

Report

	IDBA_UD	Ray	SOAPdenovo2	SPAdes
# contigs (>= 1000 bp)	568	35	86	630
# contigs (>= 5000 bp)	63	2	1	32
# contigs (>= 10000 bp)	6	2	1	5
# contigs (>= 25000 bp)	0	0	1	0
# contigs (>= 50000 bp)	0	0	0	0
Total length (>= 1000 bp)	1601432	103364	154419	1444556
Total length (>= 5000 bp)	441717	46712	28790	231311
Total length (>= 10000 bp)	67193	46712	28790	62176
Total length (>= 25000 bp)	0	0	28790	0
Total length (>= 50000 bp)	0	0	0	0
# contigs	792	393	416	962
Largest contig	13283	24057	28790	15831
Total length	1767476	333781	376199	1687463
Reference length	2090952	2090952	2090952	2090952
GC (%)	58.00	56.40	54.75	57.78
Reference GC (%)	57.72	57.72	57.72	57.72
N50	3101	729	869	2222
NG50	2575	-	-	1774
N75	1726	595	649	1287
NG75	1100	-	-	766
L50	176	111	123	227
LG50	234	-	-	329
L75	363	240	250	474
LG75	537	-	-	771
# misassemblies	19	1	3	15
# misassembled contigs	19	1	3	14
Misassembled contigs length	66575	768	3115	54403
# local misassemblies	45	5	16	33
# structural variations	3	1	1	3
# unaligned contigs	0 + 277 part	0 + 44 part	0 + 139 part	0 + 249 part
Unaligned length	203608	72983	112189	186140
Genome fraction (%)	73.307	12.329	12.281	70.546
Duplication ratio	1.020	1.012	1.028	1.018
# N's per 100 kbp	0.00	648.63	3979.01	0.00
# mismatches per 100 kbp	2298.46	1770.01	1760.60	2308.74
# indels per 100 kbp	71.76	45.38	54.13	62.50
Largest alignment	13274	2299	3922	8610
NA50	2394	598	552	1774
NGA50	1931	-	-	1301
NA75	1081	502	-	916
LA50	210	212	233	287
LGA50	286	-	-	419
LA75	481	364	-	619

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	928	1101	381	923
# relocations	267	343	88	315
# translocations	271	303	122	250
# inversions	18	3	5	8
# interspecies translocations	372	452	166	350
# possibly misassembled contigs	1455	1434	882	1286
# misassembled contigs	589	566	235	577
Misassembled contigs length	8478027	12187377	4094970	9349811
# local misassemblies	1014	1180	594	614
# structural variations	137	160	81	146
# mismatches	732101	675080	337104	779821
# indels	18431	17860	9132	19873
# short indels	16222	16361	7297	18124
# long indels	2209	1499	1835	1749
Indels length	68259	42312	52678	53946

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	38691	13394	26475	35863
Fully unaligned length	58734689	31491690	41689598	53978616
# partially unaligned contigs	4898	2058	4096	3597
# with misassembly	439	399	523	266
# both parts are significant	1102	924	673	920
Partially unaligned length	10842726	11504246	7890203	7997785
# N's	118	476832	2279043	131817

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Report

	IDBA_UD	Ray	SOAPdenovo2	SPAdes
# contigs (>= 0 bp)	55710	20766	36865	49424
# contigs (>= 1000 bp)	23695	10814	13727	20339
# contigs (>= 5000 bp)	2322	2725	1519	2283
# contigs (>= 10000 bp)	789	1386	630	908
# contigs (>= 25000 bp)	269	445	222	301
# contigs (>= 50000 bp)	122	149	103	132
Total length (>= 0 bp)	99459279	72065155	64684975	92249098
Total length (>= 1000 bp)	77350395	65266007	48925980	72172611
Total length (>= 5000 bp)	37254349	47947242	26655145	38396984
Total length (>= 10000 bp)	26853750	38598919	20575482	28960702
Total length (>= 25000 bp)	19117982	24143009	14270582	19850138
Total length (>= 50000 bp)	14013926	14105535	10168529	14017133
# contigs	55710	20766	36865	49424
Largest contig	509970	442828	560918	386771
Total length	99459279	72065155	64684975	92249098
Reference length	60553137	60553137	60553137	60553137
N50	2722	11920	2900	3135
N75	1091	3121	1019	1116
L50	5789	1152	3051	4259
L75	21056	4274	13319	17507
# misassemblies	928	1101	381	923
# misassembled contigs	589	566	235	577
Misassembled contigs length	8478027	12187377	4094970	9349811
# local misassemblies	1014	1180	594	614
# structural variations	137	160	81	146
# unaligned contigs	38691 + 4898 part	13394 + 2058 part	26475 + 4096 part	35863 + 3597 part
Unaligned length	69577415	42995936	49579801	61976401
Genome fraction (%)	45.707	38.885	24.415	46.896
Duplication ratio	1.123	1.282	1.073	1.117
# N's per 100 kbp	0.12	661.67	3523.30	142.89
# mismatches per 100 kbp	2645.18	2867.04	2280.19	2746.13
# indels per 100 kbp	66.59	75.85	61.77	69.98
Largest alignment	281176	281272	248950	281148

