

Report

	IDBA_UD	Ray	SOAPdenovo2	SPAdes
# contigs (>= 1000 bp)	854	27	276	945
# contigs (>= 5000 bp)	104	4	1	123
# contigs (>= 10000 bp)	23	2	0	31
# contigs (>= 25000 bp)	2	0	0	3
# contigs (>= 50000 bp)	1	0	0	0
Total length (>= 1000 bp)	2410400	80825	382555	2825679
Total length (>= 5000 bp)	989914	41279	5467	1117129
Total length (>= 10000 bp)	439397	30736	0	495301
Total length (>= 25000 bp)	127289	0	0	114059
Total length (>= 50000 bp)	77959	0	0	0
# contigs	1714	70	1475	1601
Largest contig	77959	16534	5467	42522
Total length	3031786	109609	1192098	3288959
Reference length	7010996	7010996	7010996	7010996
GC (%)	42.29	43.40	41.65	42.12
Reference GC (%)	42.30	42.30	42.30	42.30
N50	2480	1805	792	3062
N75	1145	907	622	1463
L50	260	9	517	259
L75	727	29	940	649
# misassemblies	30	0	8	29
# misassembled contigs	29	0	8	27
Misassembled contigs length	72888	0	11389	105962
# local misassemblies	9	8	1743	11
# structural variations	0	0	0	0
# unaligned contigs	0 + 319 part	0 + 3 part	0 + 251 part	0 + 478 part
Unaligned length	533420	3729	116993	853574
Genome fraction (%)	35.154	1.446	13.554	33.823
Duplication ratio	1.014	1.044	1.131	1.027
# N's per 100 kbp	310.25	801.03	9245.46	1429.69
# mismatches per 100 kbp	1255.84	679.54	1103.46	1423.56
# indels per 100 kbp	42.20	27.62	15.57	58.70
Largest alignment	19945	16413	5467	21502
NA50	1376	1695	596	1282
NGA50	-	-	-	-
NA75	656	823	355	-
LA50	486	10	641	585
LA75	1305	34	1238	-

