Report

	IDBA_UD	Ray	SOAPdenovo2	SPAdes
# contigs (>= 1000 bp)	52	14	18	44
# contigs (>= 5000 bp)	17	2	0	14
# contigs (>= 10000 bp)	11	2	0	9
# contigs (>= 25000 bp)	6	0	0	5
# contigs (>= 50000 bp)	3	0	0	3
Total length (>= 1000 bp)	551483	48054	24532	444302
Total length (>= 5000 bp)	468150	25645	0	376524
Total length (>= 10000 bp)	420877	25645	0	347076
Total length (>= 25000 bp)	340303	0	0	288655
Total length (>= 50000 bp)	234704	0	0	204041
# contigs	73	16	46	69
Largest contig	119910	13588	2715	85969
Total length	565313	49183	43196	461630
Reference length	2870795	2870795	2870795	2870795
GC (%)	39.51	39.73	40.94	41.05
Reference GC (%)	34.92	34.92	34.92	34.92
N50	36911	12057	1042	45766
N75	9629	2177	694	11893
L50	5	2	16	4
L75	12	6	28	9
# misassemblies	1	1	0	2
# misassembled contigs	1	1	0	2
Misassembled contigs length	2987	1480	0	5296
# local misassemblies	4	2	29	4
# structural variations	0	0	0	0
# unaligned contigs	0 + 41 part	0 + 6 part	0 + 8 part	0 + 39 part
Unaligned length	469802	31342	4035	378395
Genome fraction (%)	3.256	0.583	1.281	2.777
Duplication ratio	1.022	1.066	1.065	1.044
# N's per 100 kbp	80.49	2305.67	3974.91	447.54
# mismatches per 100 kbp	1732.11	1392.21	1571.89	1847.55
# indels per 100 kbp	59.91	47.80	16.32	65.22
Largest alignment	8456	3665	2715	12625
NA50	-	-	799	-
NGA50	-	-	-	-
NA75	-	-	548	-
LA50	-	-	18	-
LA75	-	-	34	-

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).
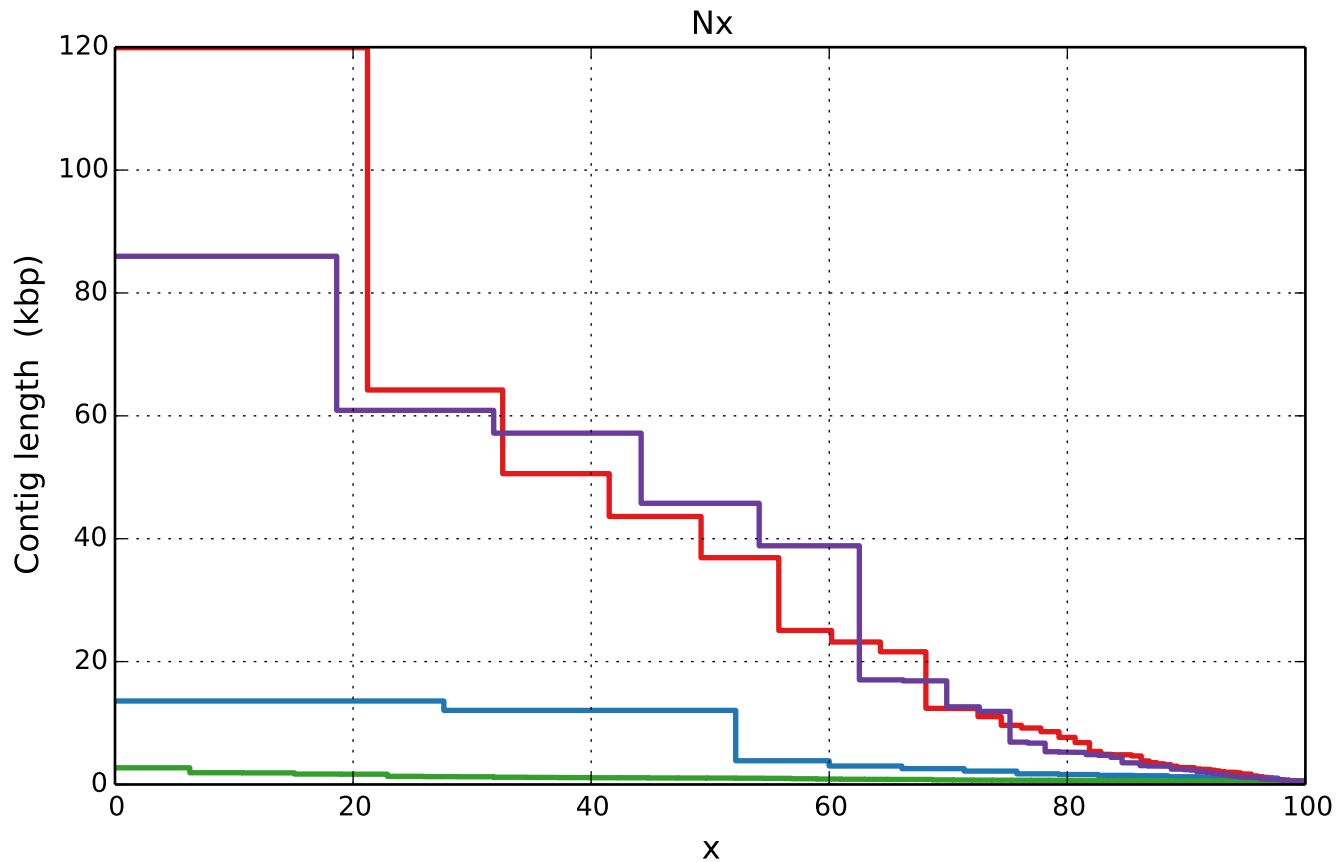
Misassemblies report

