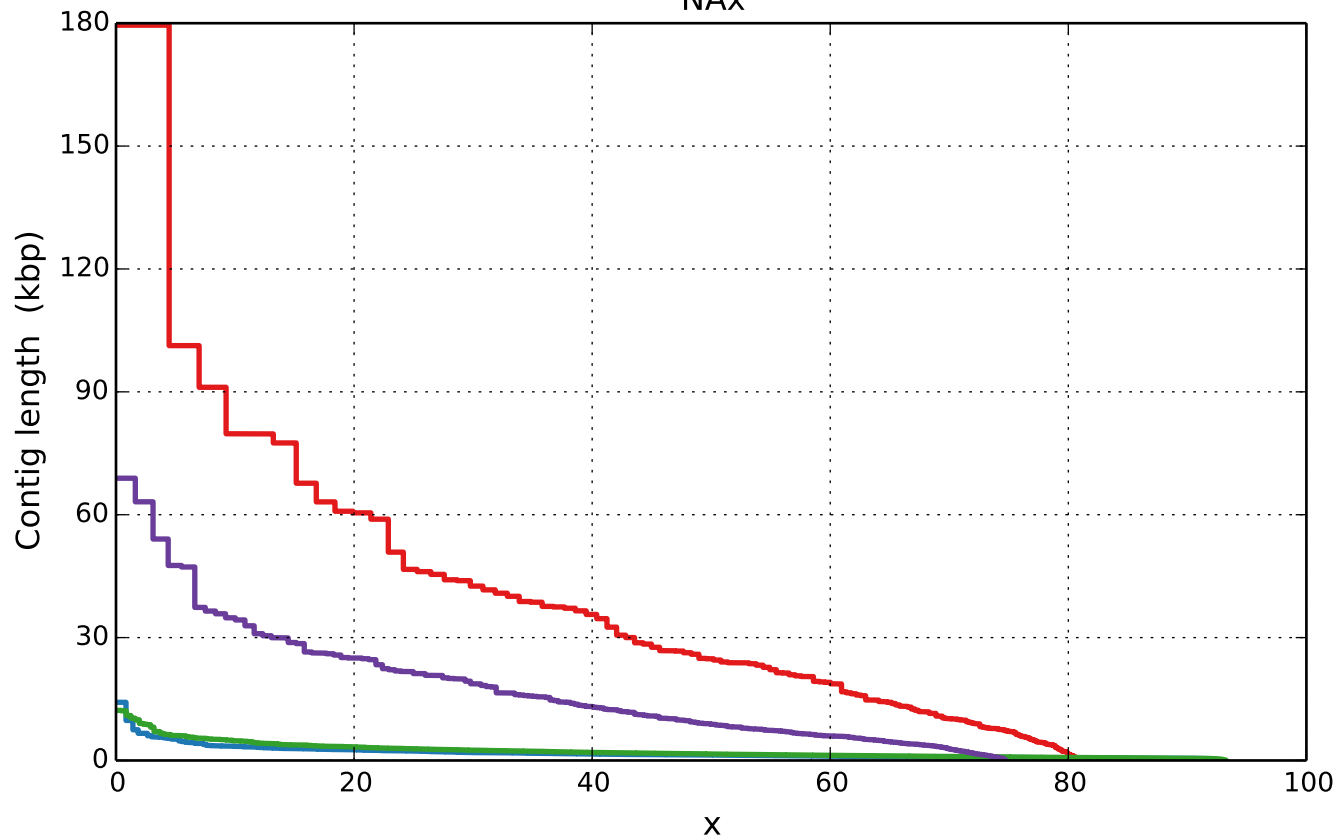
— SPAdes

Misassemblies



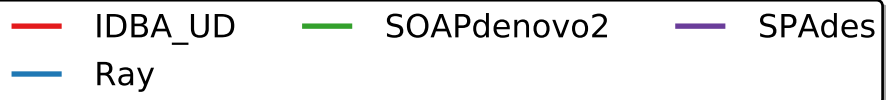
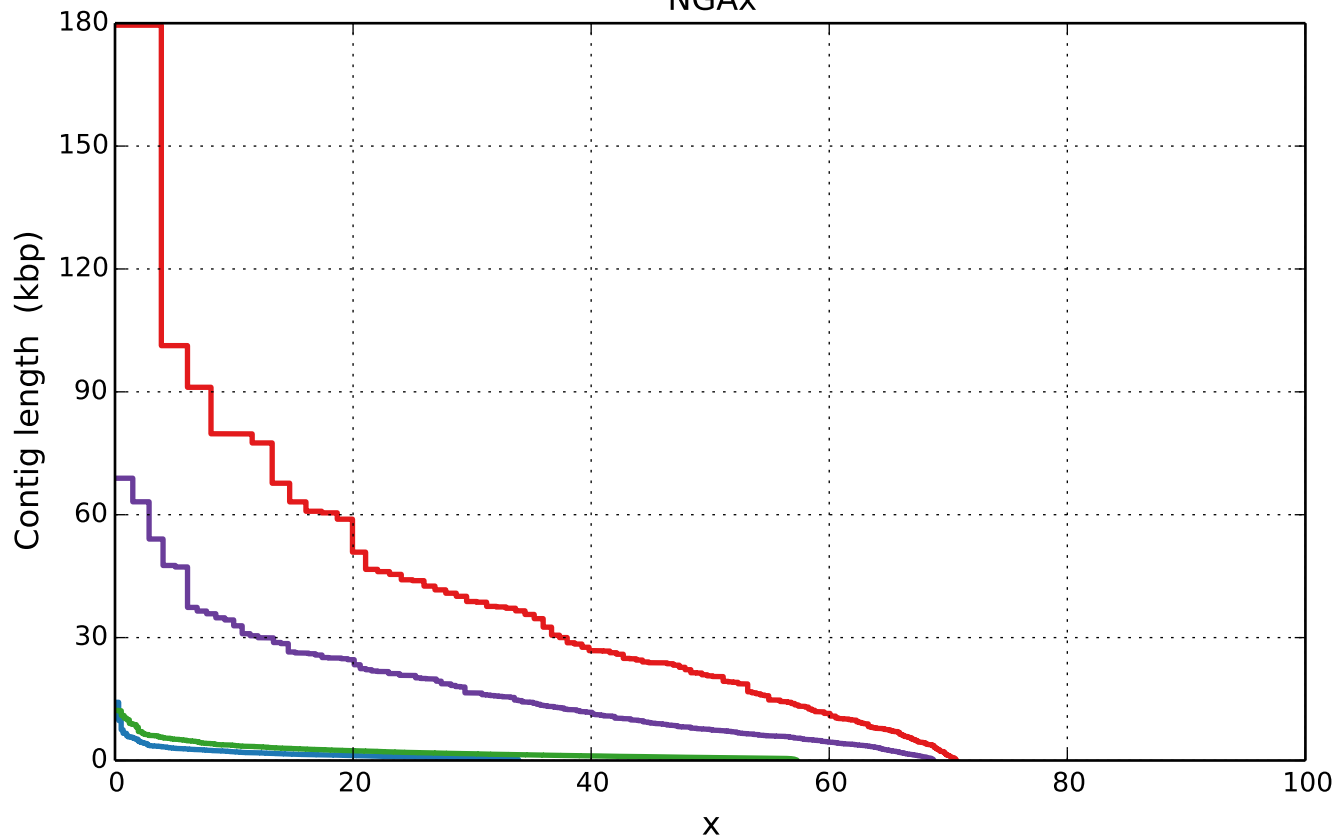