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

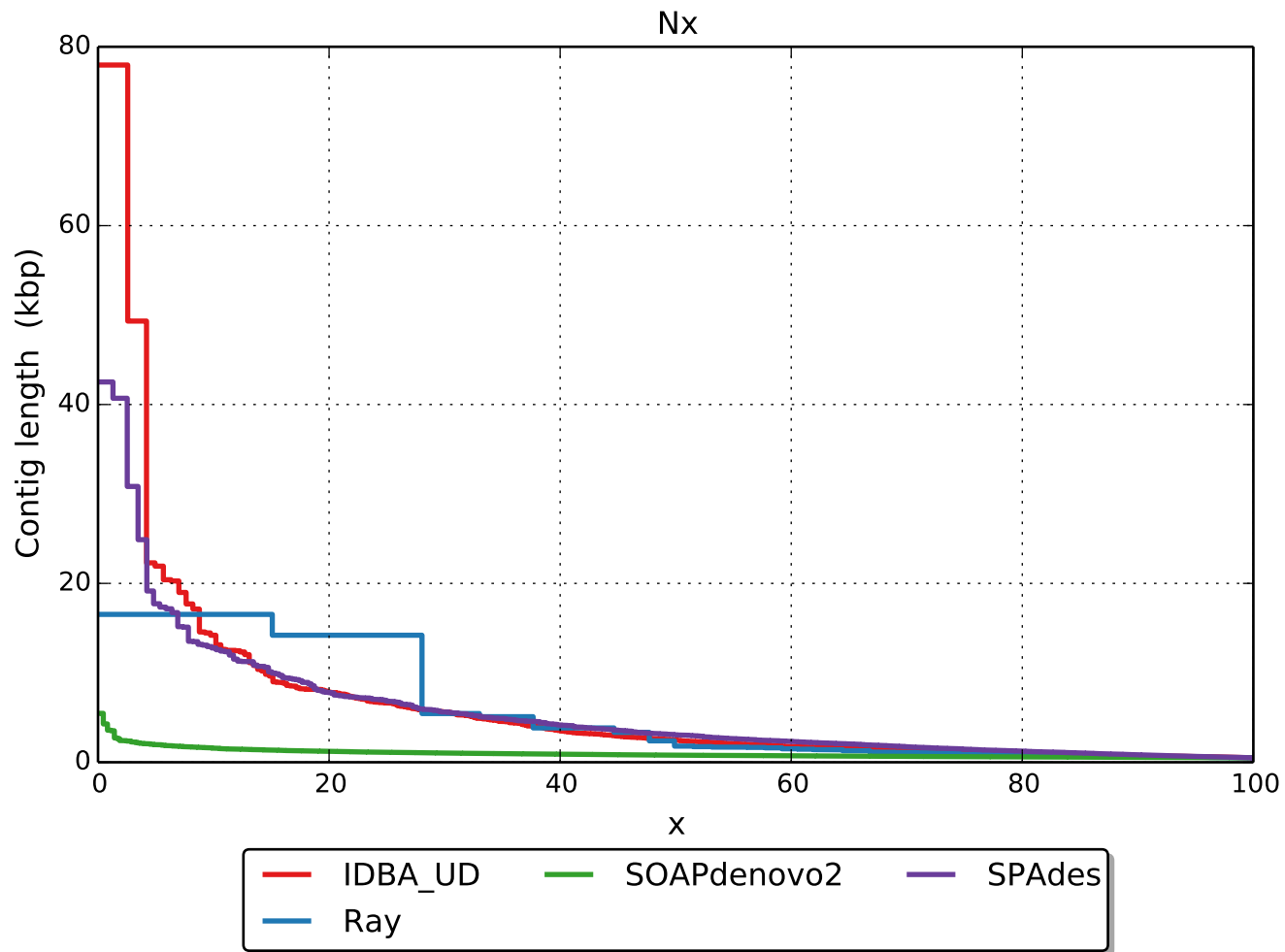
	IDBA_UD	Ray	SOAPdenovo2	SPAdes
# misassemblies	30	0	8	29
# relocations	12	0	2	18
# translocations	15	0	5	10
# inversions	3	0	1	1
# possibly misassembled contigs	71	1	16	179
# misassembled contigs	29	0	8	27
Misassembled contigs length	72888	0	11389	105962
# local misassemblies	9	8	1743	11
# structural variations	0	0	0	0
# mismatches	30952	689	10486	33757
# indels	1040	28	148	1392
# short indels	889	26	133	1068
# long indels	151	2	15	324
Indels length	3113	57	369	5606

