Report

	IDBA_UD	Ray	SOAPdenovo2	SPAdes
# contigs (>= 1000 bp)	1033	18	650	1095
# contigs (>= 5000 bp)	228	7	4	244
# contigs (>= 10000 bp)	71	4	2	61
# contigs (>= 25000 bp)	5	1	0	8
# contigs (>= 50000 bp)	1	1	0	2
Total length (>= 1000 bp)	4199060	170328	948088	4423419
Total length (>= 5000 bp)	2246299	153011	43579	2370932
Total length (>= 10000 bp)	1169695	129884	32464	1126334
Total length (>= 25000 bp)	230295	88128	0	393160
Total length (>= 50000 bp)	103500	88128	0	183607
# contigs	1360	95	2552	1447
Largest contig	103500	88128	19665	118876
Total length	4440942	217268	2268621	4678634
Reference length	6760735	6760735	6760735	6760735
GC (%)	43.52	44.98	42.92	43.35
Reference GC (%)	43.02	43.02	43.02	43.02
N50	5158	14202	906	5076
NG50	2640	-	-	2914
N75	2761	1491	675	2678
L50	223	3	847	238
LG50	544	-	-	509
L75	525	12	1574	555
# misassemblies	43	6	23	55
# misassembled contigs	34	2	21	41
Misassembled contigs length	201859	90348	22731	402495
# local misassemblies	33	6	2634	27
# structural variations	0	0	0	0
# unaligned contigs	0 + 391 part	0 + 4 part	0 + 392 part	0 + 545 part
Unaligned length	569238	41723	163645	996757
Genome fraction (%)	56.013	2.451	28.257	51.908
Duplication ratio	1.022	1.059	1.102	1.049
# N's per 100 kbp	300.25	691.77	6857.07	766.10
# mismatches per 100 kbp	1298.77	316.26	1146.72	1495.04
# indels per 100 kbp	44.60	8.45	17.95	50.84
Largest alignment	27284	42955	19665	40751
NA50	3653	1491	718	2543
NGA50	1331	-	-	752
NA75	1443	506	493	528
LA50	318	12	1007	454
LGA50	827	-	-	1171
LA75	791	91	1959	1373