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	19	1	3	15
# relocations	7	0	0	5
# translocations	12	1	3	9
# inversions	0	0	0	1
# possibly misassembled contigs	49	3	10	41
# misassembled contigs	19	1	3	14
Misassembled contigs length	66575	768	3115	54403
# local misassemblies	45	5	16	33
# structural variations	3	1	1	3
# mismatches	35231	4563	4521	34056
# indels	1100	117	139	922
# short indels	922	111	98	781
# long indels	178	6	41	141
Indels length	4245	210	1228	3173

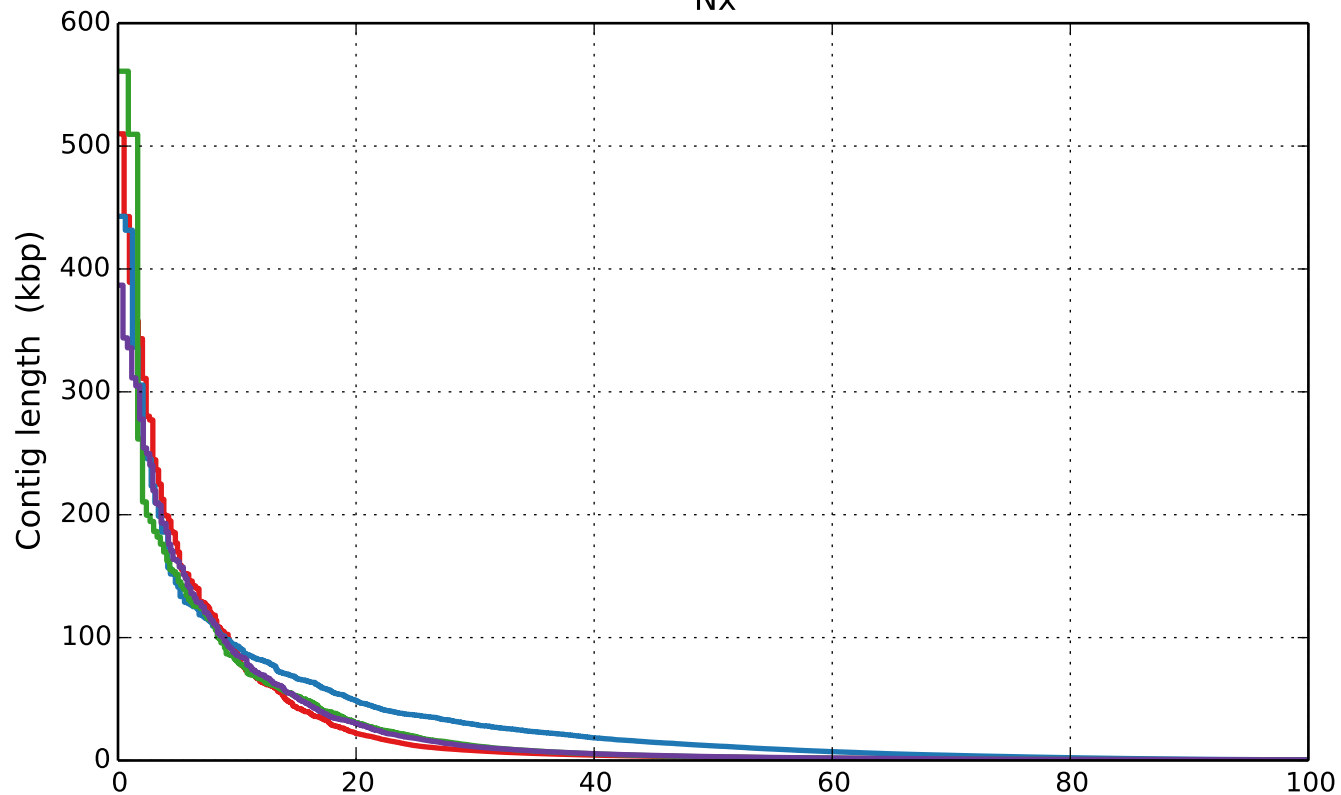
All statistics are based on contigs of size ≥ 500 bp, unless otherwise noted (e.g., "# contigs (≥ 0 bp)" and "Total length (≥ 0 bp)" include all contigs).