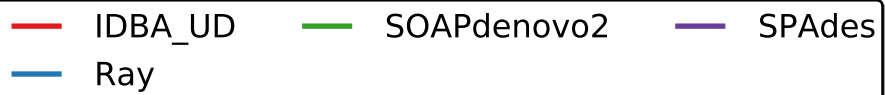
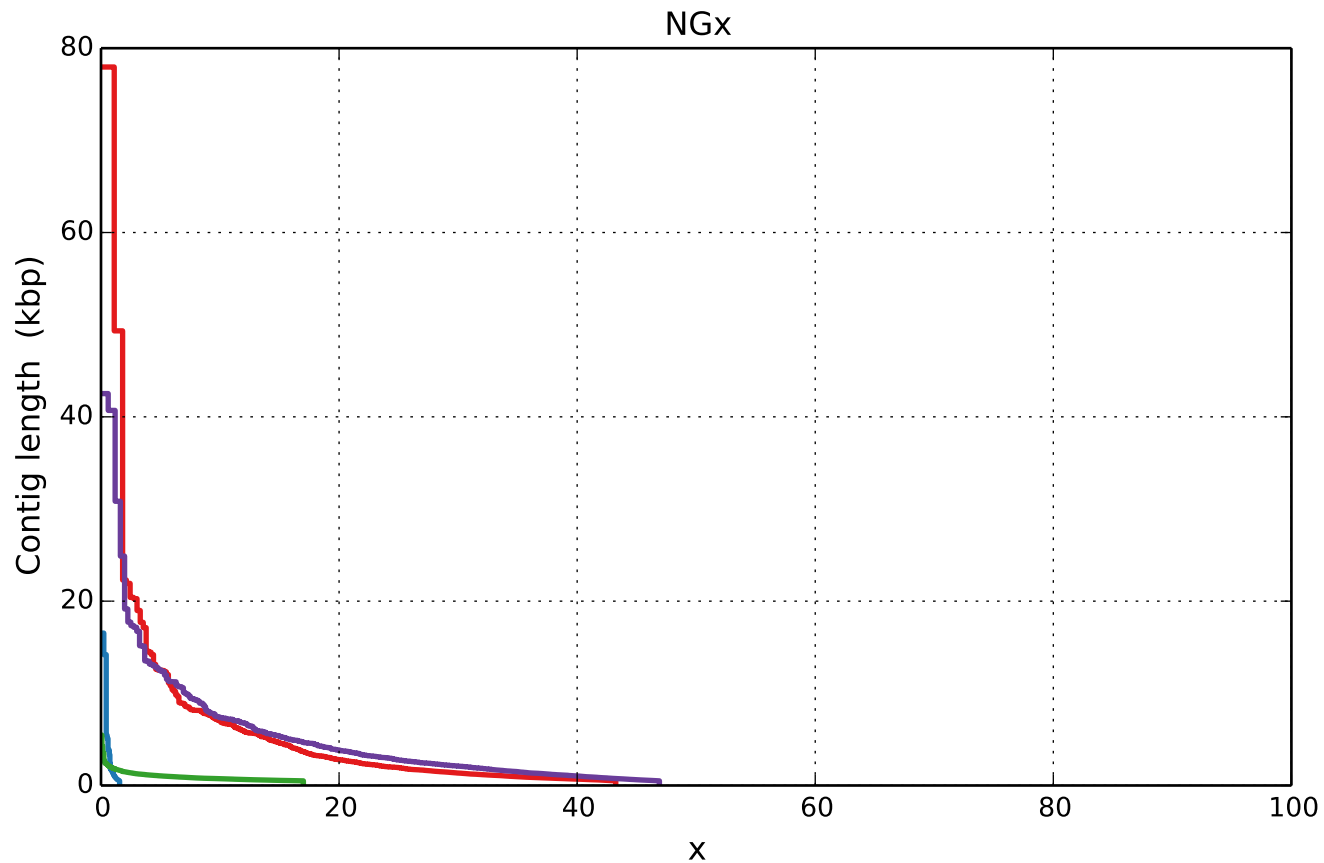
All statistics are based on contigs of size ≥ 500 bp, unless otherwise noted (e.g., "# contigs (≥ 0 bp)" and "Total length (≥ 0 bp)" include all contigs).

