

Report

	IDBA_UD	Ray	SOAPdenovo2	SPAdes
# contigs (>= 1000 bp)	27	13	3	14
# contigs (>= 5000 bp)	6	2	0	7
# contigs (>= 10000 bp)	2	2	0	5
# contigs (>= 25000 bp)	1	0	0	2
# contigs (>= 50000 bp)	1	0	0	0
Total length (>= 1000 bp)	169853	46658	5186	125929
Total length (>= 5000 bp)	119680	25999	0	115282
Total length (>= 10000 bp)	86909	25999	0	101777
Total length (>= 25000 bp)	71408	0	0	53940
Total length (>= 50000 bp)	71408	0	0	0
# contigs	42	20	18	25
Largest contig	71408	15783	2763	28342
Total length	180974	51510	16369	133809
Reference length	3932923	3932923	3932923	3932923
GC (%)	47.47	46.09	44.90	49.90
Reference GC (%)	50.18	50.18	50.18	50.18
N50	9700	10216	848	18482
N75	3775	1688	716	12780
L50	3	2	7	3
L75	10	7	12	5
# misassemblies	3	1	0	2
# misassembled contigs	3	1	0	2
Misassembled contigs length	10050	2877	0	13575
# local misassemblies	0	1	5	0
# structural variations	0	0	0	0
# unaligned contigs	0 + 23 part	0 + 6 part	0 + 5 part	0 + 14 part
Unaligned length	136355	28731	1172	89568
Genome fraction (%)	1.070	0.537	0.373	1.008
Duplication ratio	1.061	1.078	1.035	1.116
# N's per 100 kbp	175.16	1452.15	2193.17	125.55
# mismatches per 100 kbp	1575.98	1656.10	816.94	2100.56
# indels per 100 kbp	45.16	23.66	27.23	37.83
Largest alignment	7081	2381	2665	11133
NA50	-	-	845	-
NGA50	-	-	-	-
NA75	-	-	658	-
LA50	-	-	7	-
LA75	-	-	13	-

