Report

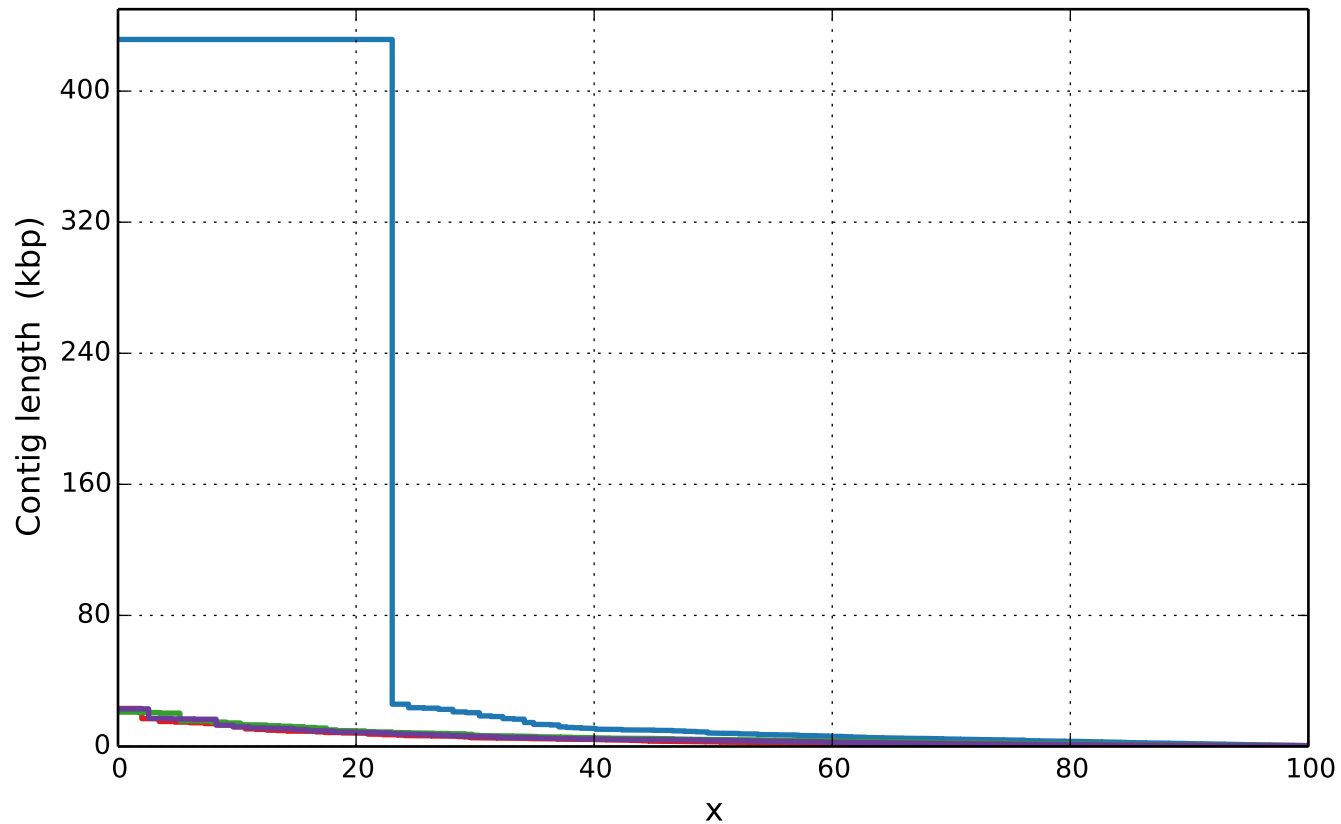|	IDBA_UD	Ray	SOAPdenovo2	SPAdes
# contigs (>= 1000 bp)	315	310	291	221
# contigs (>= 5000 bp)	46	87	60	36
# contigs (>= 10000 bp)	10	29	15	10
# contigs (>= 25000 bp)	0	2	0	0
# contigs (>= 50000 bp)	0	1	0	0
Total length (>= 1000 bp)	930307	1793577	1055002	738979
Total length (>= 5000 bp)	394795	1244060	521704	323093
Total length (>= 10000 bp)	145101	843217	218930	142151
Total length (>= 25000 bp)	0	457331	0	0
Total length (>= 50000 bp)	0	431523	0	0
# contigs	641	421	489	438
Largest contig	23191	431523	20974	22957
Total length	1158721	1873375	1192250	892035
Reference length	2431995	2431995	2431995	2431995
GC (%)	65.19	63.83	65.32	64.85
Reference GC (%)	65.25	65.25	65.25	65.25
N50	2851	8194	4239	3705
NG50	-	5154	-	-
N75	1173	3908	2014	1431
NG75	-	811	-	-
L50	96	40	77	65
LG50	-	82	-	-
L75	259	124	177	162
LG75	-	345	-	-
# misassemblies	6	5	5	5
# misassembled contigs	6	5	5	5
Misassembled contigs length	16479	20516	18009	24954
# local misassemblies	10	45	18	4
# structural variations	0	0	0	1
# unaligned contigs	0 + 222 part	0 + 224 part	0 + 404 part	0 + 164 part
Unaligned length	497862	1175843	931495	335242
Genome fraction (%)	23.120	24.460	9.679	21.343
Duplication ratio	1.175	1.173	1.108	1.073
# N's per 100 kbp	0.00	2521.71	6422.39	182.62
# mismatches per 100 kbp	3721.99	3867.84	3231.04	3657.65
# indels per 100 kbp	50.51	53.96	44.60	53.37
Largest alignment	10446	13161	5653	21788
NA50	558	-	-	749
NGA50	-	-	-	-
LA50	439	-	-	240

