Report

	IDBA_UD	Ray	SOAPdenovo2	SPAdes
# contigs (>= 1000 bp)	237	101	39	92
# contigs (>= 5000 bp)	18	53	2	31
# contigs (>= 10000 bp)	3	34	0	16
# contigs (>= 25000 bp)	1	18	0	3
# contigs (>= 50000 bp)	1	10	0	1
Total length (>= 1000 bp)	602449	1639870	84963	566721
Total length (>= 5000 bp)	207988	1519735	11948	456209
Total length (>= 10000 bp)	104709	1386283	0	344171
Total length (>= 25000 bp)	77531	1116983	0	151096
Total length (>= 50000 bp)	77531	853325	0	85767
# contigs	610	118	225	298
Largest contig	77531	127463	6744	85767
Total length	863785	1651869	210304	708375
Reference length	2107814	2107814	2107814	2107814
GC (%)	40.89	39.30	39.01	41.19
Reference GC (%)	39.22	39.22	39.22	39.22
N50	1704	51621	880	9564
NG50	-	29305	-	-
N75	883	18194	649	1390
NG75	-	2947	-	-
L50	104	10	61	18
LG50	-	16	-	-
L75	286	24	132	62
LG75	-	70	-	-
# misassemblies	3	2	1	16
# misassembled contigs	3	2	1	11
Misassembled contigs length	1986	23763	1184	133364
# local misassemblies	27	10	2	8
# structural variations	1	0	0	1
# unaligned contigs	0 + 128 part	0 + 43 part	0 + 41 part	0 + 35 part
Unaligned length	269248	1069655	26931	174377
Genome fraction (%)	23.743	19.856	8.577	22.673
Duplication ratio	1.188	1.391	1.014	1.117
# N's per 100 kbp	1.51	206.07	1317.62	1521.93
# mismatches per 100 kbp	3403.02	4244.69	2404.55	3738.57
# indels per 100 kbp	43.56	59.26	41.49	57.75
Largest alignment	15597	28387	6744	20480
NA50	719	-	749	1001
NGA50	-	-	-	-
NA75	-	-	536	-
LA50	326	-	72	97
LA75	-	-	156	-

