Report

	IDBA_UD	Ray	SOAPdenovo2	SPAdes
# contigs (>= 1000 bp)	516	324	260	326
# contigs (>= 5000 bp)	34	156	13	60
# contigs (>= 10000 bp)	8	100	2	24
# contigs (>= 25000 bp)	1	18	0	3
# contigs (>= 50000 bp)	0	2	0	0
Total length (>= 1000 bp)	1221868	2799355	532027	1163518
Total length (>= 5000 bp)	298690	2363531	98228	648263
Total length (>= 10000 bp)	116462	1975505	28688	395906
Total length (>= 25000 bp)	33954	707725	0	116474
Total length (>= 50000 bp)	0	174625	0	0
# contigs	1095	397	835	646
Largest contig	33954	102776	17473	48732
Total length	1626023	2850649	924010	1387192
Reference length	2138805	2138805	2138805	2138805
GC (%)	39.72	40.03	39.98	40.06
Reference GC (%)	39.93	39.93	39.93	39.93
N50	1870	15018	1194	3985
NG50	1264	19580	-	1319
N75	1005	7604	743	1426
NG75	517	13970	-	-
L50	214	56	196	71
LG50	381	35	-	244
L75	514	120	450	223
LG75	1052	68	-	-
# misassemblies	12	44	2	32
# misassembled contigs	11	37	2	28
Misassembled contigs length	29179	508578	6778	239131
# local misassemblies	57	67	29	17
# structural variations	3	11	2	3
# unaligned contigs	0 + 209 part	0 + 132 part	0 + 273 part	0 + 136 part
Unaligned length	389913	854130	307731	232141
Genome fraction (%)	49.436	61.217	26.886	49.064
Duplication ratio	1.169	1.525	1.072	1.101