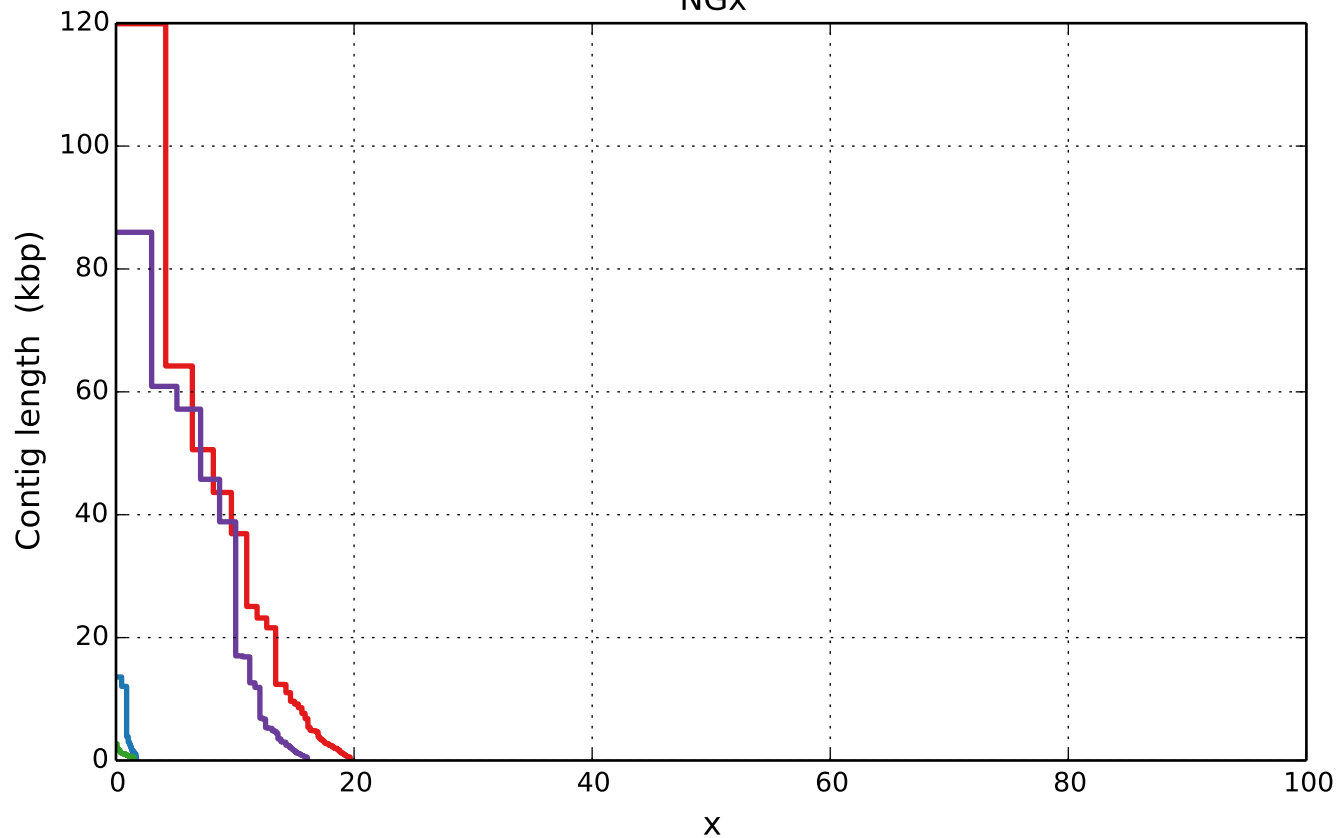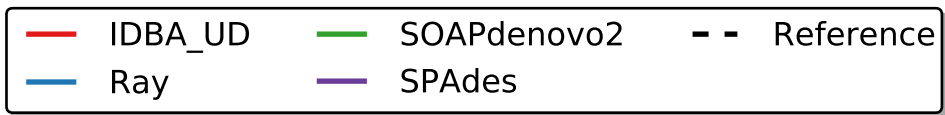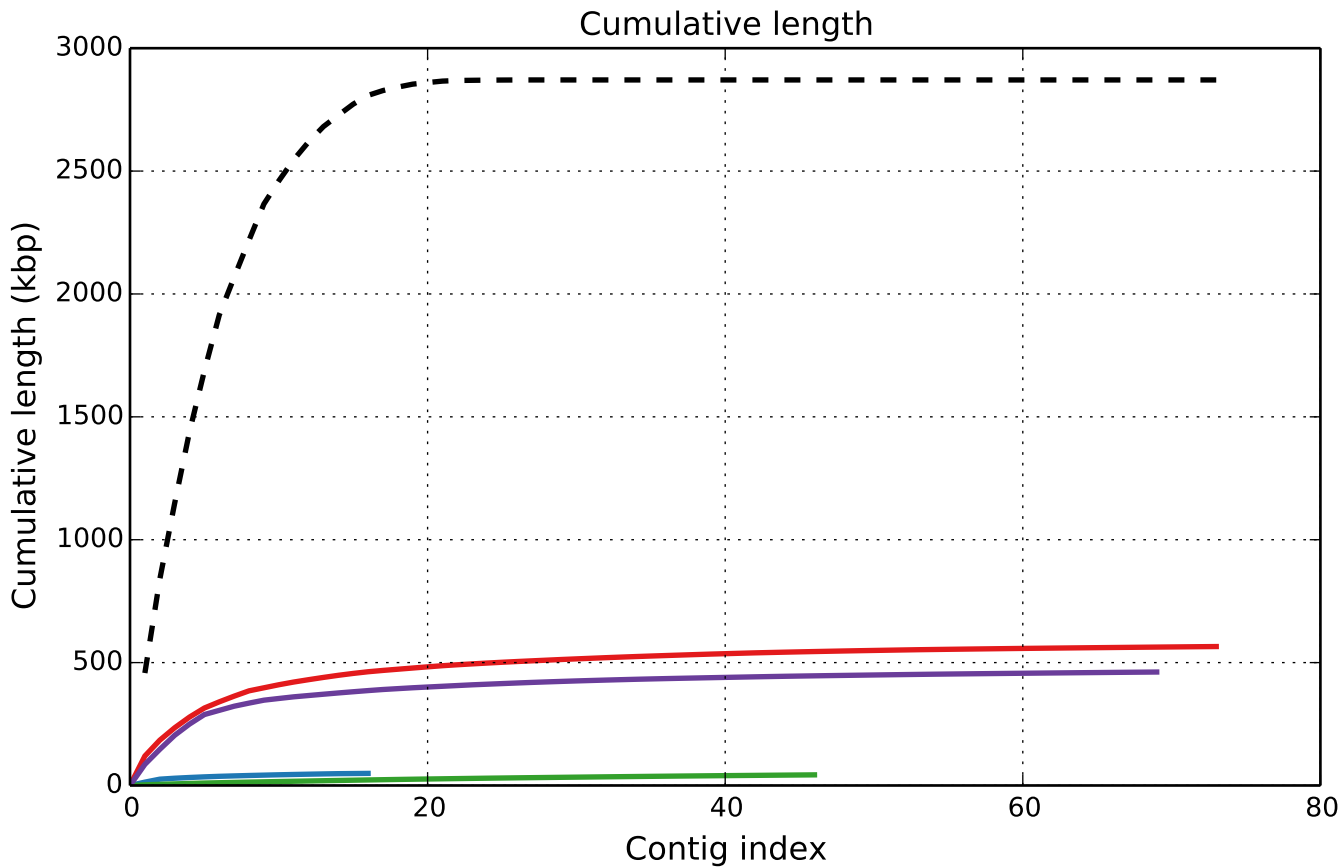|	IDBA_UD	Ray	SOAPdenovo2	SPAdes
# misassemblies	1	1	0	2
# relocations	0	0	0	1
# translocations	1	1	0	1
# inversions	0	0	0	0
# possibly misassembled contigs	8	4	1	11
# misassembled contigs	1	1	0	2
Misassembled contigs length	2987	1480	0	5296
# local misassemblies	4	2	29	4
# structural variations	0	0	0	0
# mismatches	1619	233	578	1473
# indels	56	8	6	52
# short indels	50	8	6	45
# long indels	6	0	0	7
Indels length	137	12	7	151