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).
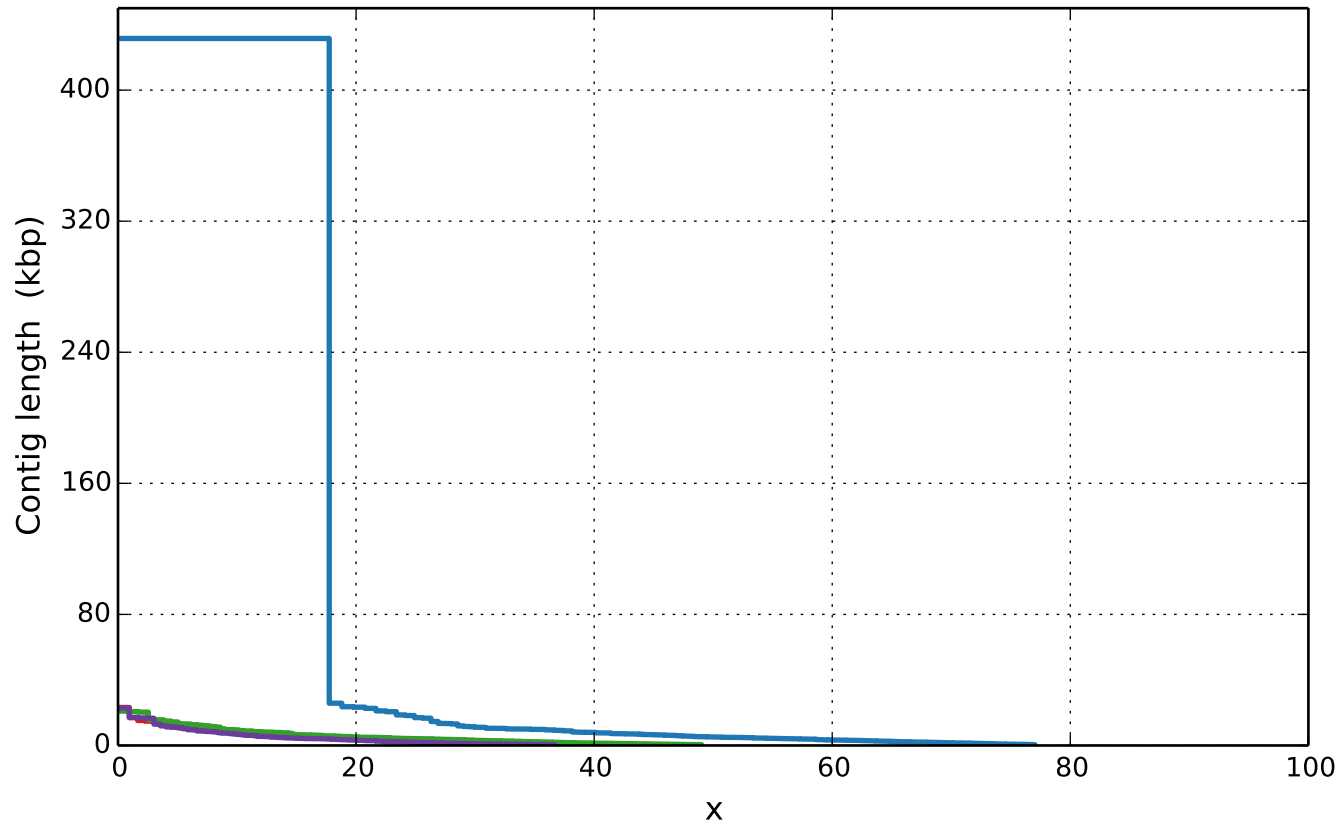
Misassemblies report