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

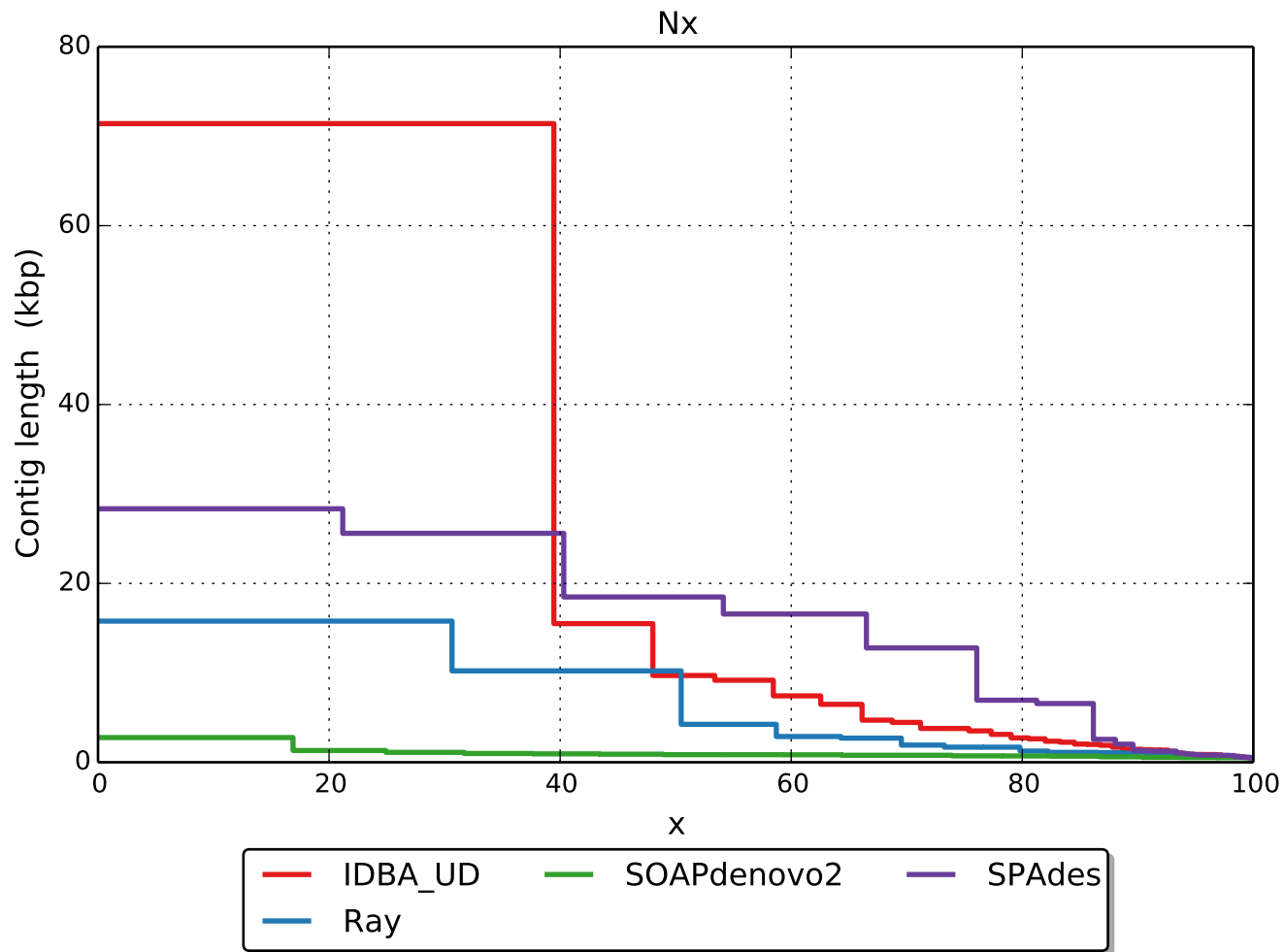
	IDBA_UD	Ray	SOAPdenovo2	SPAdes
# misassemblies	3	1	0	2
# relocations	3	1	0	2
# translocations	0	0	0	0
# inversions	0	0	0	0
# possibly misassembled contigs	5	2	0	9
# misassembled contigs	3	1	0	2
Misassembled contigs length	10050	2877	0	13575
# local misassemblies	0	1	5	0
# structural variations	0	0	0	0
# mismatches	663	350	120	833
# indels	19	5	4	15
# short indels	17	4	4	15
# long indels	2	1	0	0
Indels length	42	10	4	21