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).
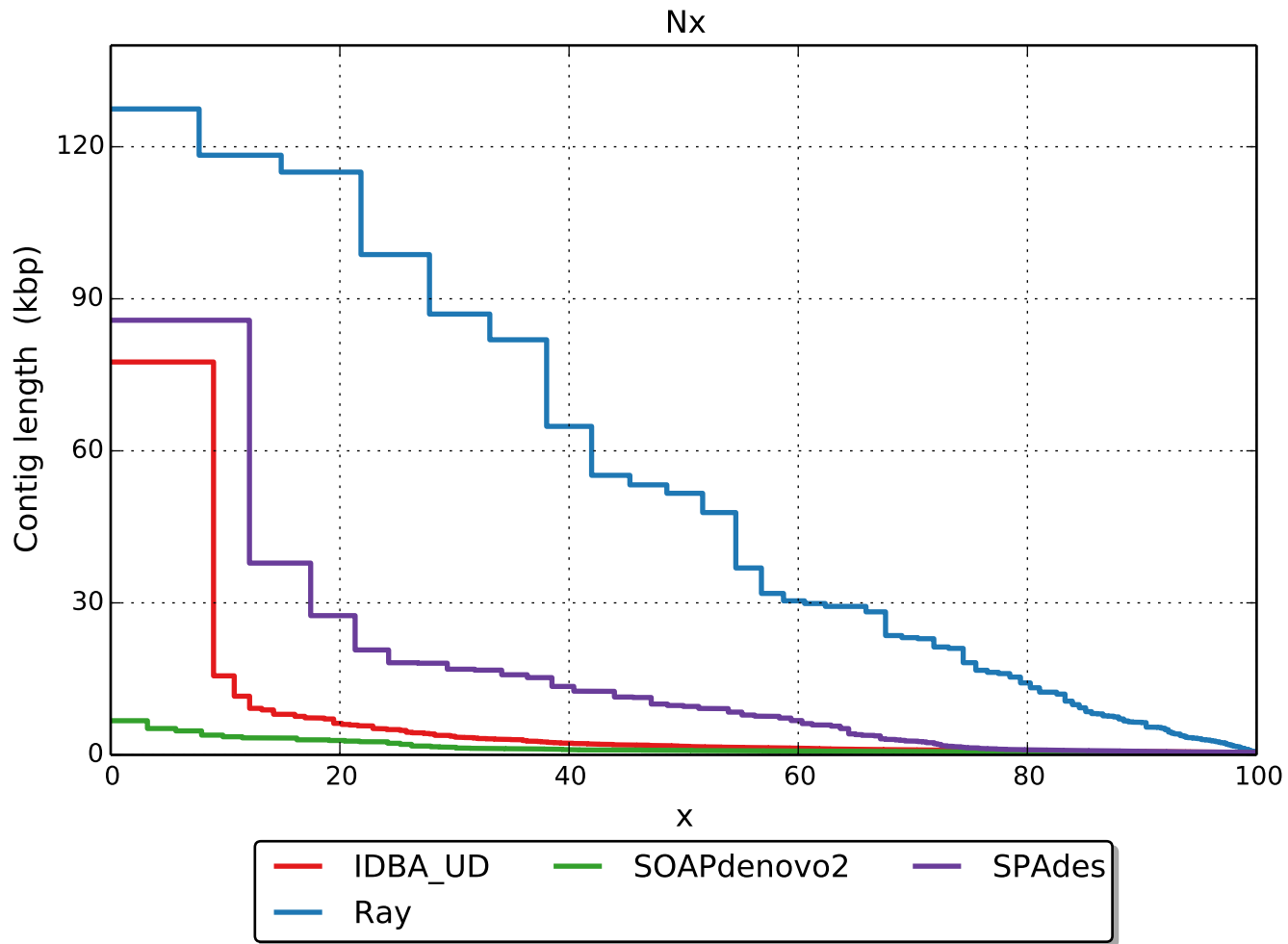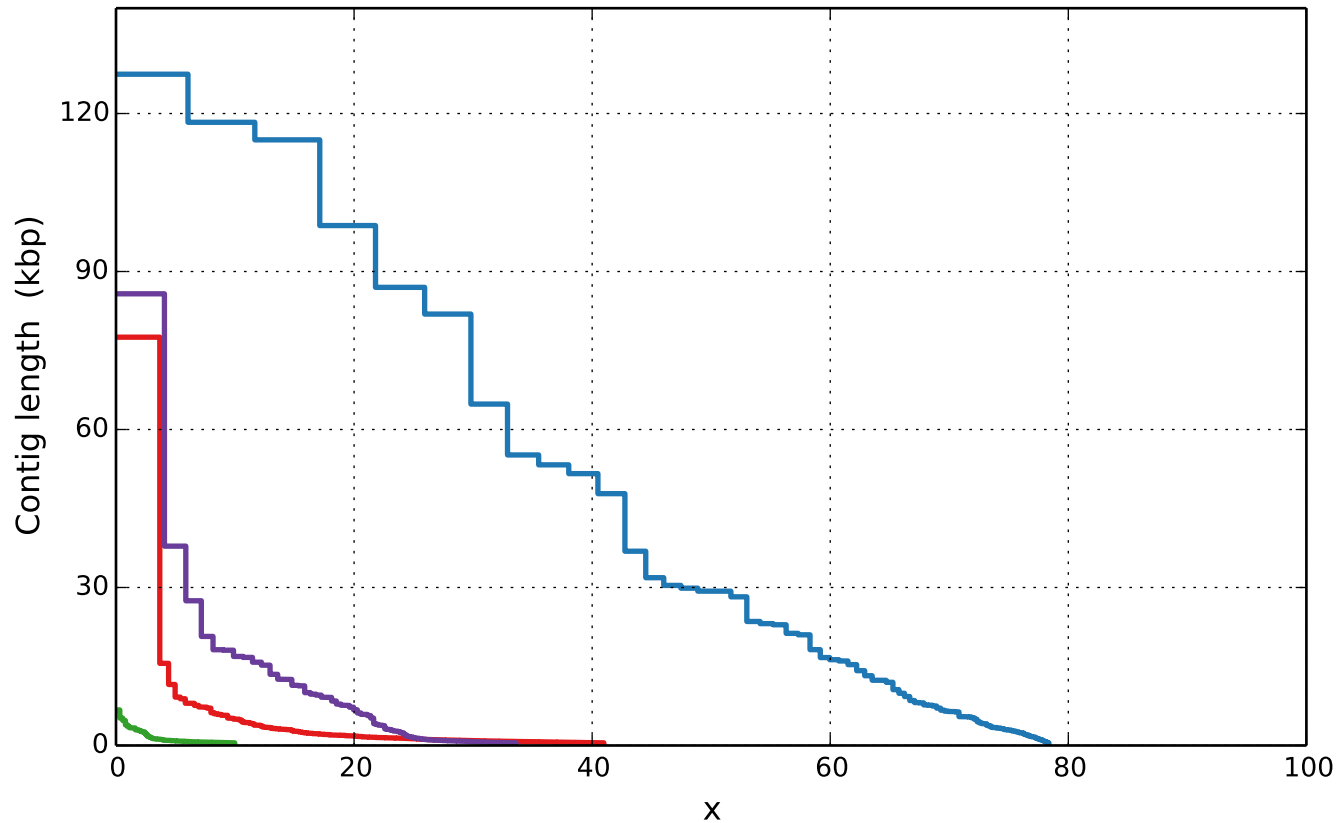
Misassemblies report