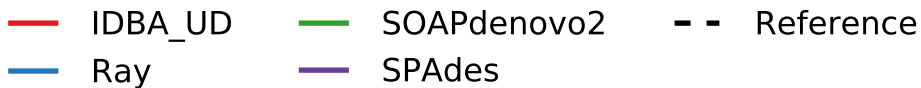
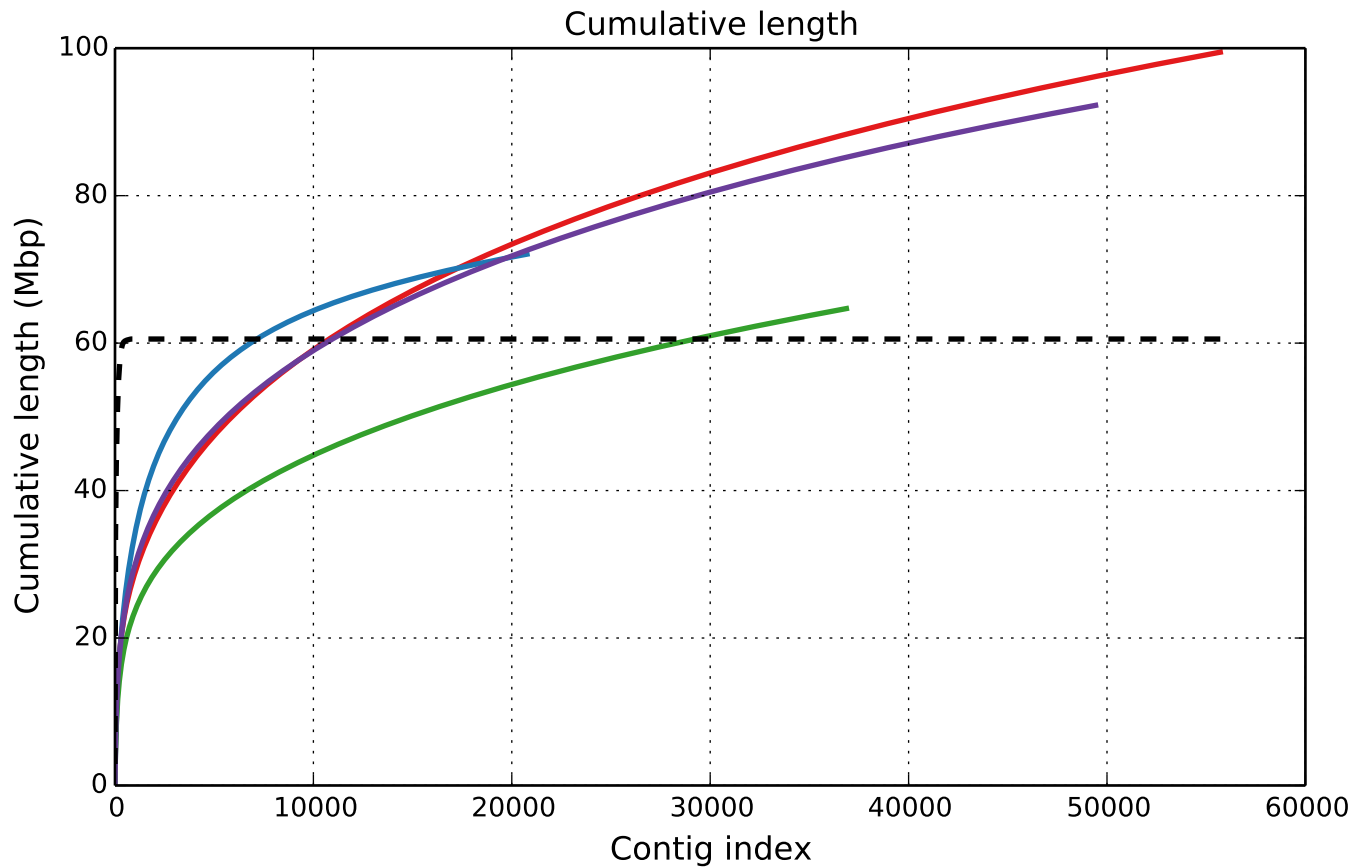
Unaligned report