# N's per 100 kbp	0.00	395.00	2964.90	719.01
# mismatches per 100 kbp	2697.89	3159.97	2568.17	2805.93
# indels per 100 kbp	55.23	69.35	47.13	55.84
Largest alignment	10976	37275	11215	21659
NA50	981	3800	574	1908
NGA50	630	7444	-	575
NA75	200	-	-	623
NGA75	-	2269	-	-
LA50	426	146	466	137
LGA50	754	79	-	526
LA75	1052	-	-	477
LGA75	-	208	-	-

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).
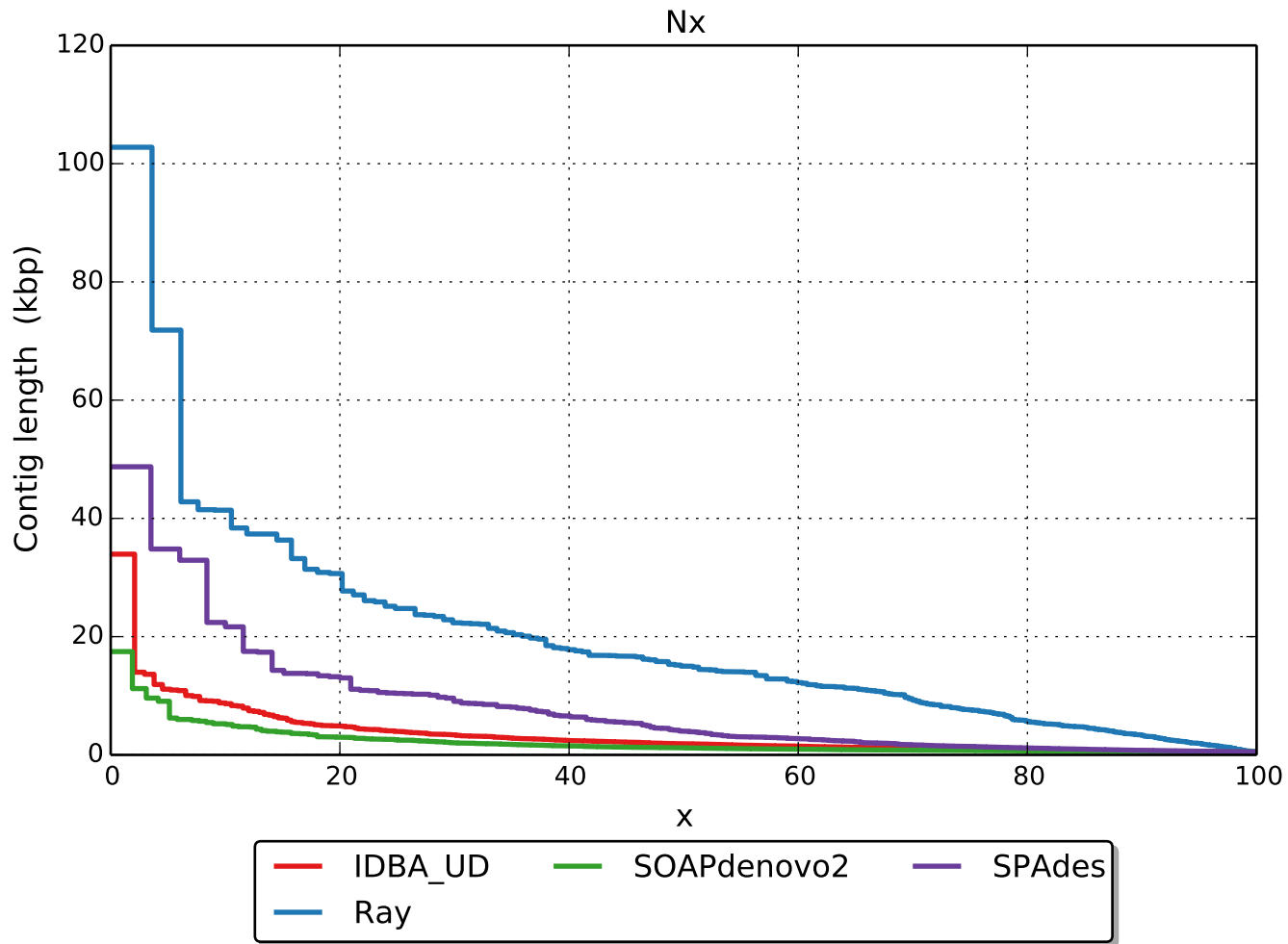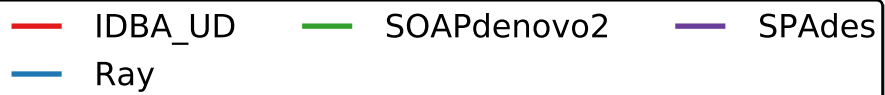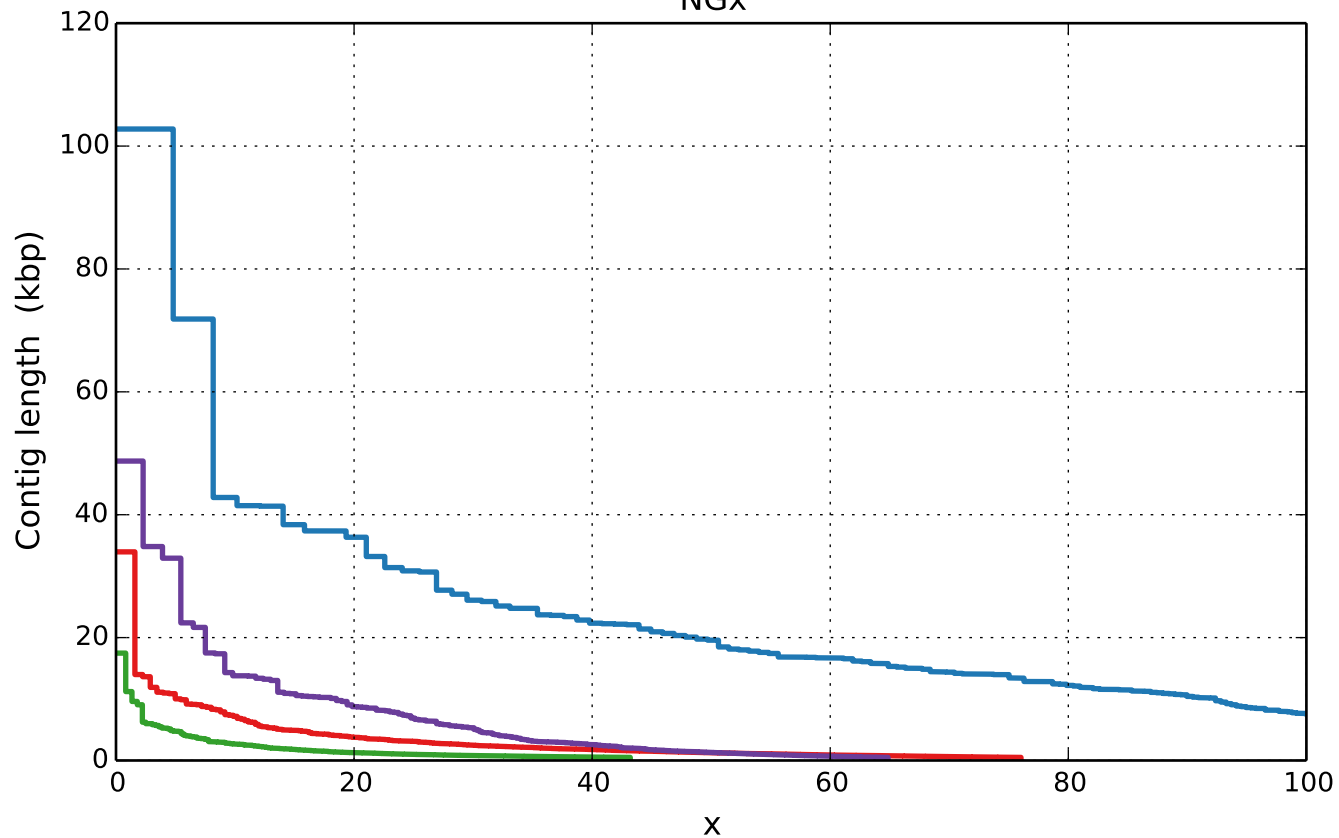
Misassemblies report

|	IDBA_UD	Ray	SOAPdenovo2	SPAdes
# misassemblies	12	44	2	32
# relocations	12	44	2	32
# translocations	0	0	0	0
# inversions	0	0	0	0
# possibly misassembled contigs	61	111	35	57
# misassembled contigs	11	37	2	28
Misassembled contigs length	29179	508578	6778	239131