	IDBA_UD	Ray	SOAPdenovo2	SPAdes
# misassemblies	6	5	5	5
# relocations	3	2	5	4
# translocations	3	3	0	0
# inversions	0	0	0	1
# possibly misassembled contigs	55	164	89	68
# misassembled contigs	6	5	5	5
Misassembled contigs length	16479	20516	18009	24954
# local misassemblies	10	45	18	4
# structural variations	0	0	0	1
# mismatches	20928	23008	7606	18985
# indels	284	321	105	277
# short indels	255	313	81	268
# long indels	29	8	24	9
Indels length	920	472	698	543

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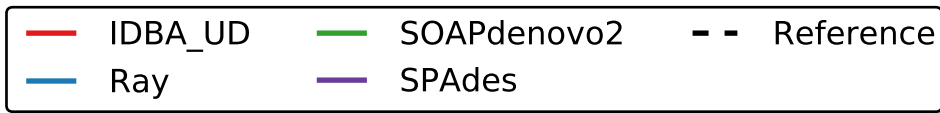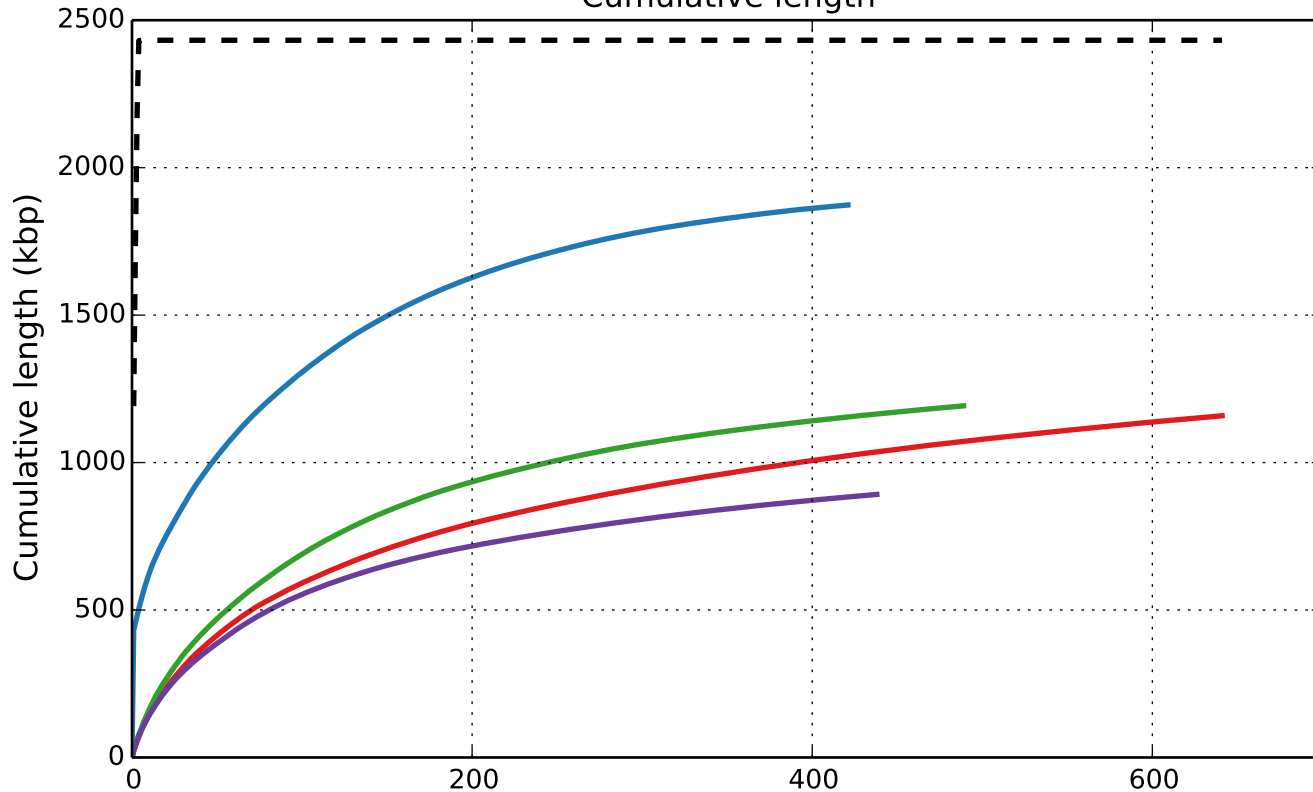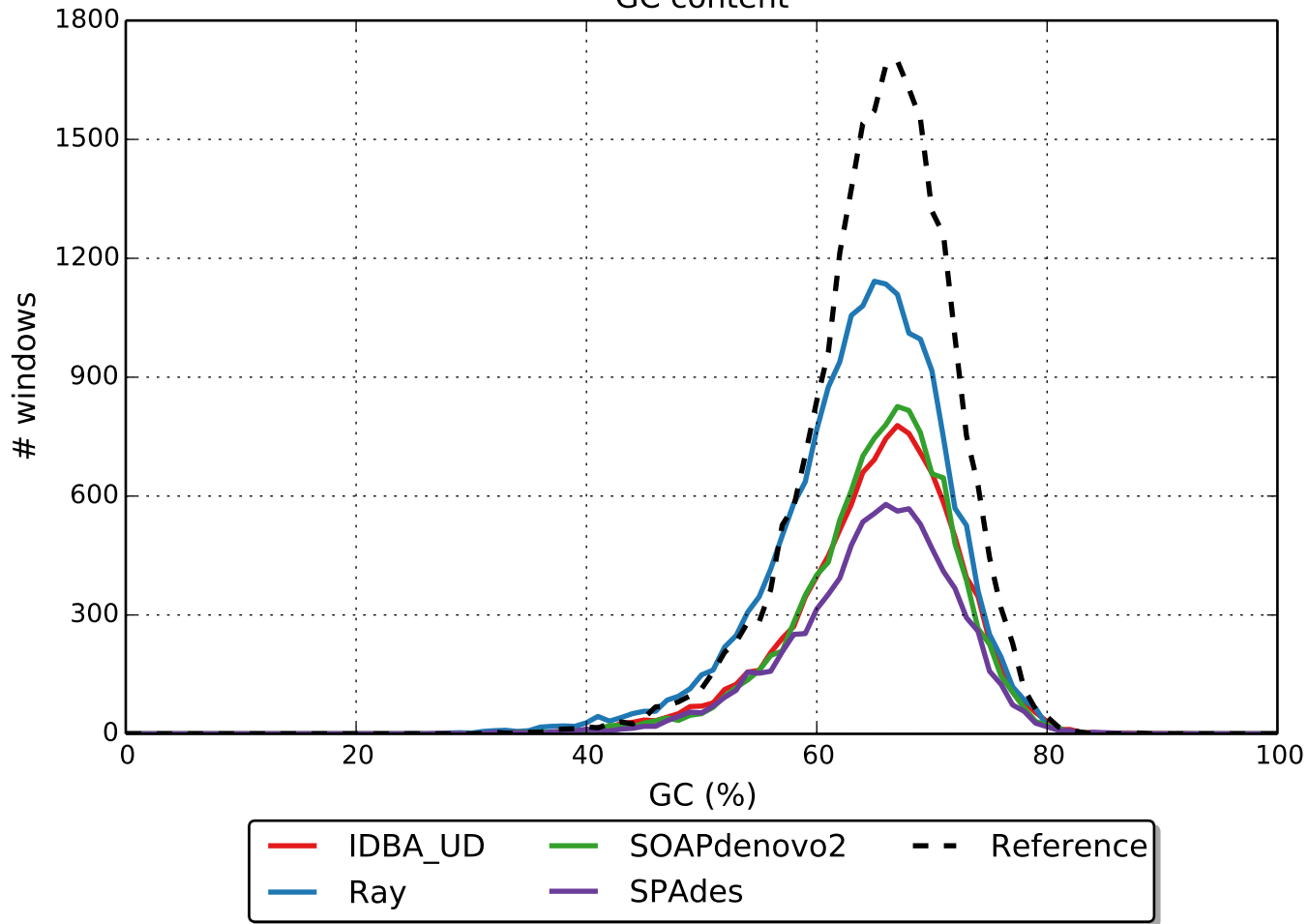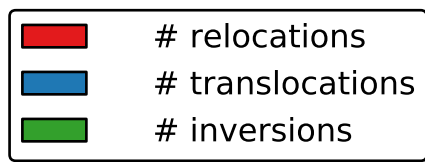(e.g., "# contigs (>= 0 bp)" and "Total length (>= 0 bp)" include all contigs).