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).
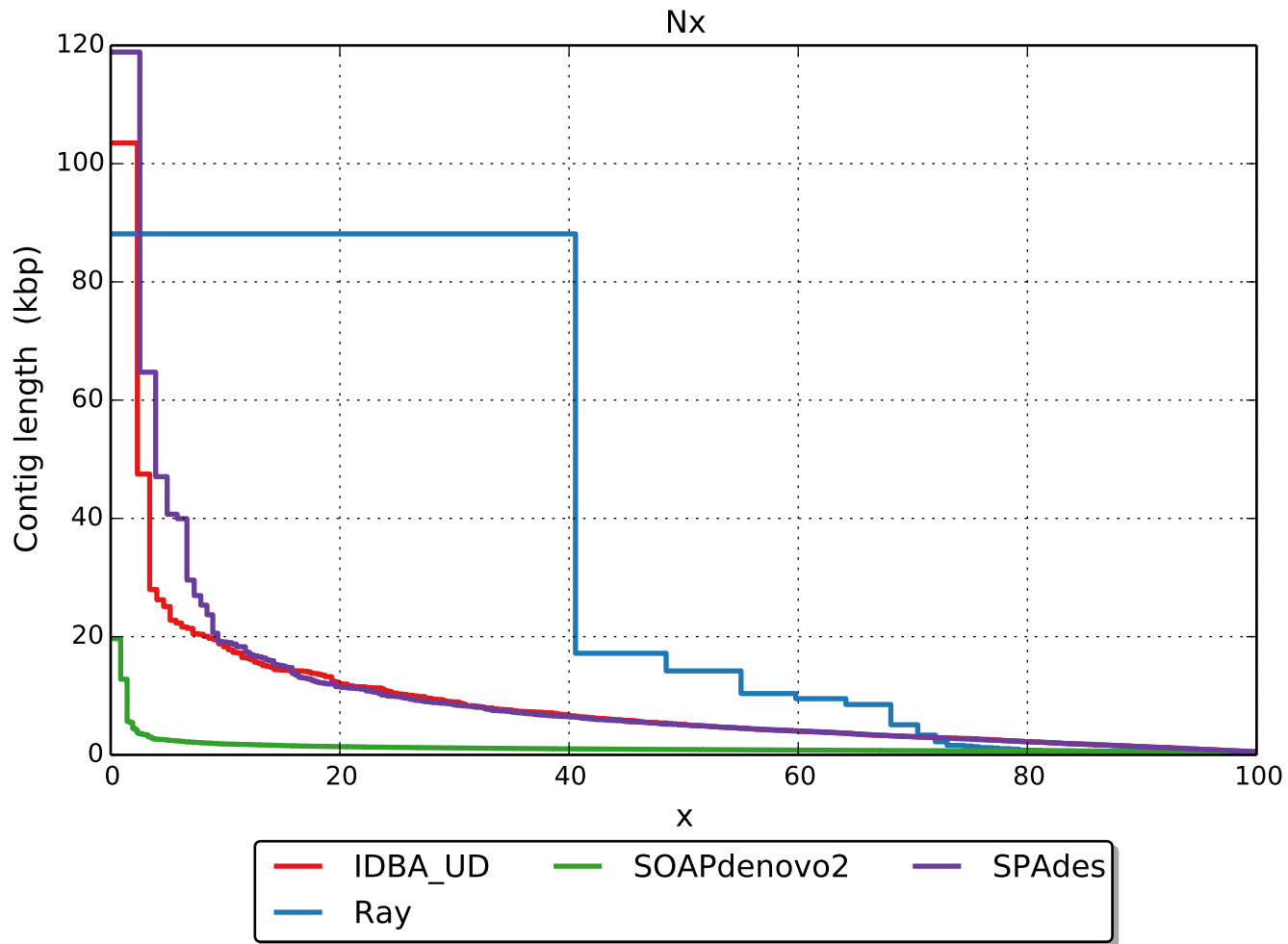