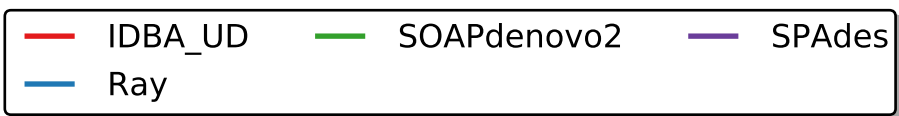
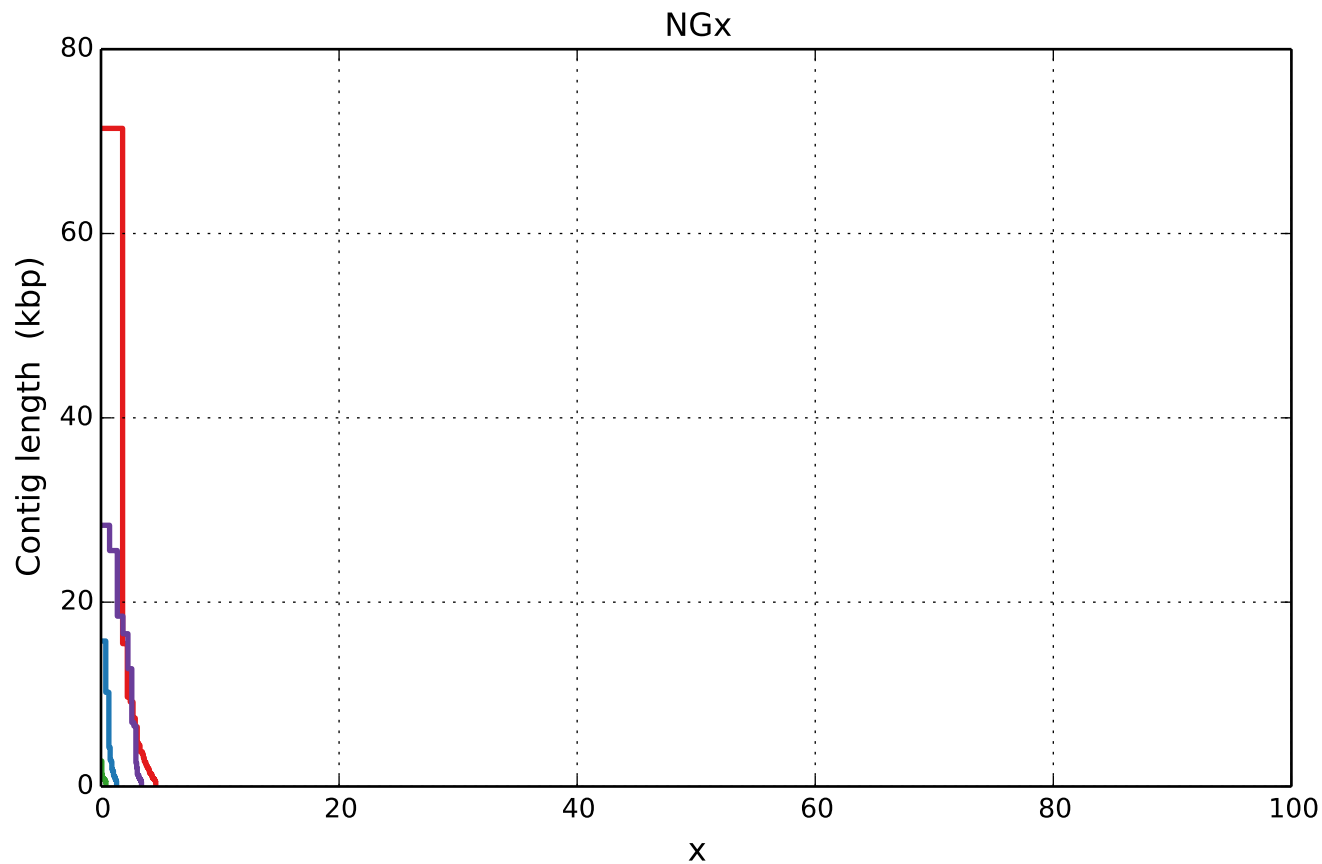
All statistics are based on contigs of size ≥ 500 bp, unless otherwise noted (e.g., "# contigs (≥ 0 bp)" and "Total length (≥ 0 bp)" include all contigs).