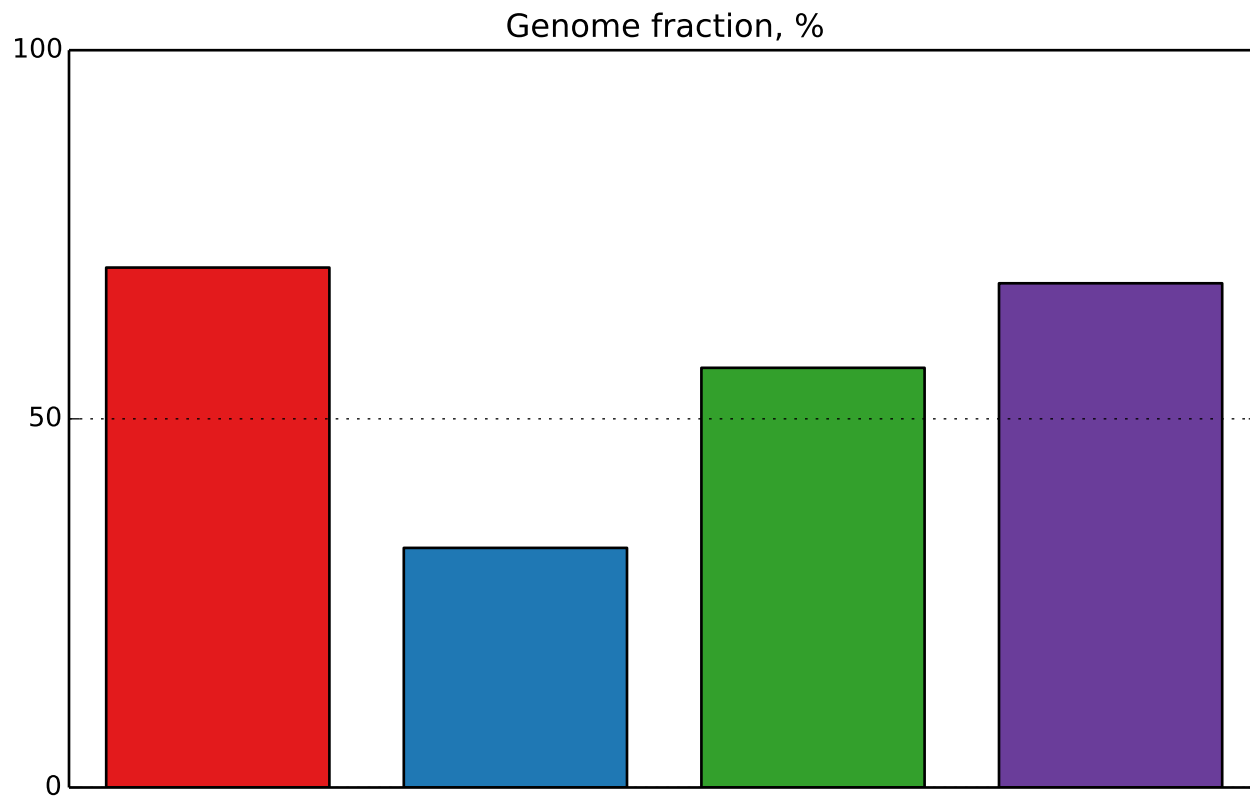
NAx



— IDBA_UD — SOAPdenovo2 — SPAdes
— Ray

NGAx





IDBA_UD

SOAPdenovo2

SPAdes

Ray