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
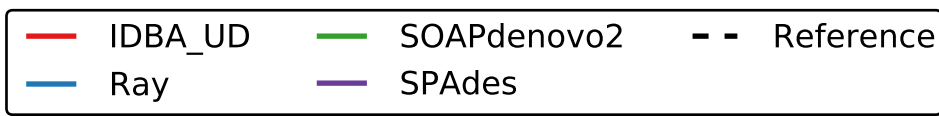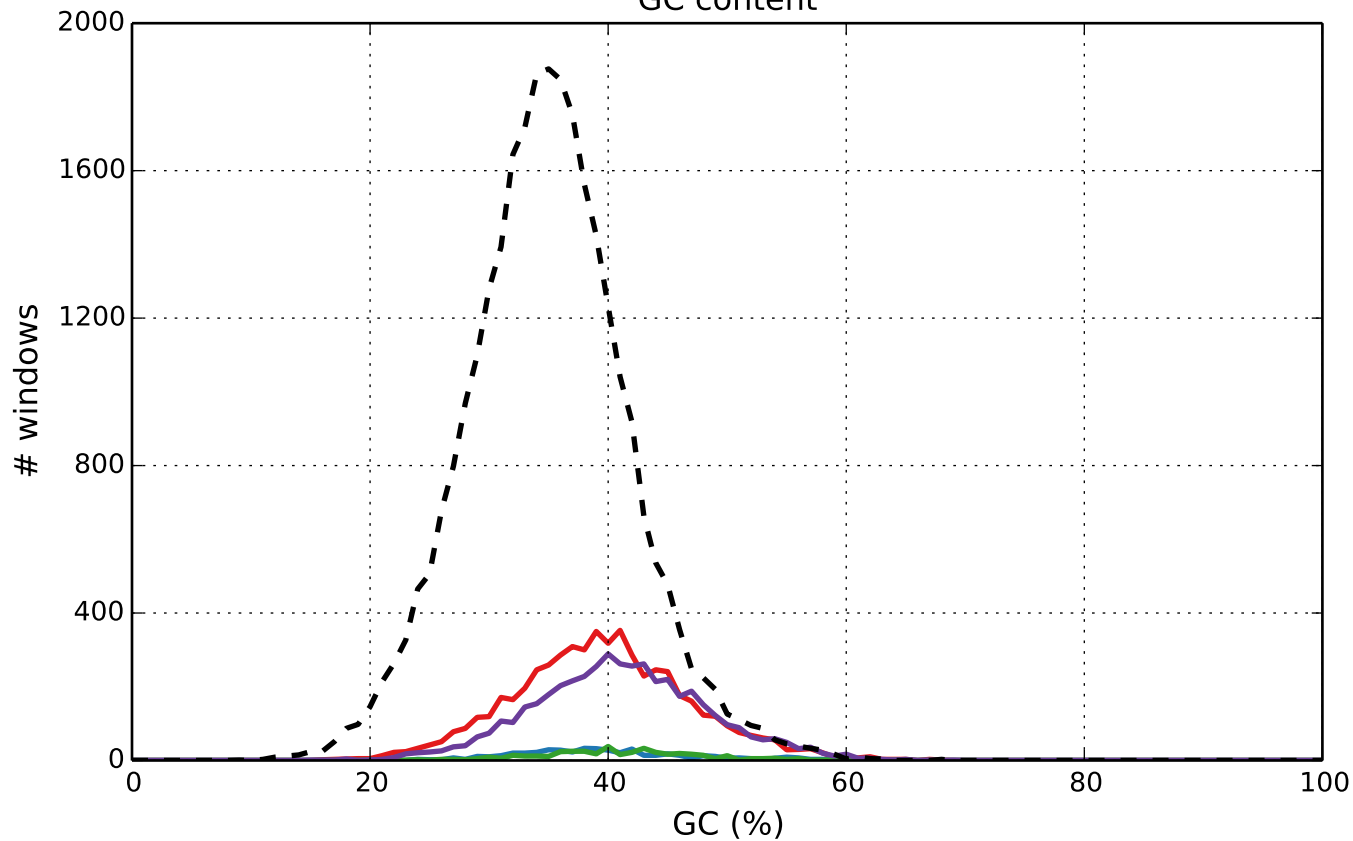
	IDBA_UD	Ray	SOAPdenovo2	SPAdes
# fully unaligned contigs	0	0	0	0
Fully unaligned length	0	0	0	0
# partially unaligned contigs	41	6	8	39
# with misassembly	2	2	0	4
# both parts are significant	8	4	1	9
Partially unaligned length	469802	31342	4035	378395
# N's	455	1134	1717	2066