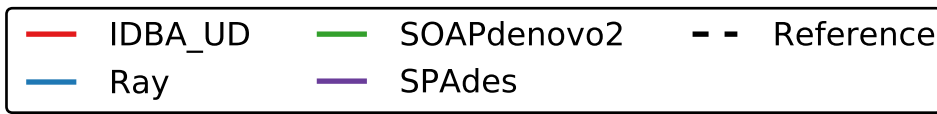
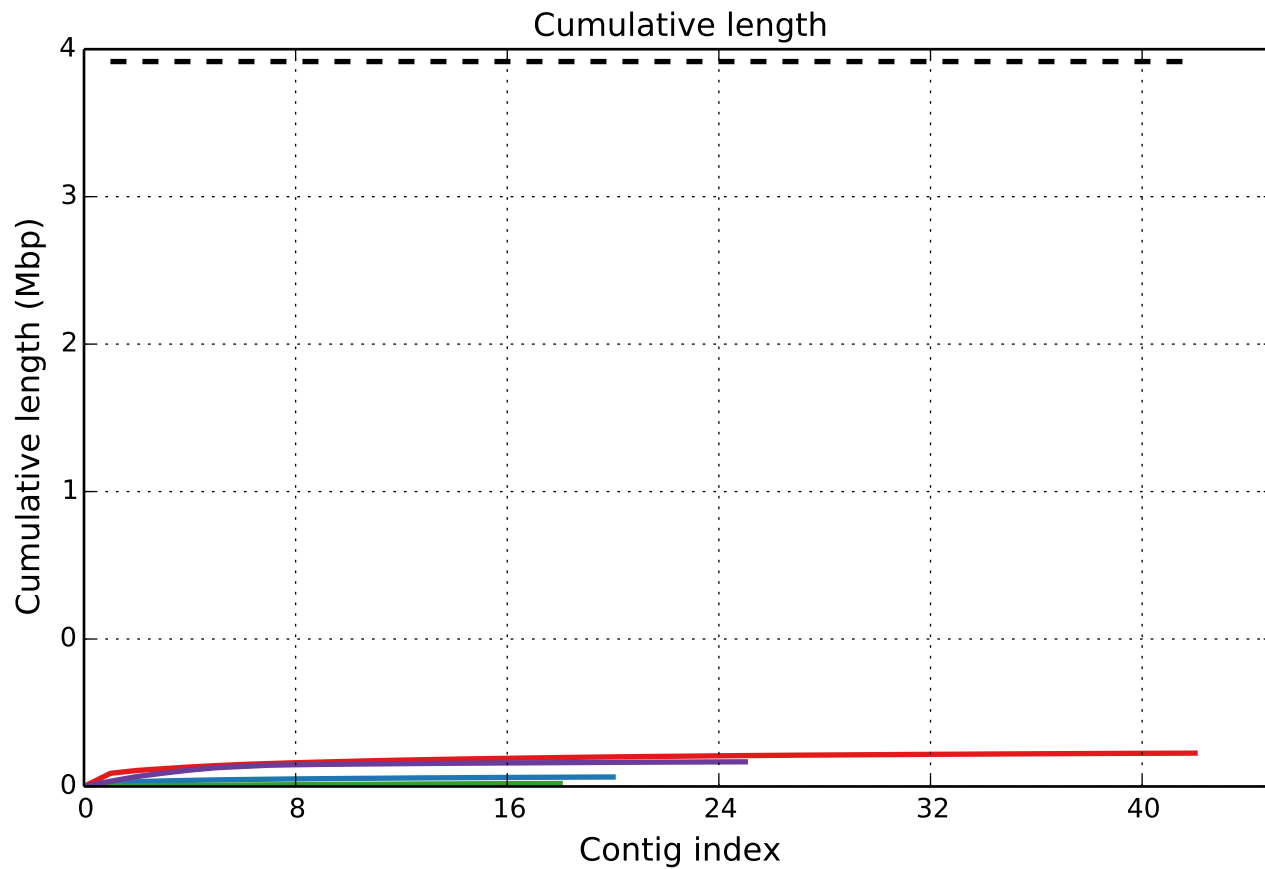
Unaligned report

	IDBA_UD	Ray	SOAPdenovo2	SPAdes
# fully unaligned contigs	0	0	0	0
Fully unaligned length	0	0	0	0
# partially unaligned contigs	23	6	5	14
# with misassembly	1	1	0	0
# both parts are significant	5	2	0	8
Partially unaligned length	136355	28731	1172	89568
# N's	317	748	359	168