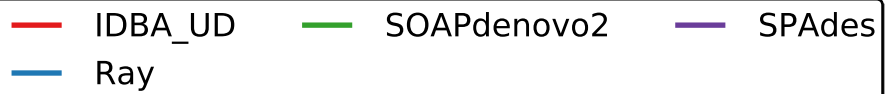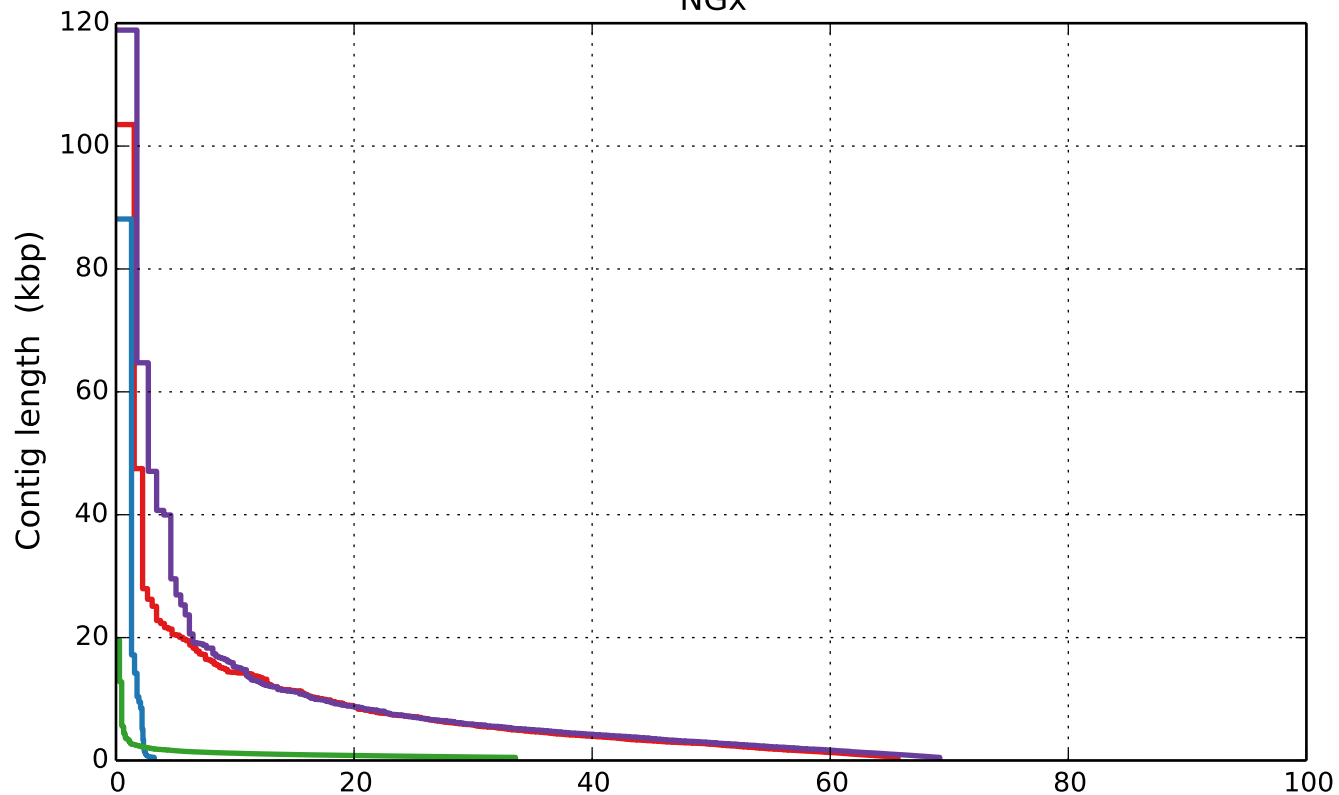
Misassemblies report