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).

Cumulative length

GC content

windows vs GC (%)

Legend:
- IDBA_UD
- Ray
- SOAPdenovo2
- SPAdes
- Reference
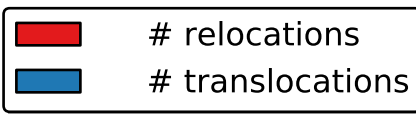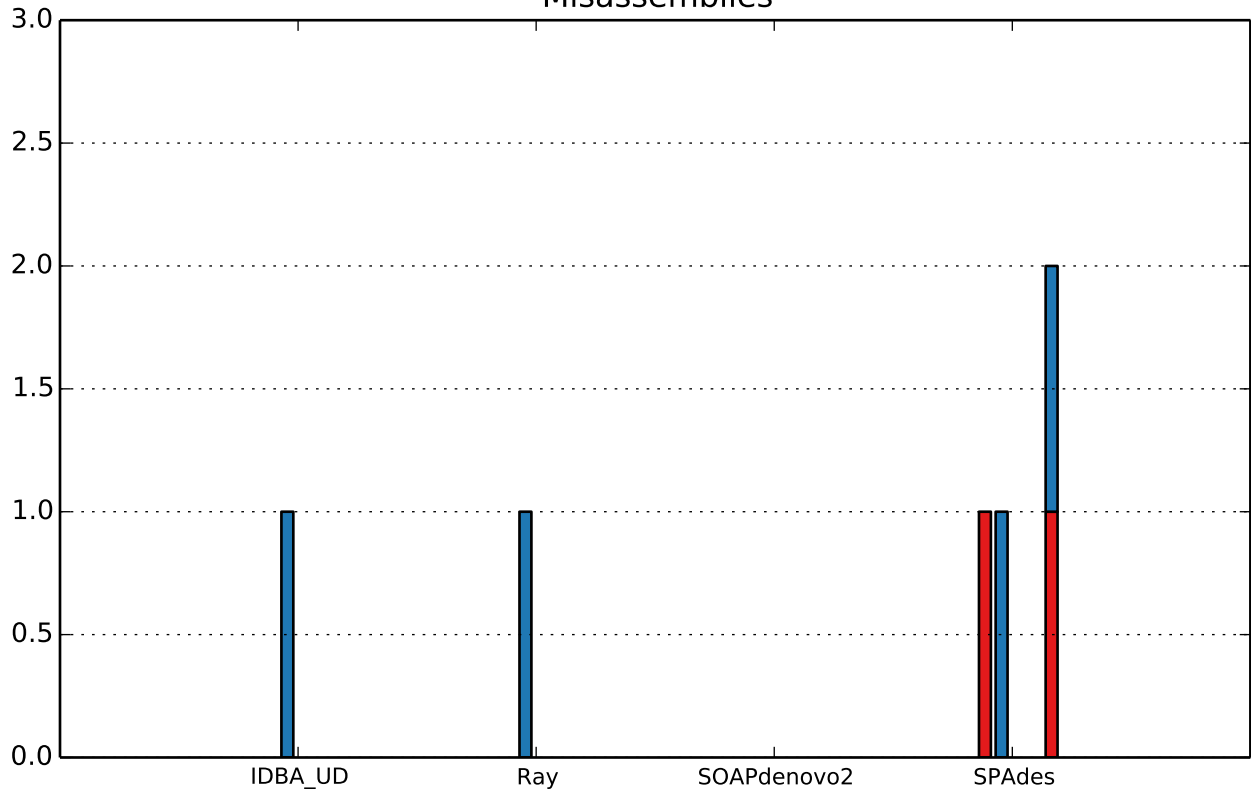