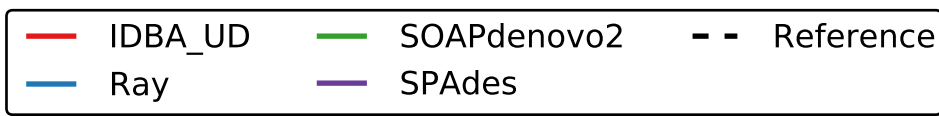
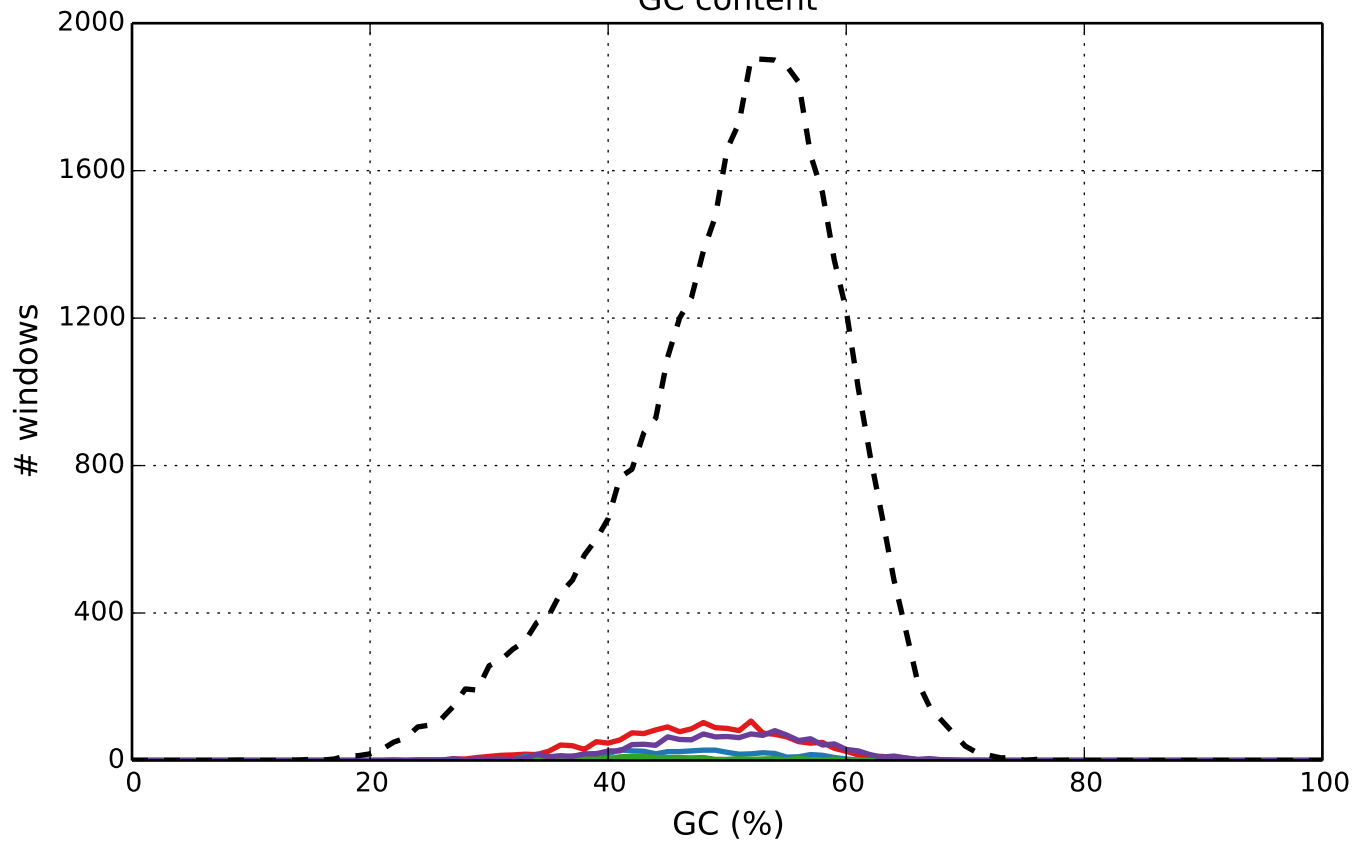
All statistics are based on contigs of size ≥ 500 bp, unless otherwise noted (e.g., "# contigs (≥ 0 bp)" and "Total length (≥ 0 bp)" include all contigs).