	IDBA_UD	Ray	SOAPdenovo2	SPAdes
# fully unaligned contigs	0	0	0	0
Fully unaligned length	0	0	0	0
# partially unaligned contigs	277	44	139	249
# with misassembly	6	1	4	6
# both parts are significant	39	3	8	36
Partially unaligned length	203608	72983	112189	186140
# N's	0	2165	14969	0

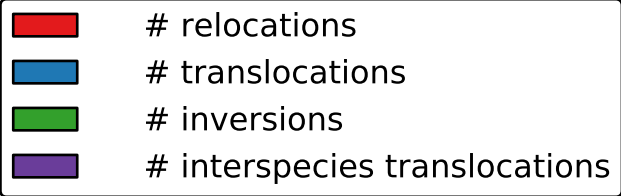
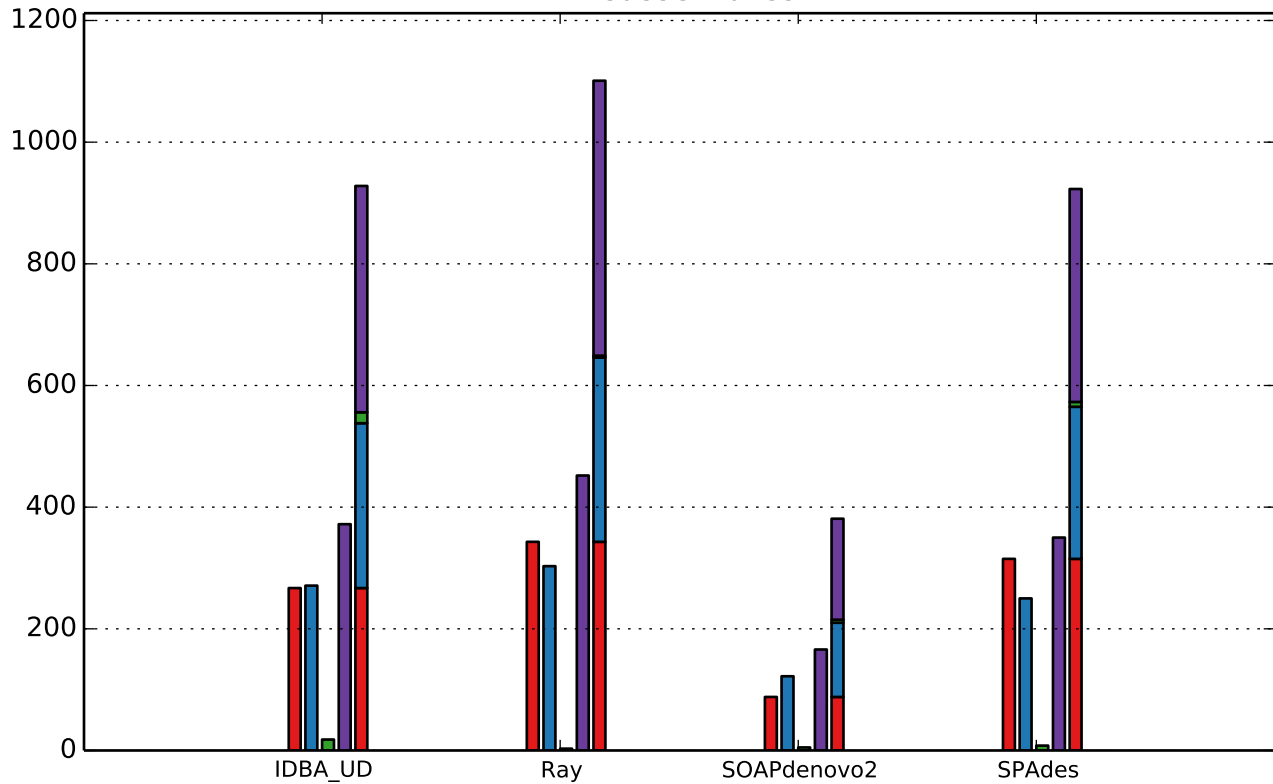
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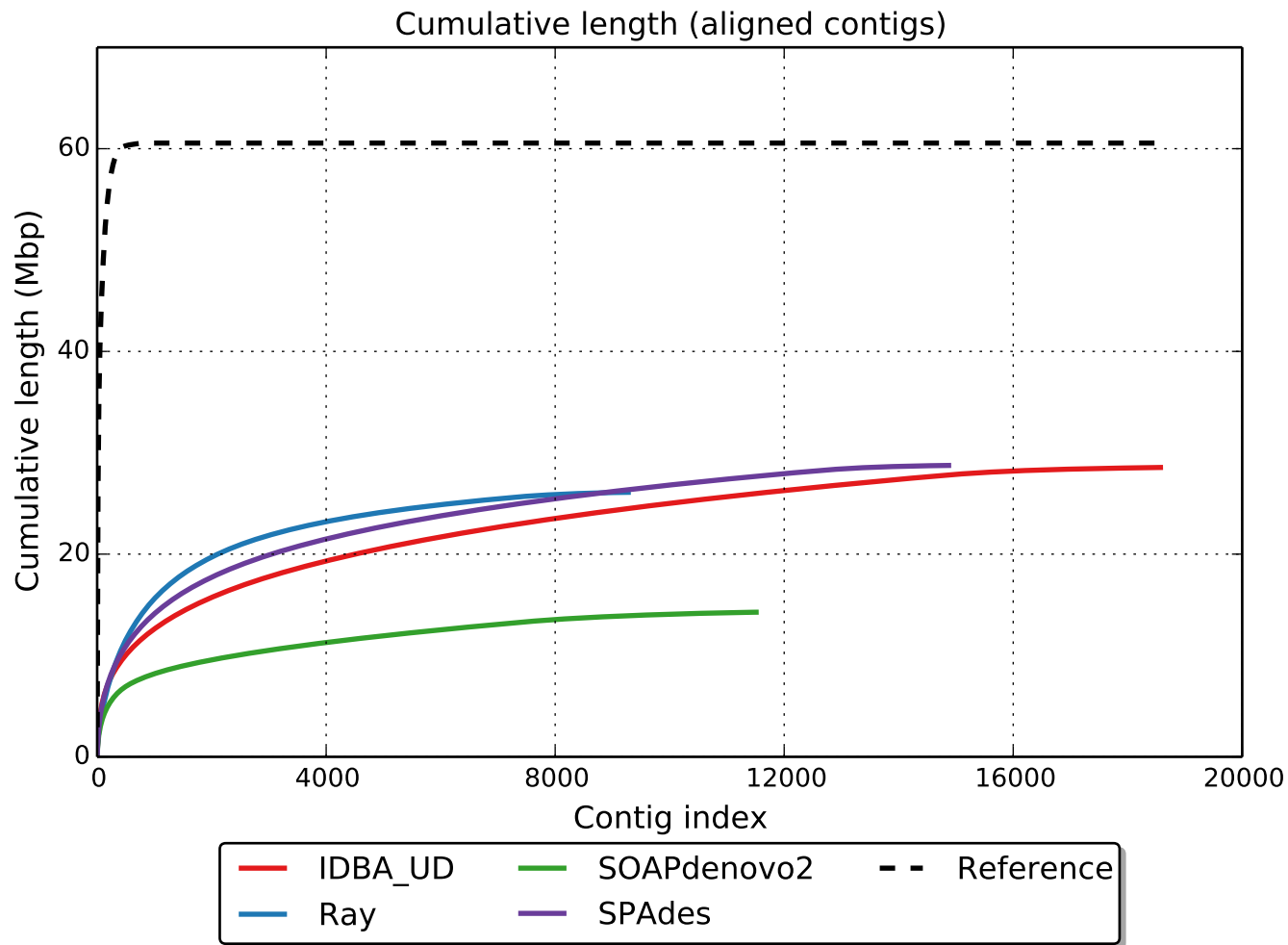
Nx