	IDBA_UD	Ray	SOAPdenovo2	SPAdes
# misassemblies	43	6	23	55
# relocations	18	4	9	20
# translocations	18	2	10	32
# inversions	7	0	4	3
# possibly misassembled contigs	144	4	37	275
# misassembled contigs	34	2	21	41
Misassembled contigs length	201859	90348	22731	402495
# local misassemblies	33	6	2634	27
# structural variations	0	0	0	0
# mismatches	49183	524	21907	52466
# indels	1689	14	343	1784
# short indels	1473	14	312	1511
# long indels	216	0	31	273
Indels length	5111	15	737	5880

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).
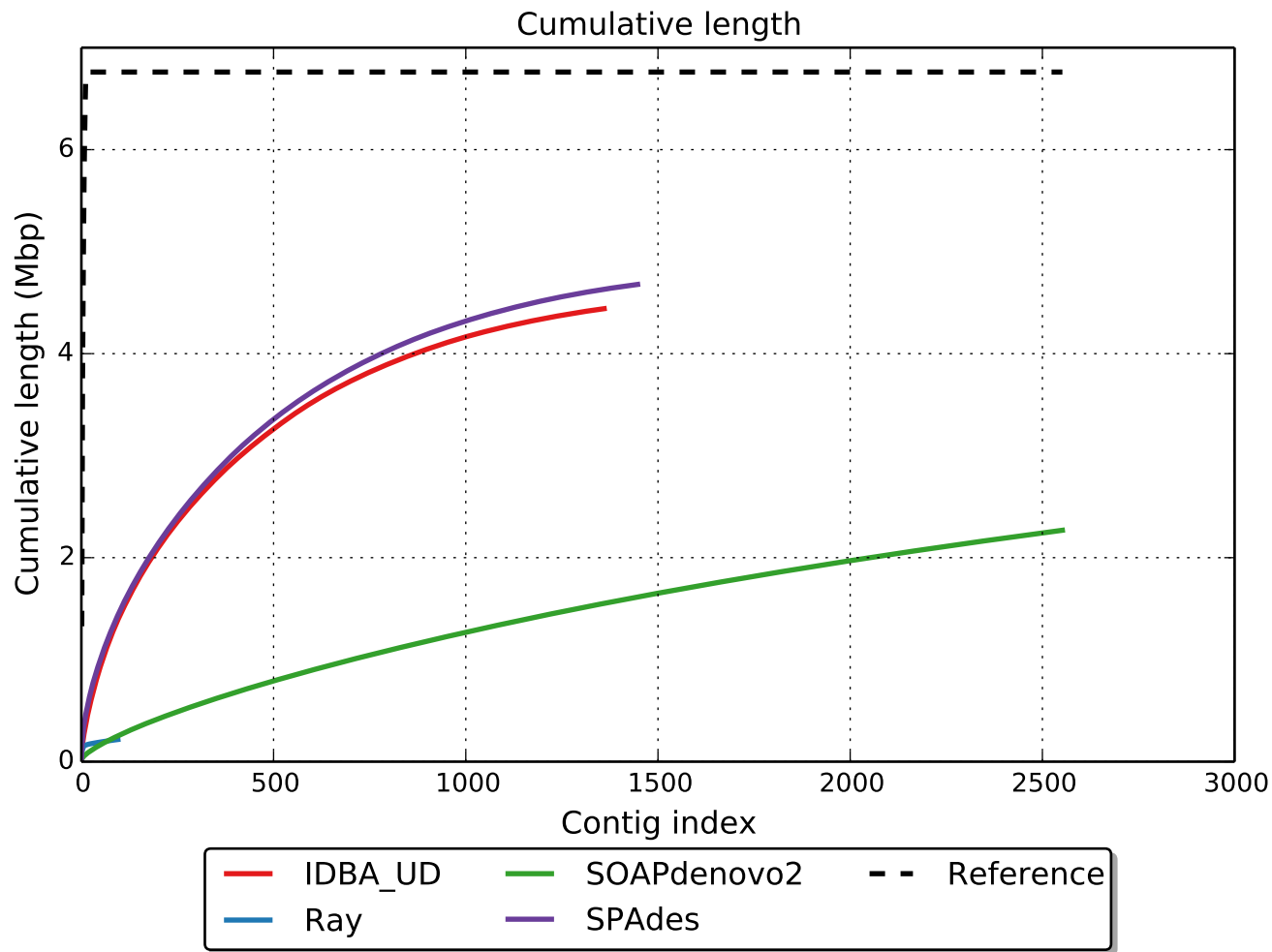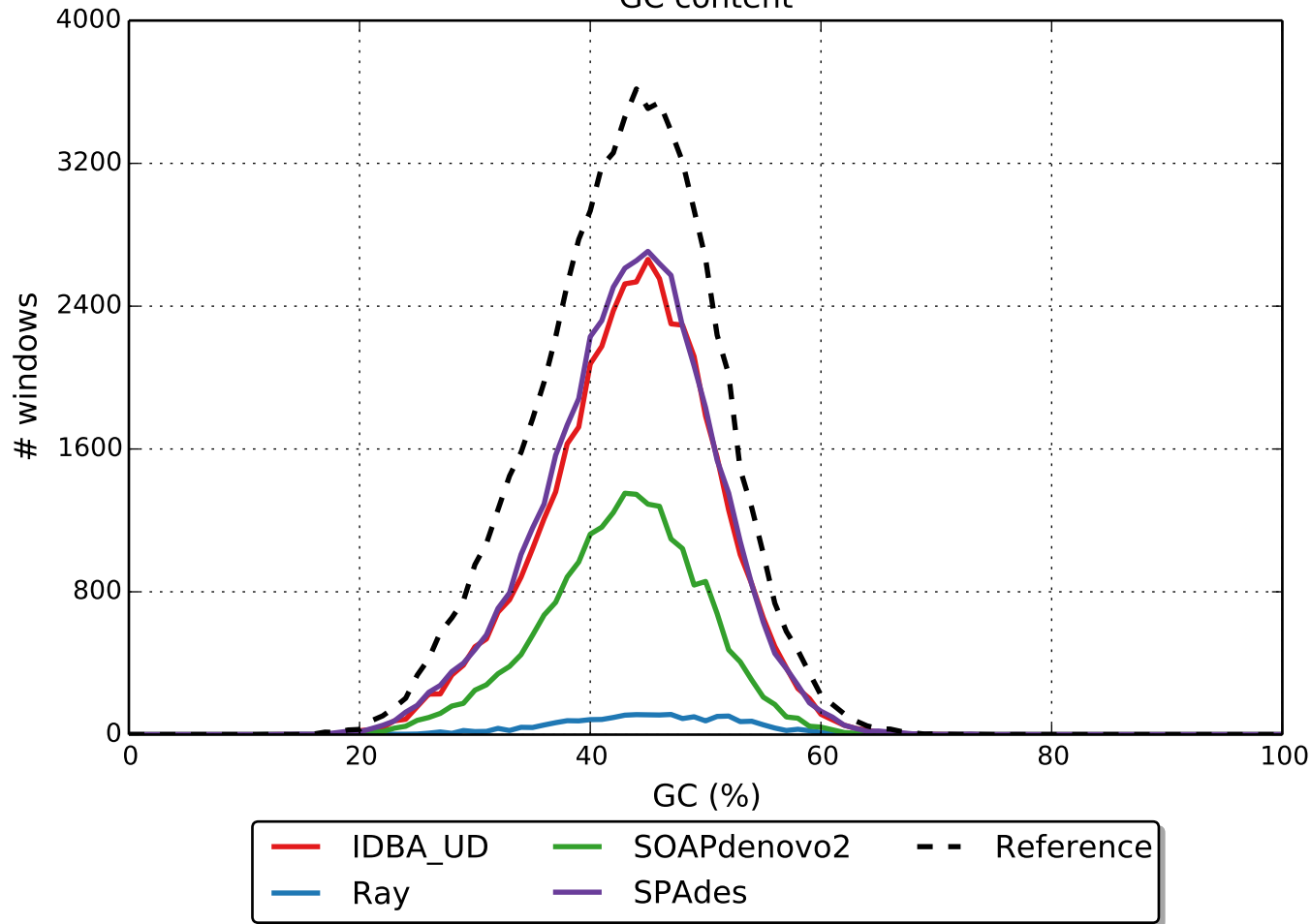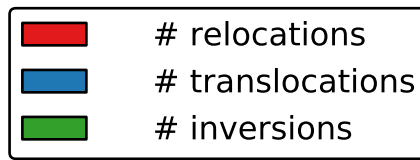
Unaligned report