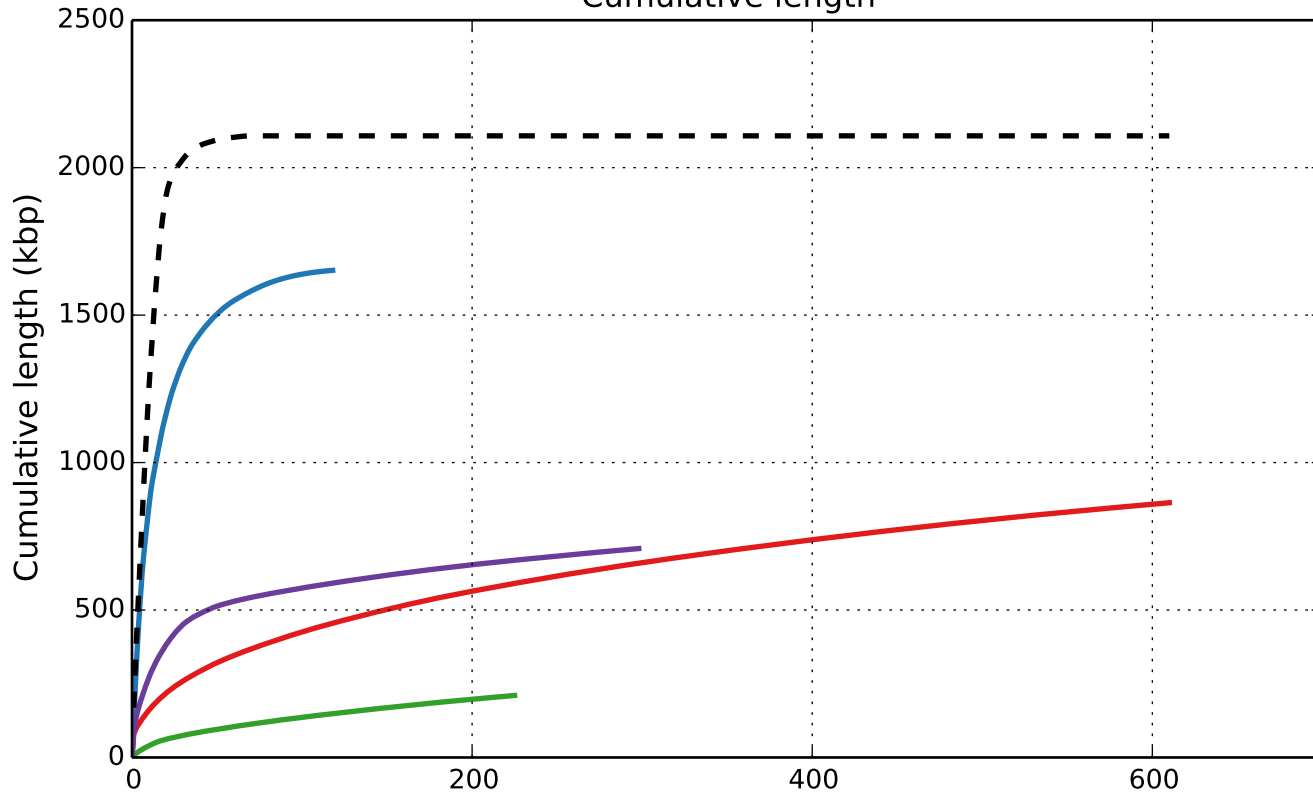|	IDBA_UD	Ray	SOAPdenovo2	SPAdes
# misassemblies	3	2	1	16
# relocations	1	0	0	10
# translocations	2	2	1	6
# inversions	0	0	0	0
# possibly misassembled contigs	53	36	1	23
# misassembled contigs	3	2	1	11
Misassembled contigs length	1986	23763	1184	133364
# local misassemblies	27	10	2	8
# structural variations	1	0	0	1
# mismatches	17031	17765	4347	17867
# indels	218	248	75	276
# short indels	196	240	73	253
# long indels	22	8	2	23
Indels length	946	401	100	935