Unaligned report

	IDBA_UD	Ray	SOAPdenovo2	SPAdes
# fully unaligned contigs	0	0	0	0
Fully unaligned length	0	0	0	0
# partially unaligned contigs	222	224	404	164
# with misassembly	7	30	47	5
# both parts are significant	48	138	81	63
Partially unaligned length	497862	1175843	931495	335242
# N's	0	47241	76571	1629

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

Contig length (kbp)

x

IDBA_UD   SOAPdenovo2   SPAdes
Ray

Cumulative length

Contig index

IDBA_UD SOAPdenovo2 --- Reference
Ray SPAdes

GC content

Misassemblies

relocations
translocations
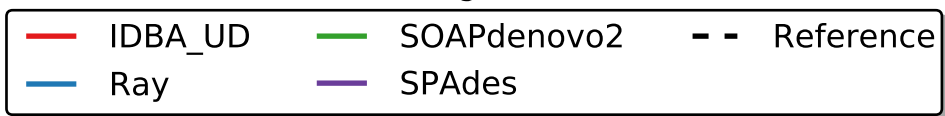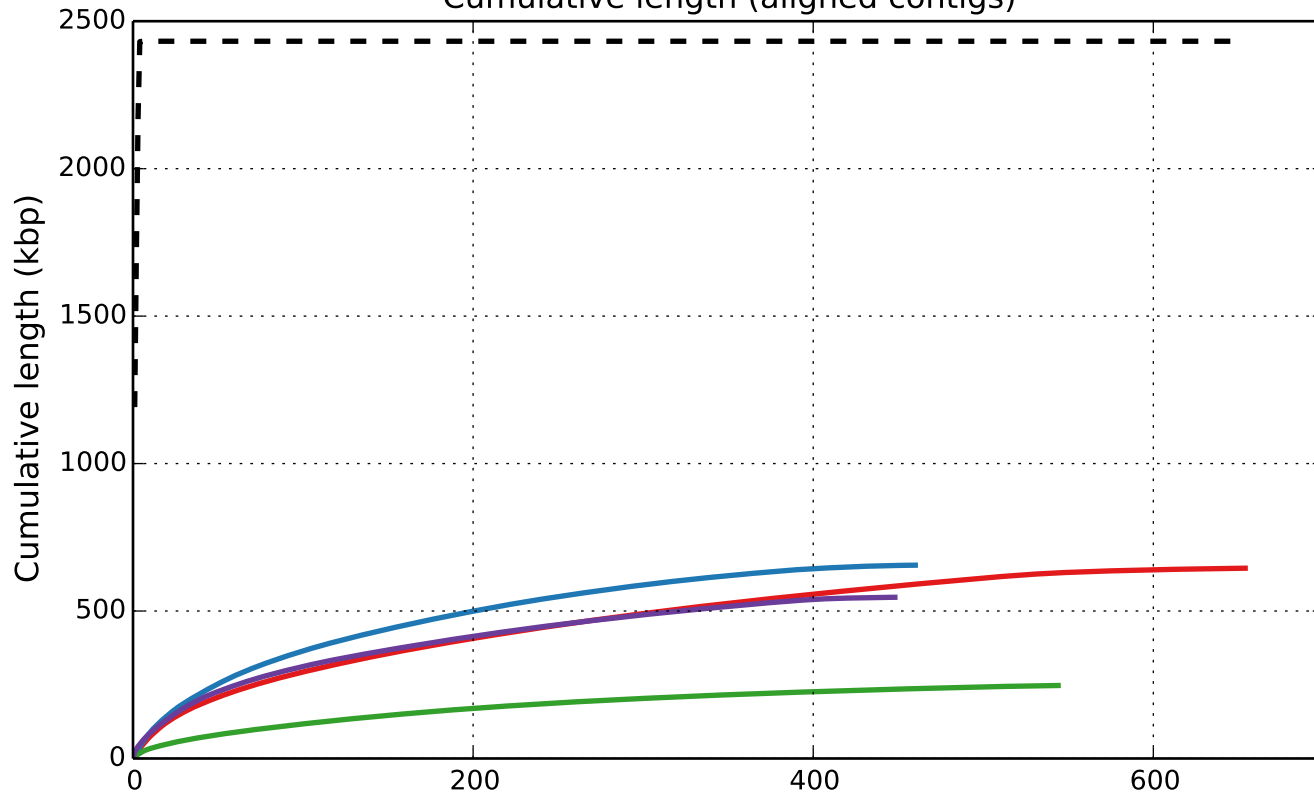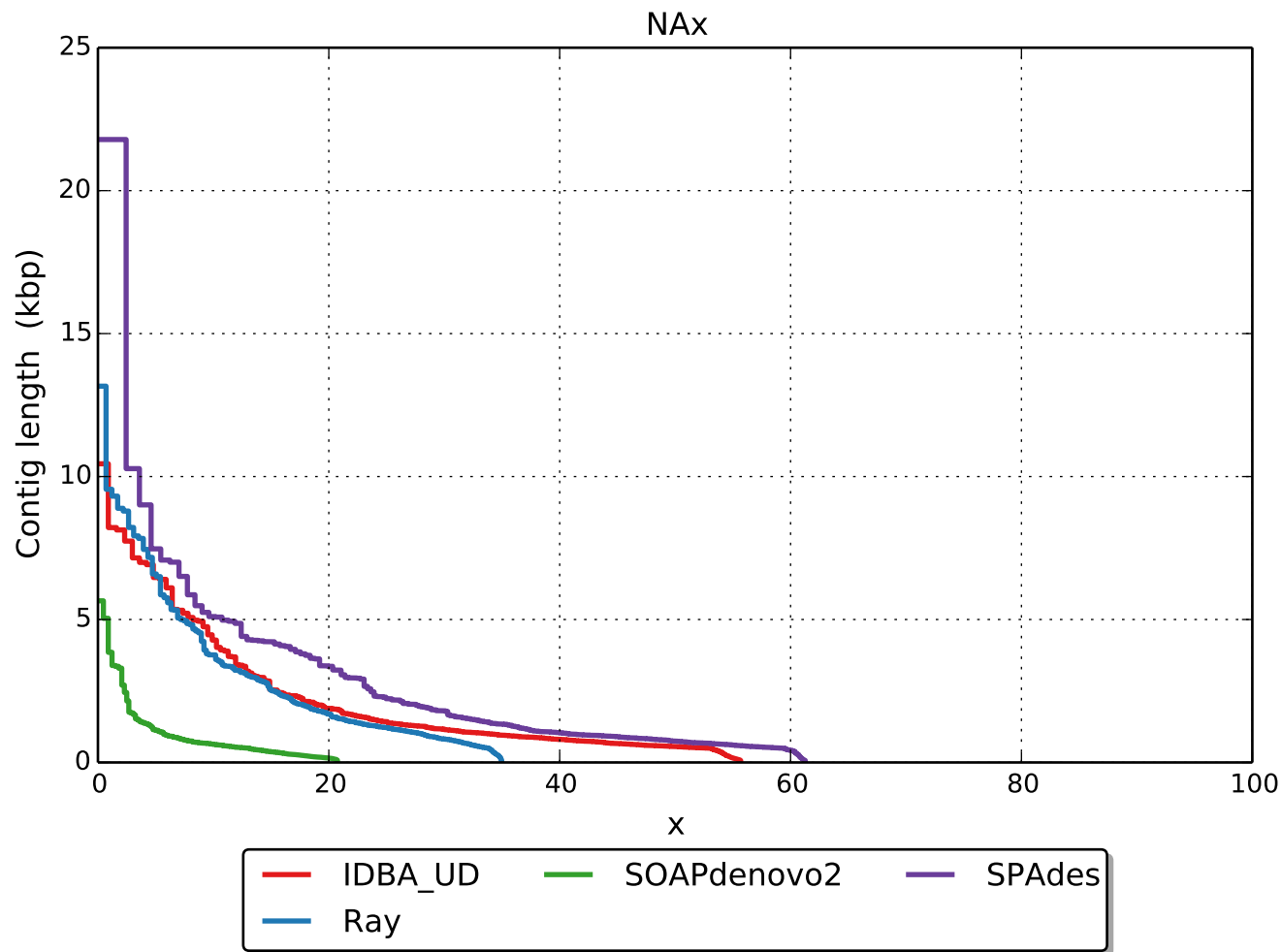# inversions
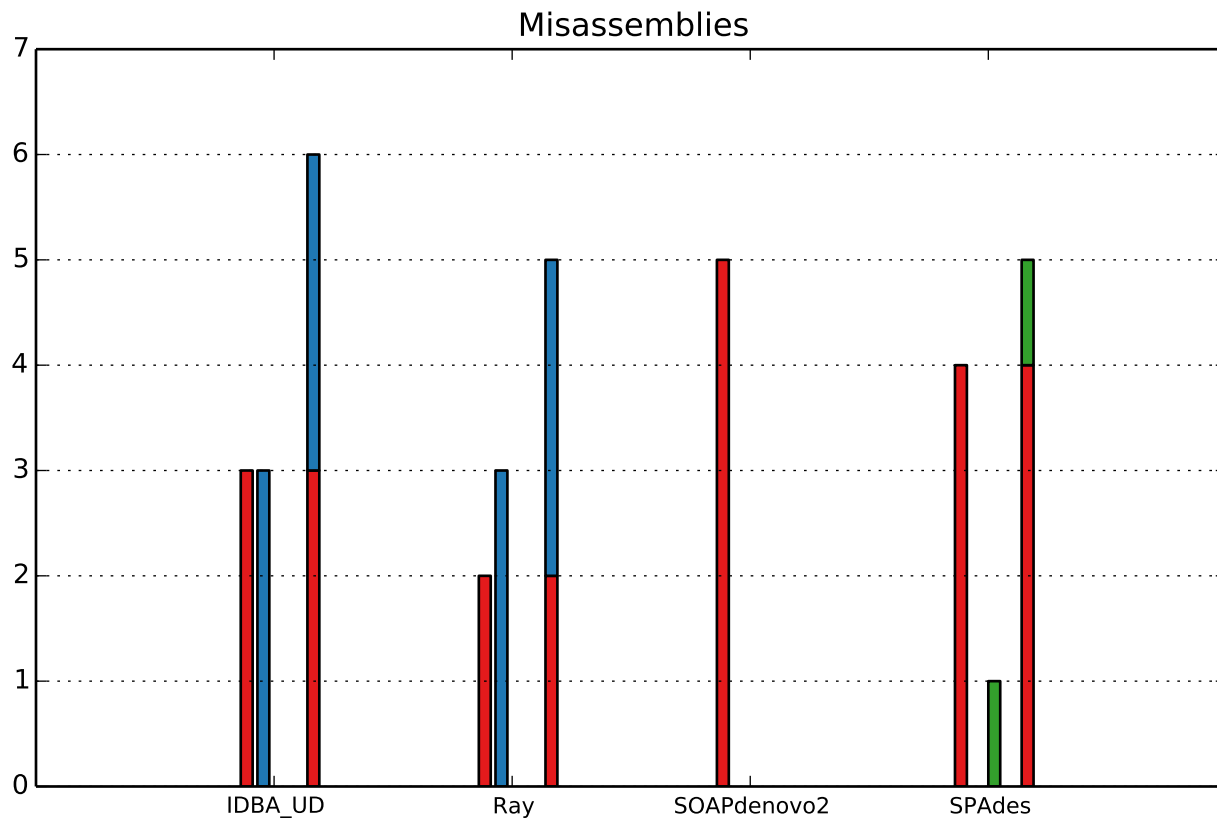
Cumulative length (aligned contigs)

NAx

Contig length (kbp) vs x

Legend:
- IDBA_UD
- Ray
- SOAPdenovo2
- SPAdes

Genome fraction, %