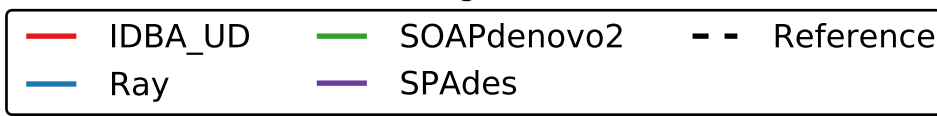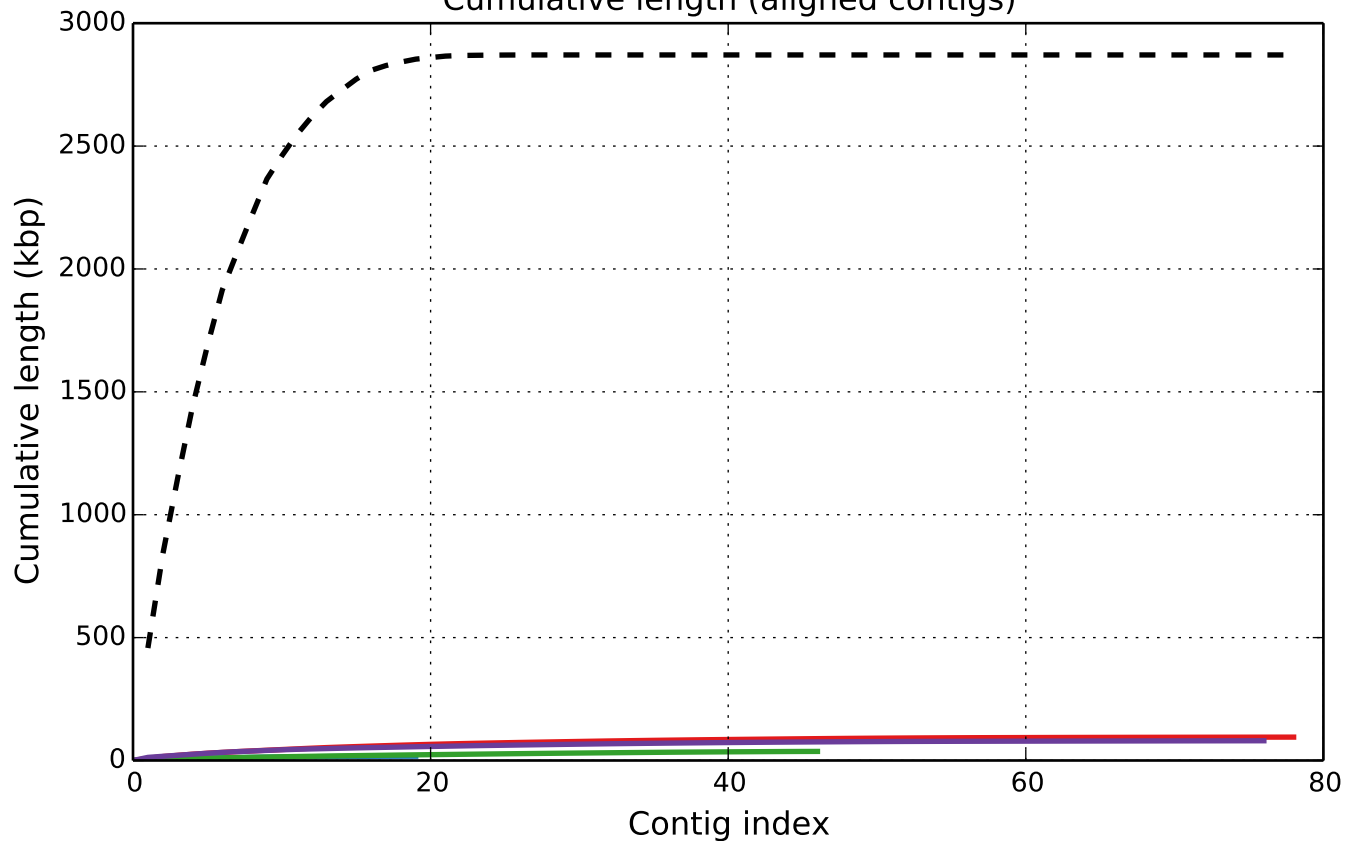
Misassemblies

Cumulative length (aligned contigs)

NAx

Contig length (kbp)

x

IDBA_UD   SOAPdenovo2   SPAdes
Ray

NGAx

Genome fraction, %