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).
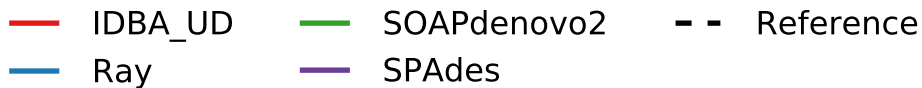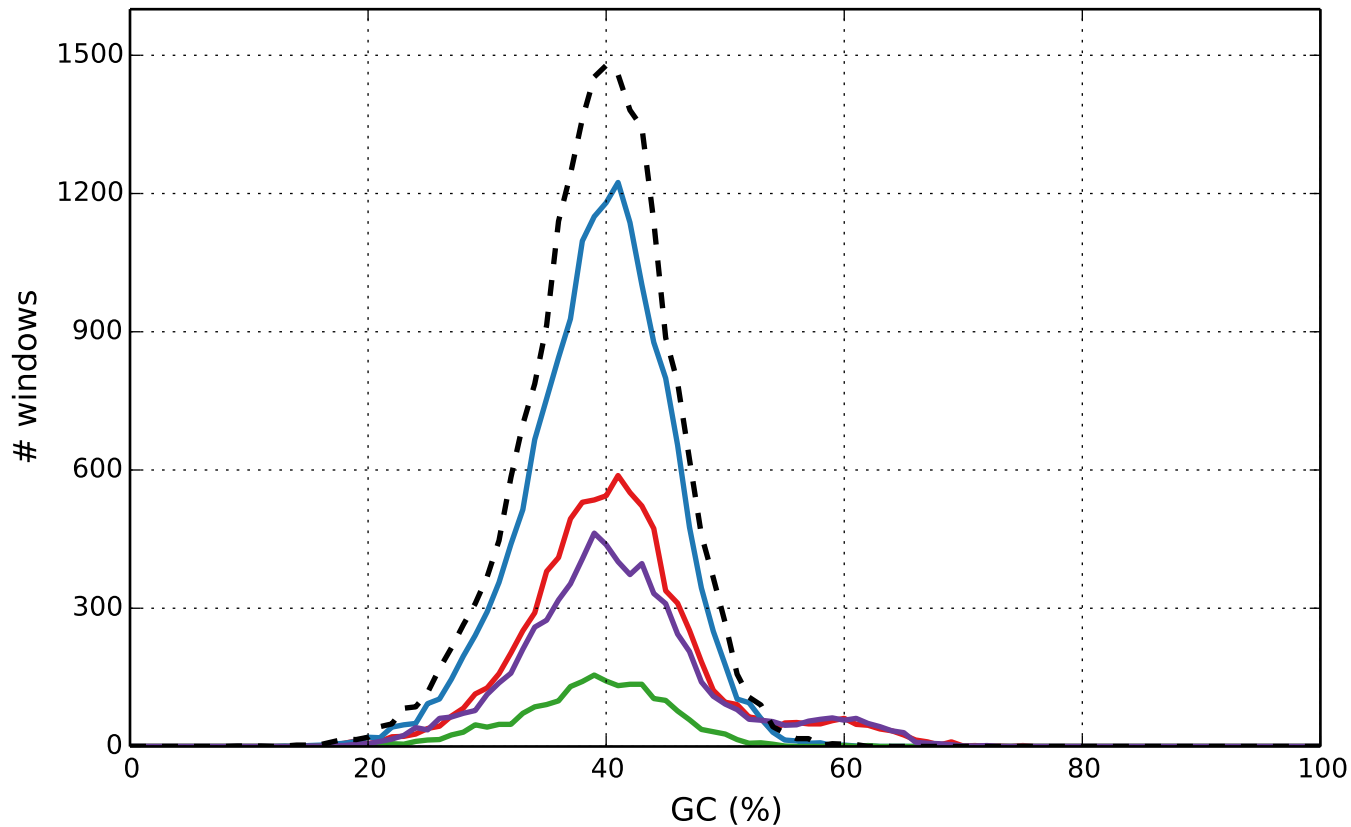
Unaligned report