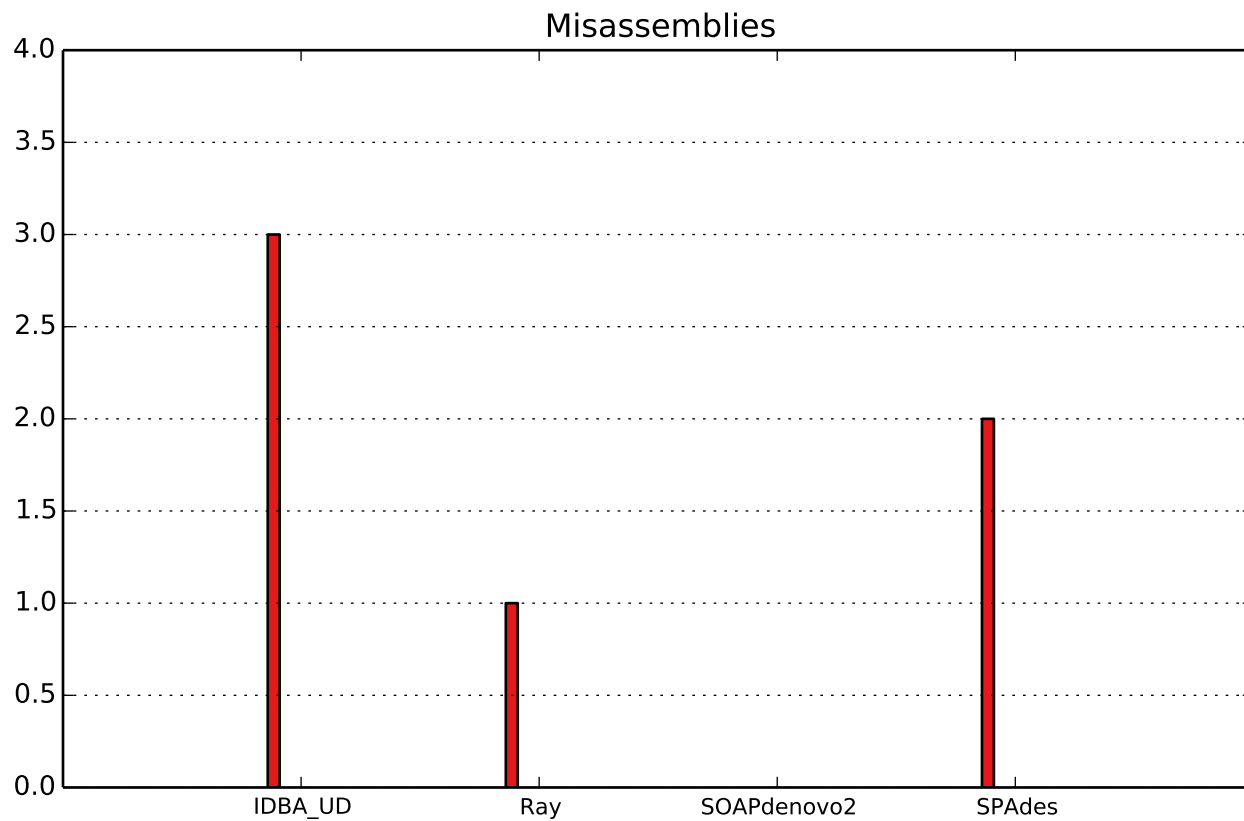






GC content





 # relocations