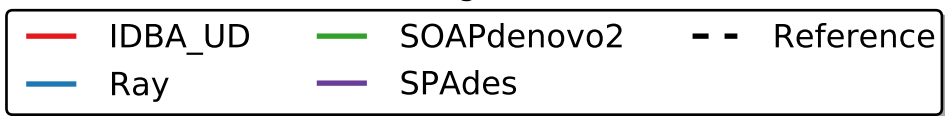
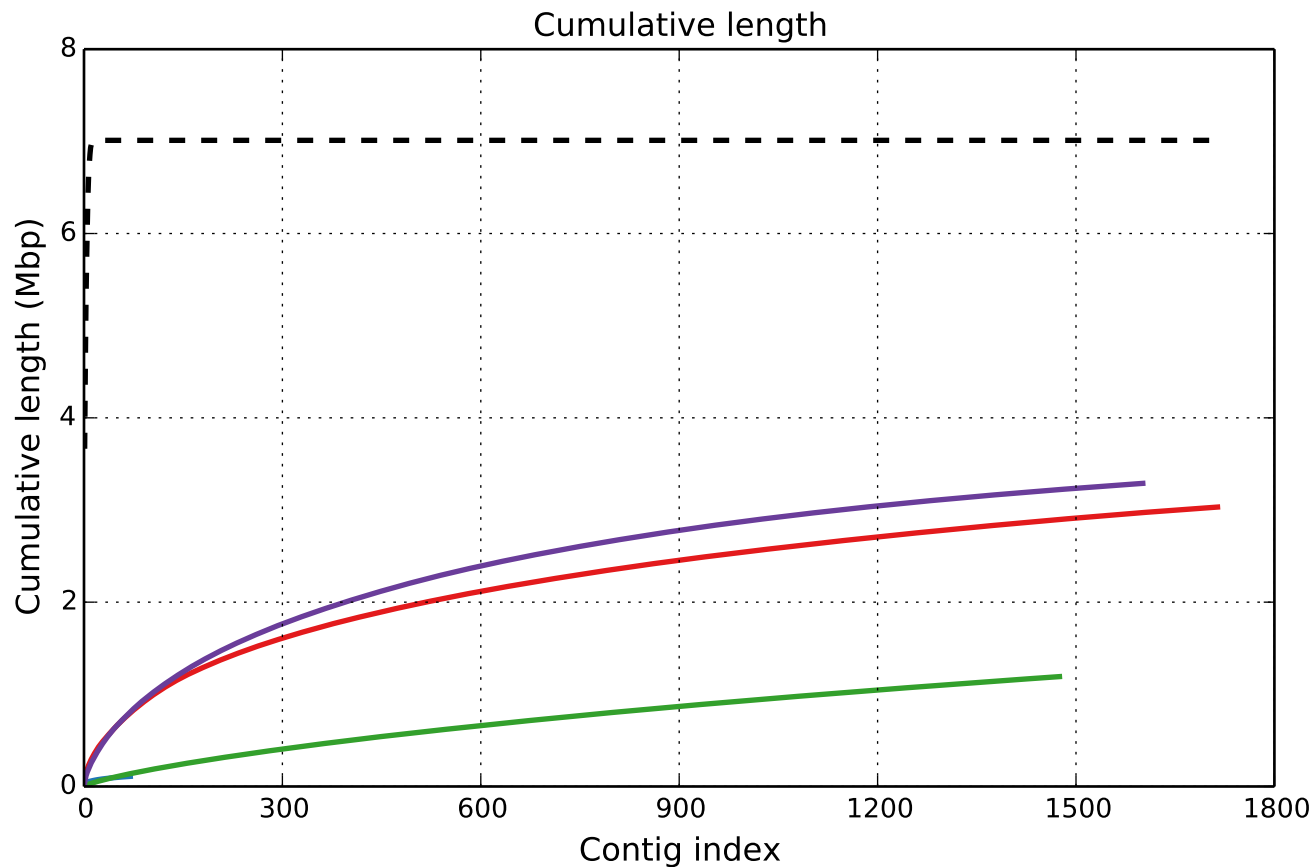
Unaligned report

	IDBA_UD	Ray	SOAPdenovo2	SPAdes
# fully unaligned contigs	0	0	0	0
Fully unaligned length	0	0	0	0
# partially unaligned contigs	319	3	251	478
# with misassembly	6	0	55	19
# both parts are significant	67	0	6	158
Partially unaligned length	533420	3729	116993	853574
# N's	9406	878	110215	47022