	IDBA_UD	Ray	SOAPdenovo2	SPAdes
# fully unaligned contigs	0	0	0	0
Fully unaligned length	0	0	0	0
# partially unaligned contigs	128	43	41	35
# with misassembly	7	11	0	6
# both parts are significant	44	31	1	12
Partially unaligned length	269248	1069655	26931	174377
# N's	13	3404	2771	10781

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).
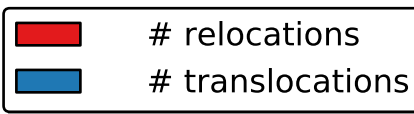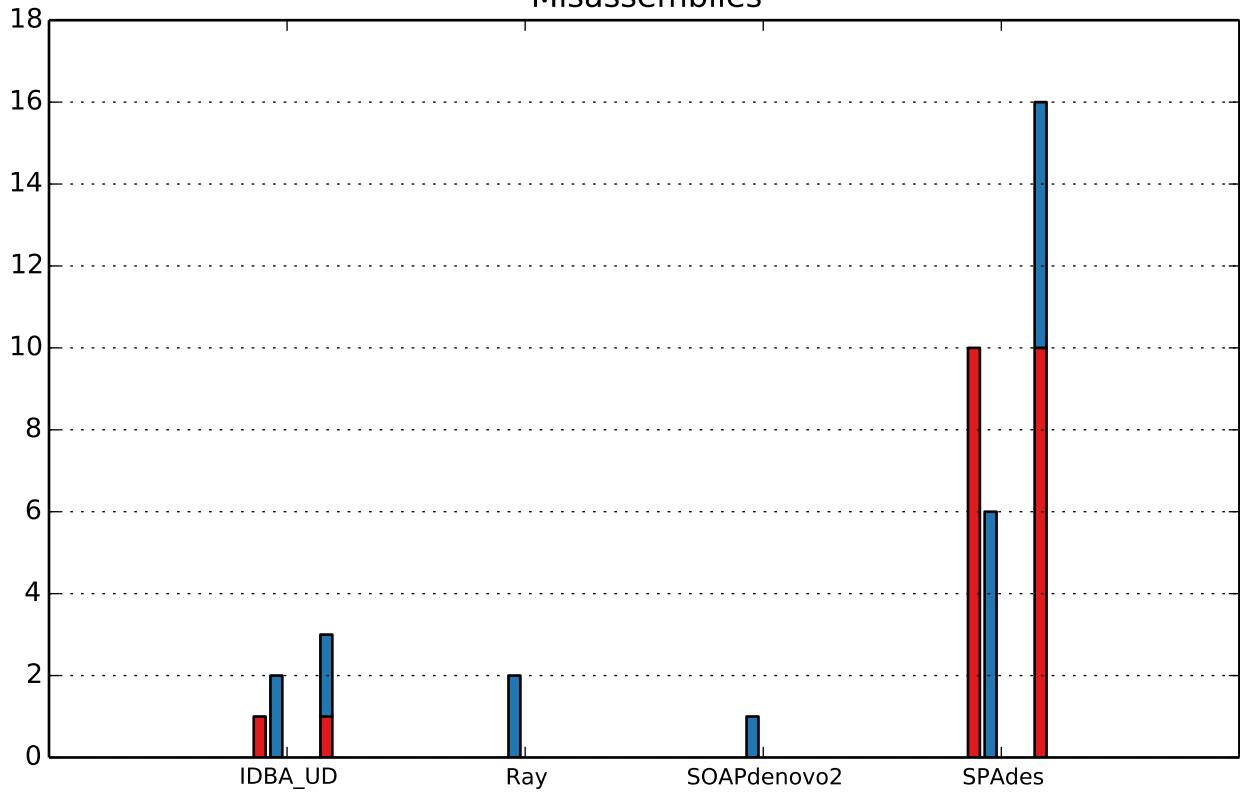
Cumulative length

GC content

Misassemblies

Genome fraction, %

IDBA_UD
Ray
SOAPdenovo2
SPAdes