# local misassemblies	57	67	29	17
# structural variations	3	11	2	3
# mismatches	28526	41374	14768	29445
# indels	584	908	271	586
# short indels	508	853	244	538
# long indels	76	55	27	48
Indels length	2508	1872	1404	2131

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	209	132	273	136
# with misassembly	17	20	16	7
# both parts are significant	58	71	33	42
Partially unaligned length	389913	854130	307731	232141
# N's	0	11260	27396	9974

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).
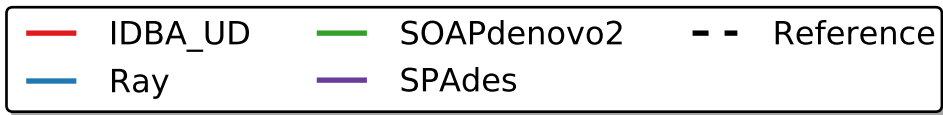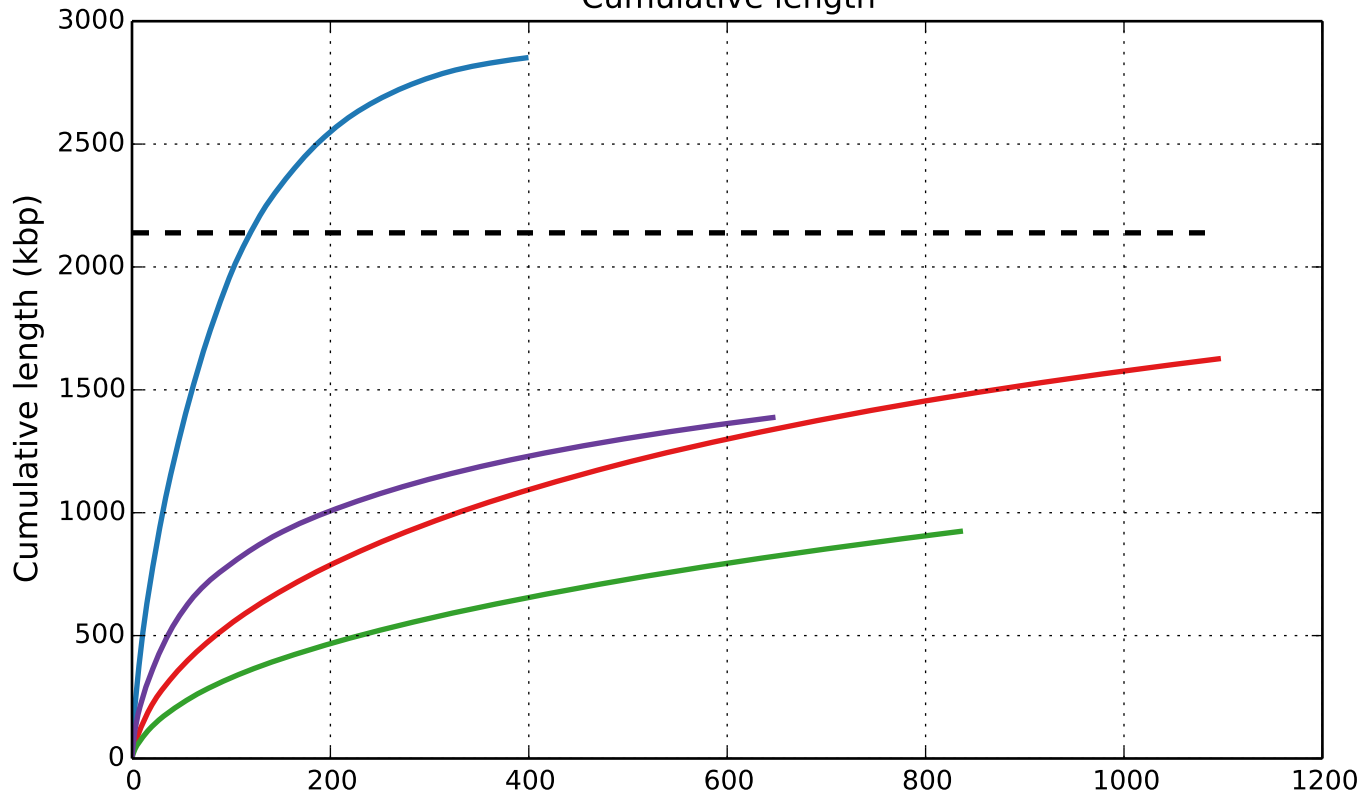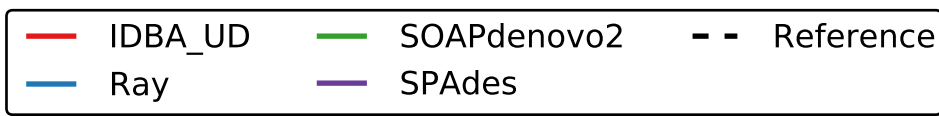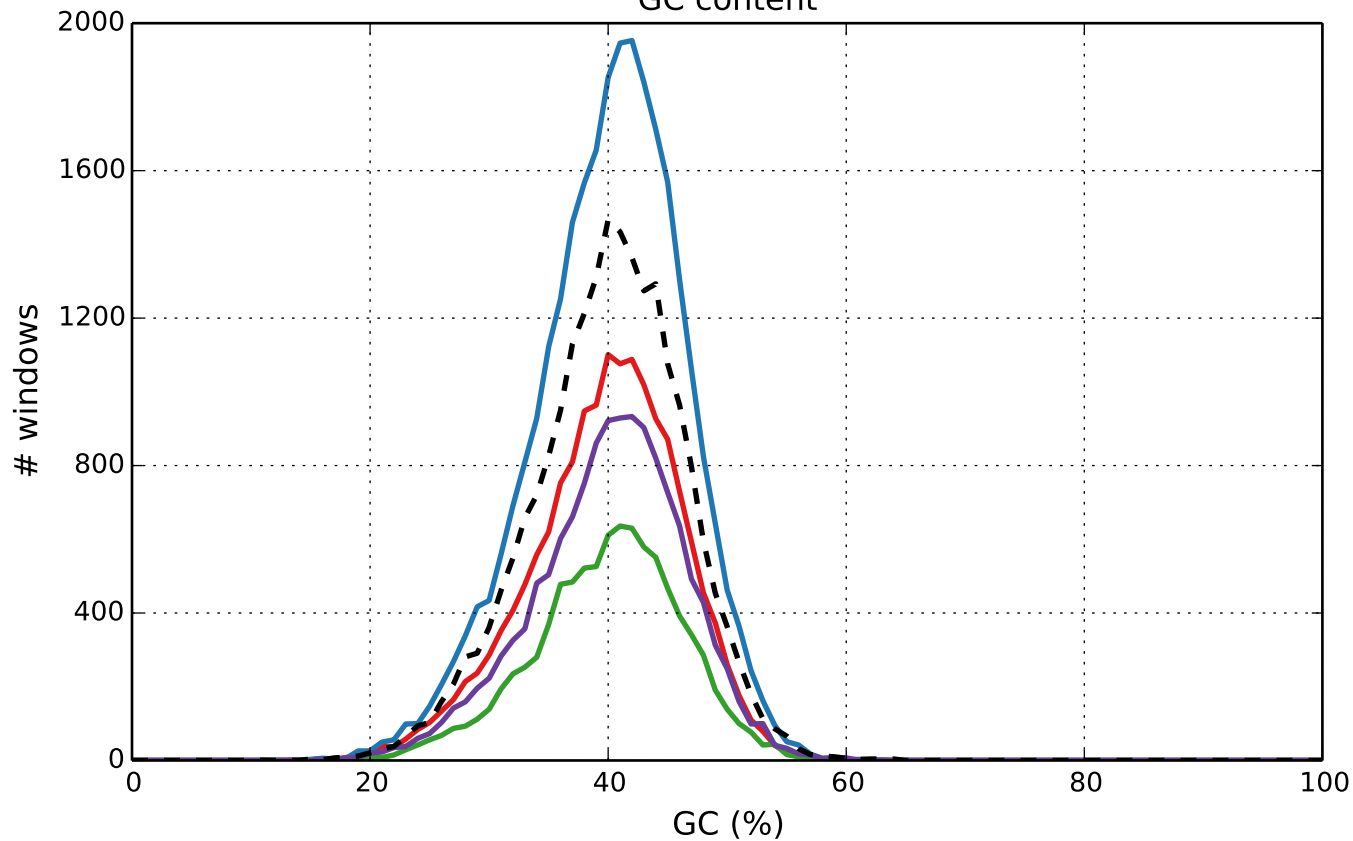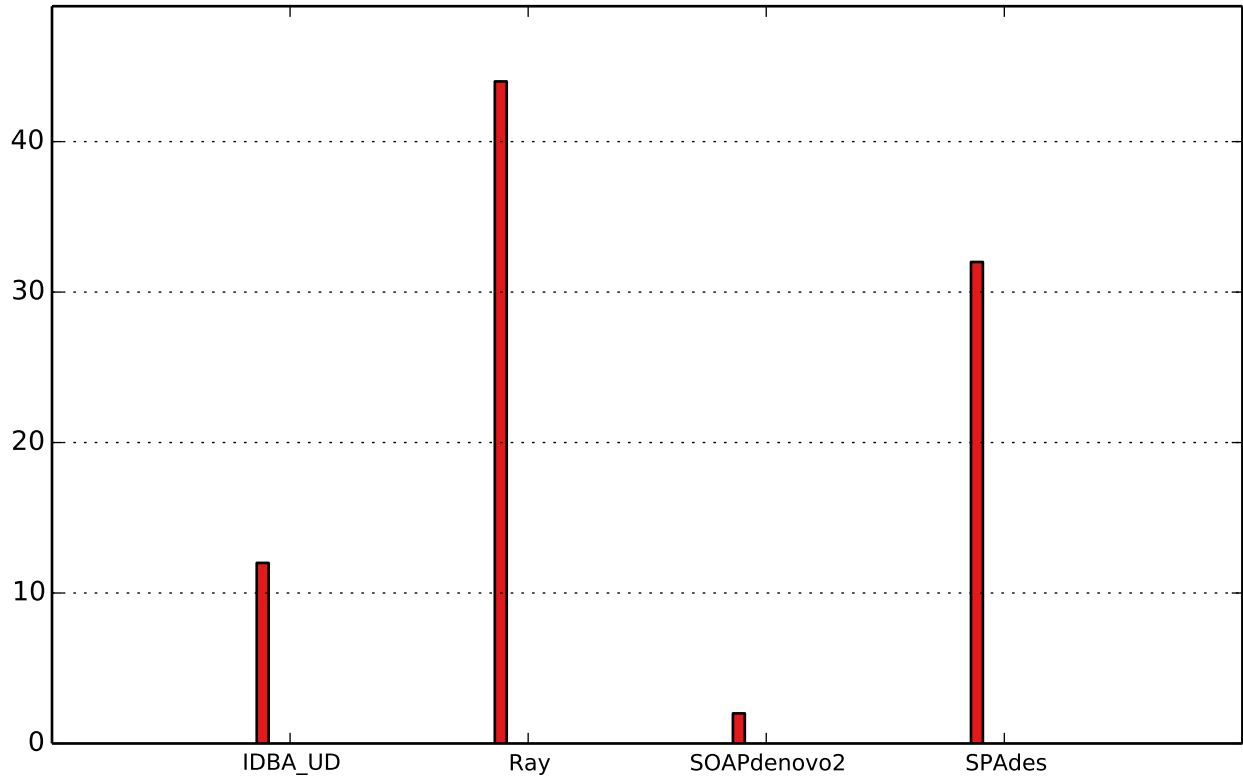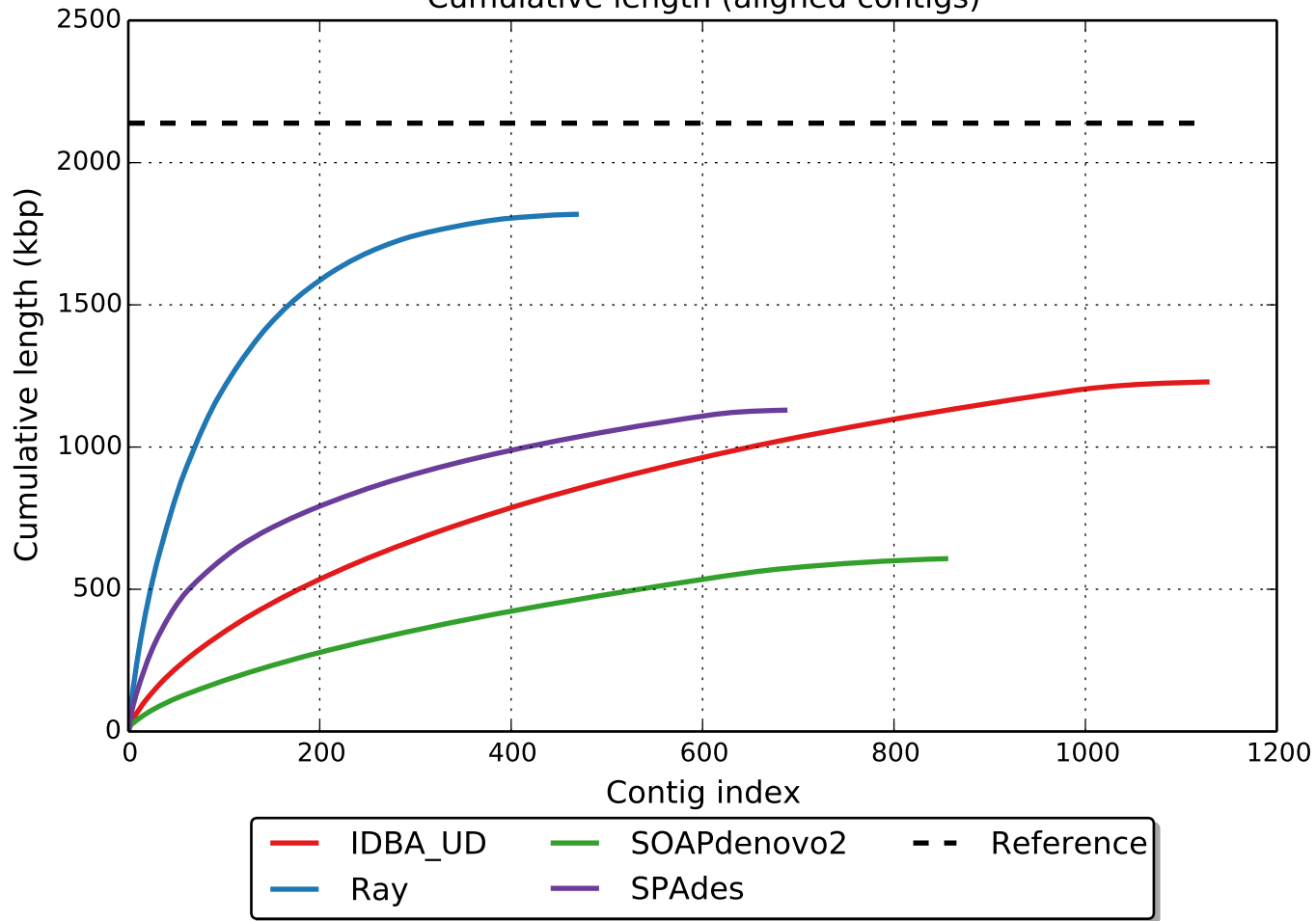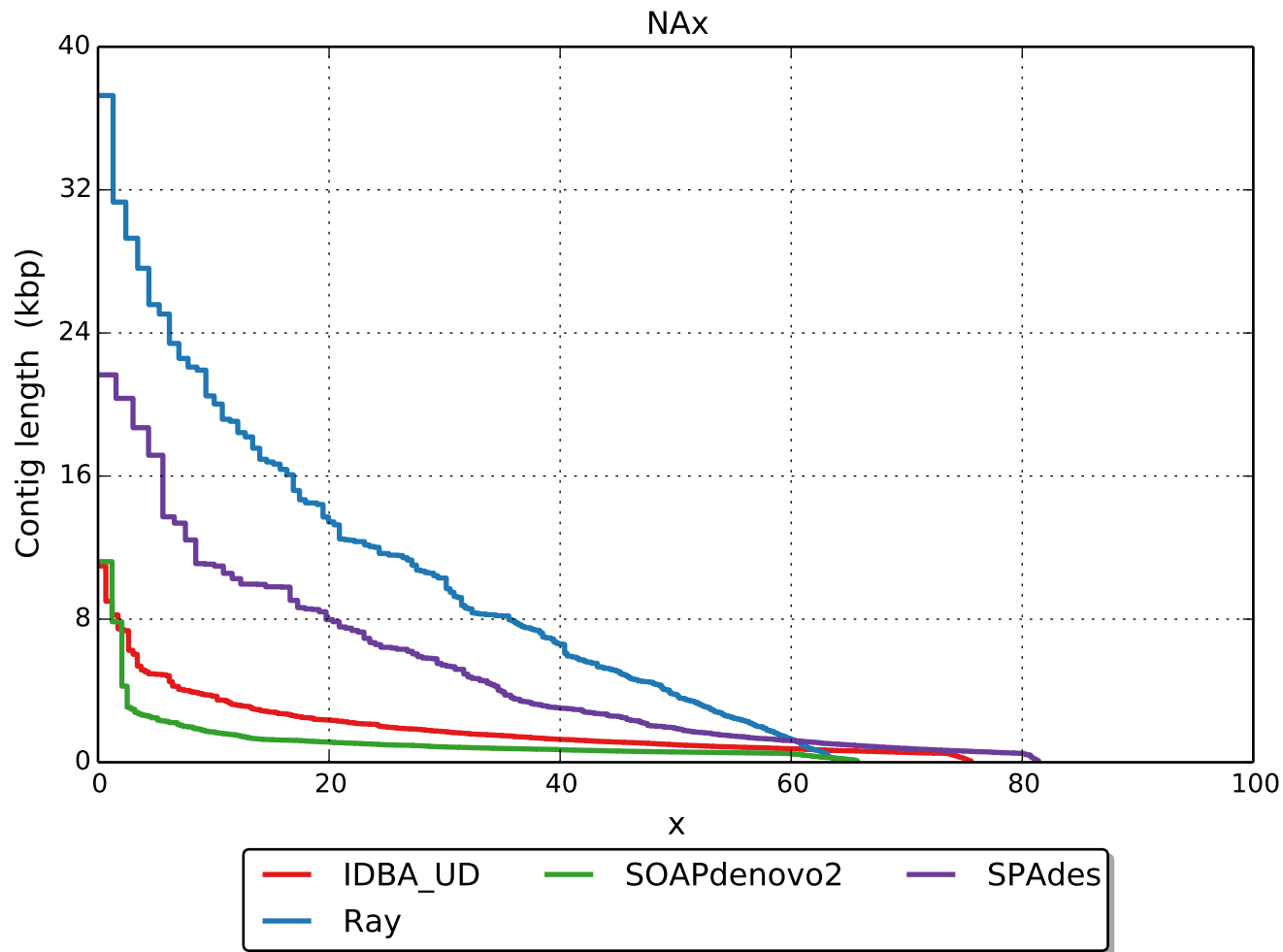
Cumulative length

Misassemblies

Cumulative length (aligned contigs)

Genome fraction, %