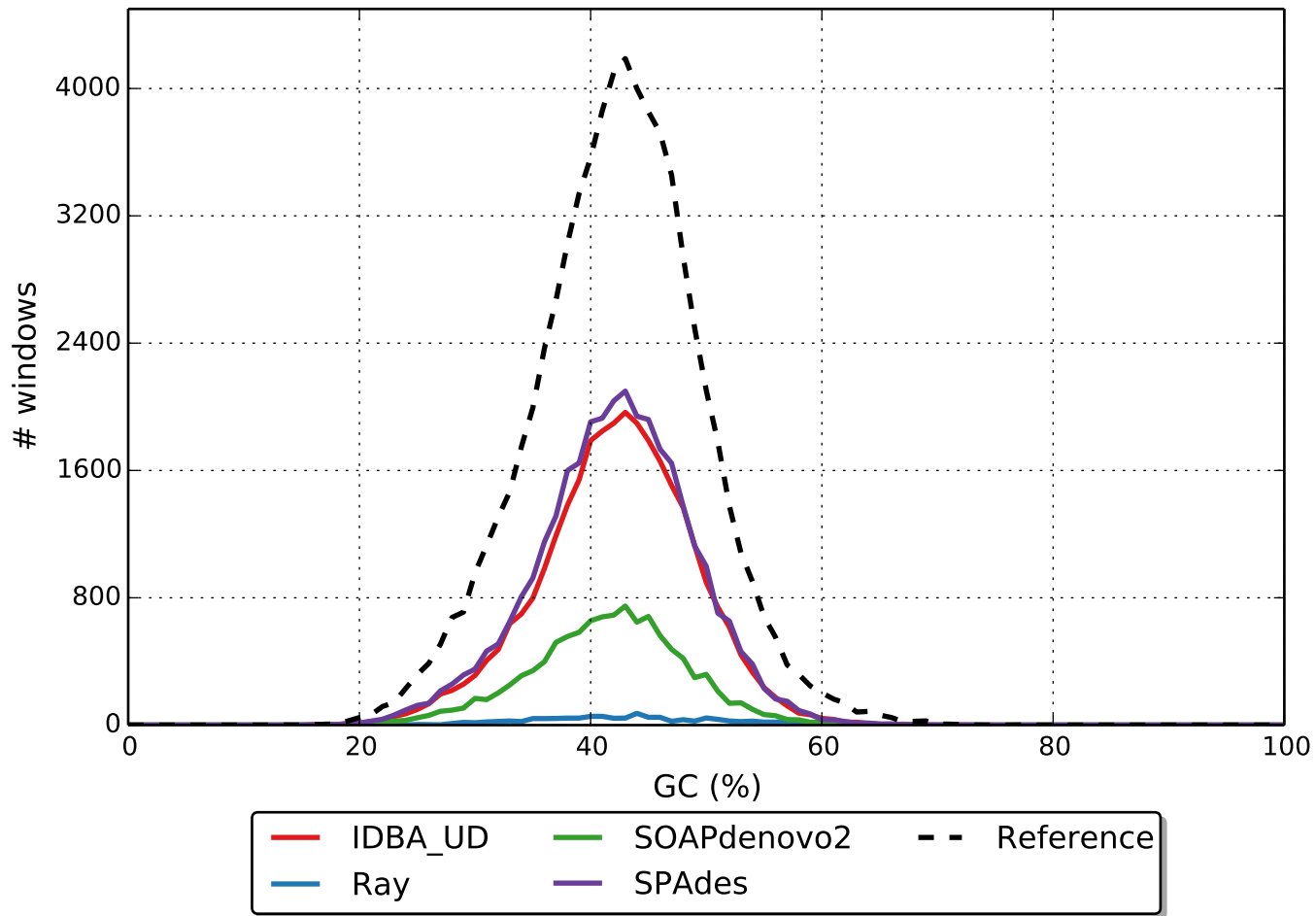
All statistics are based on contigs of size ≥ 500 bp, unless otherwise noted (e.g., "# contigs (≥ 0 bp)" and "Total length (≥ 0 bp)" include all contigs).







GC content



Misassemblies