	IDBA_UD	Ray	SOAPdenovo2	SPAdes
# fully unaligned contigs	0	0	0	0
Fully unaligned length	0	0	0	0
# partially unaligned contigs	391	4	392	545
# with misassembly	10	0	69	14
# both parts are significant	121	2	20	238
Partially unaligned length	569238	41723	163645	996757
# N's	13334	1503	155561	35843

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).
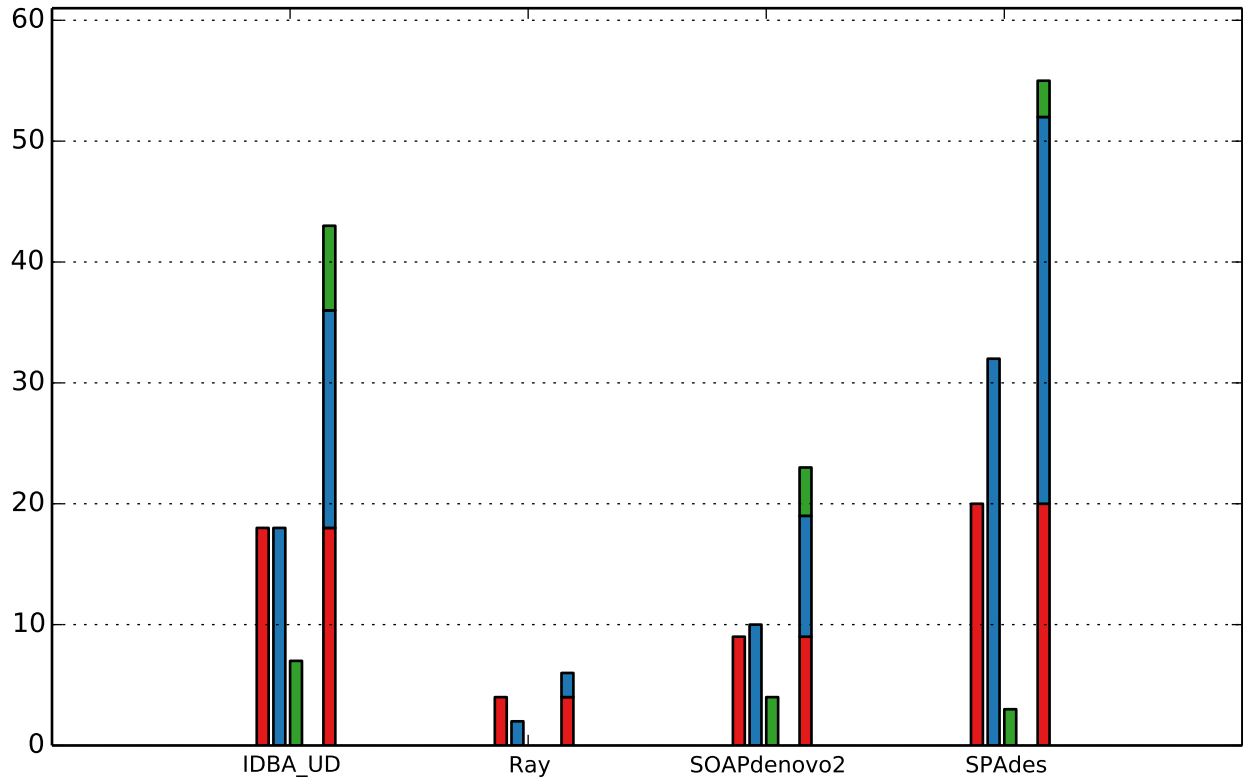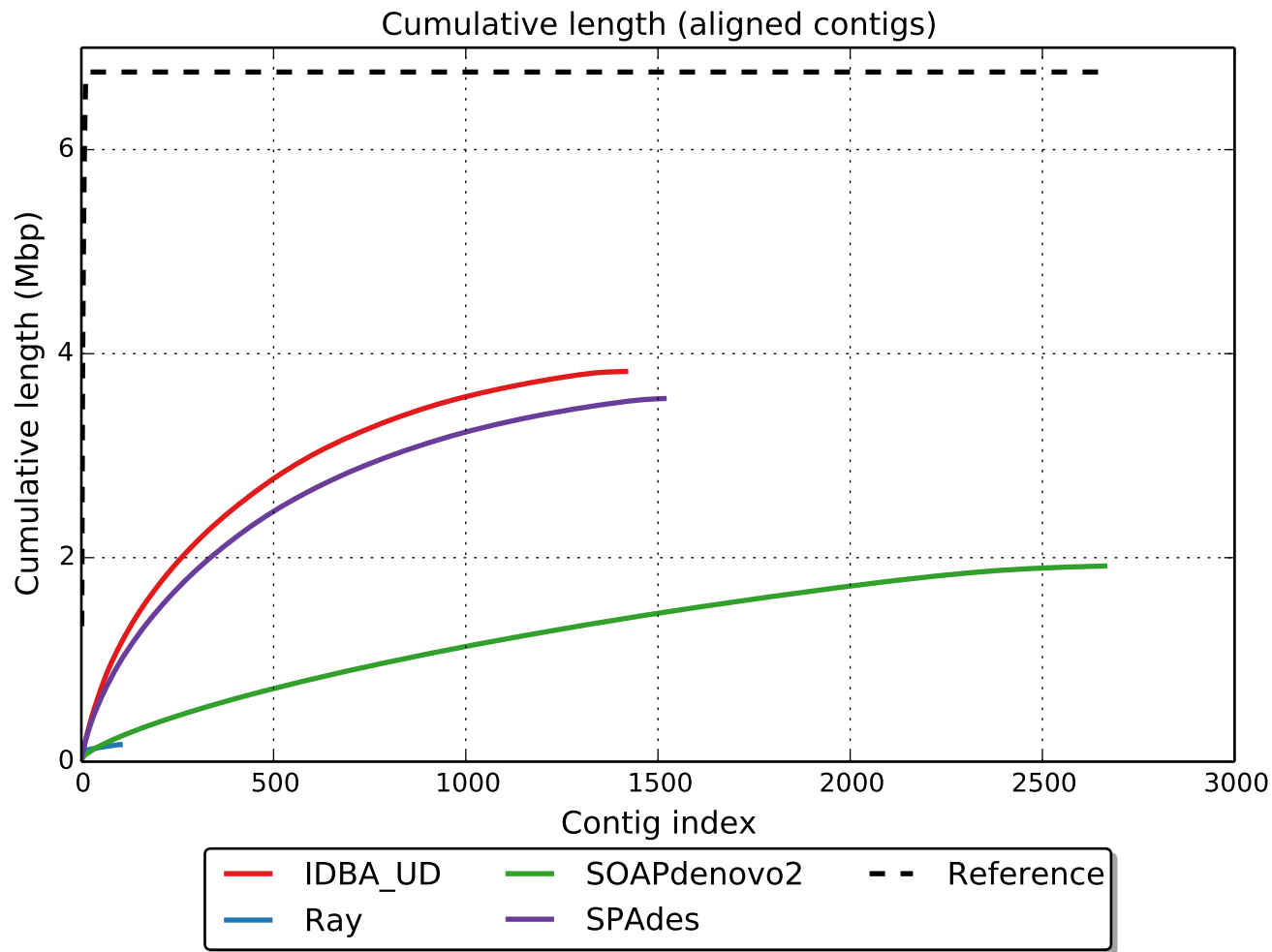
NGx

IDBA_UD	SOAPdenovo2	SPAdes
Ray		

Misassemblies

Cumulative length (aligned contigs)

NGAx

Genome fraction, %