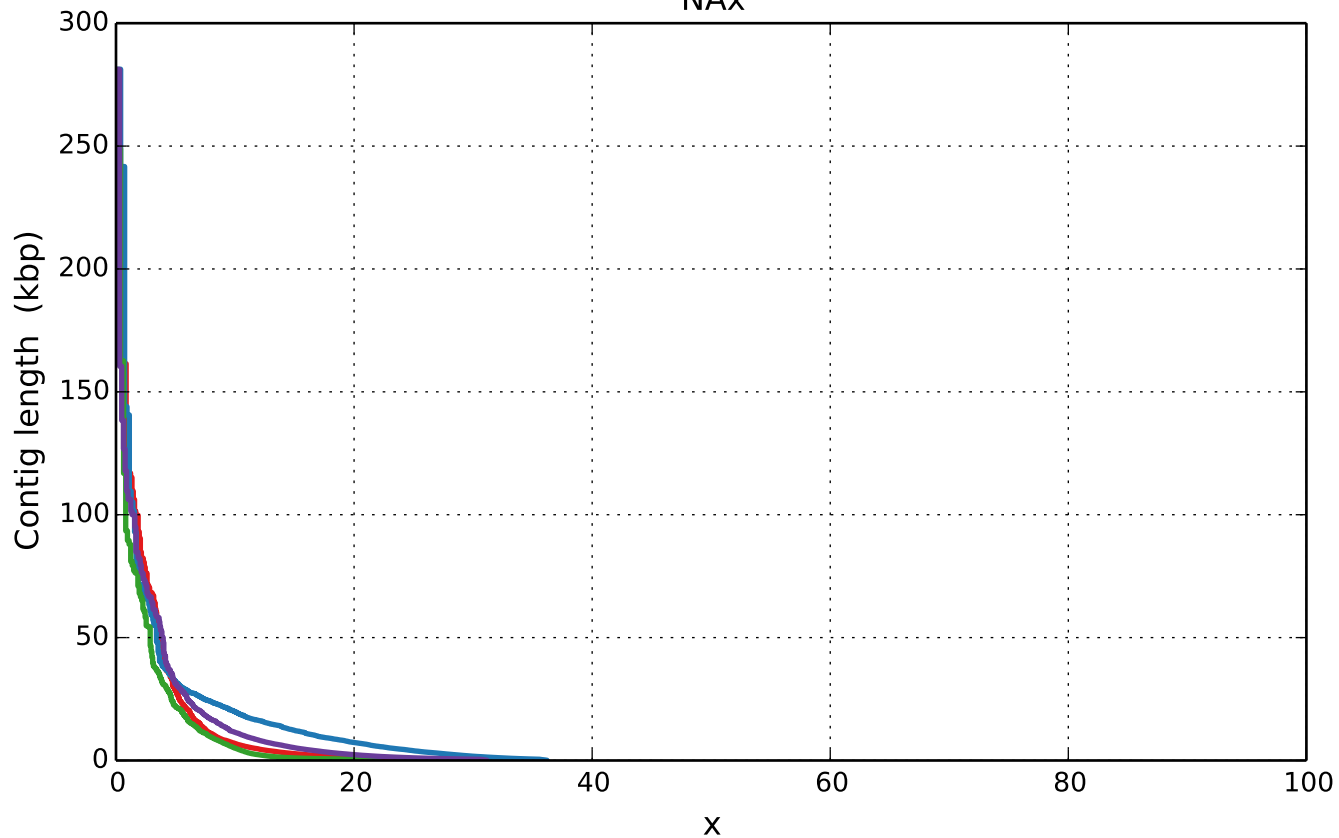


Misassemblies





NAx

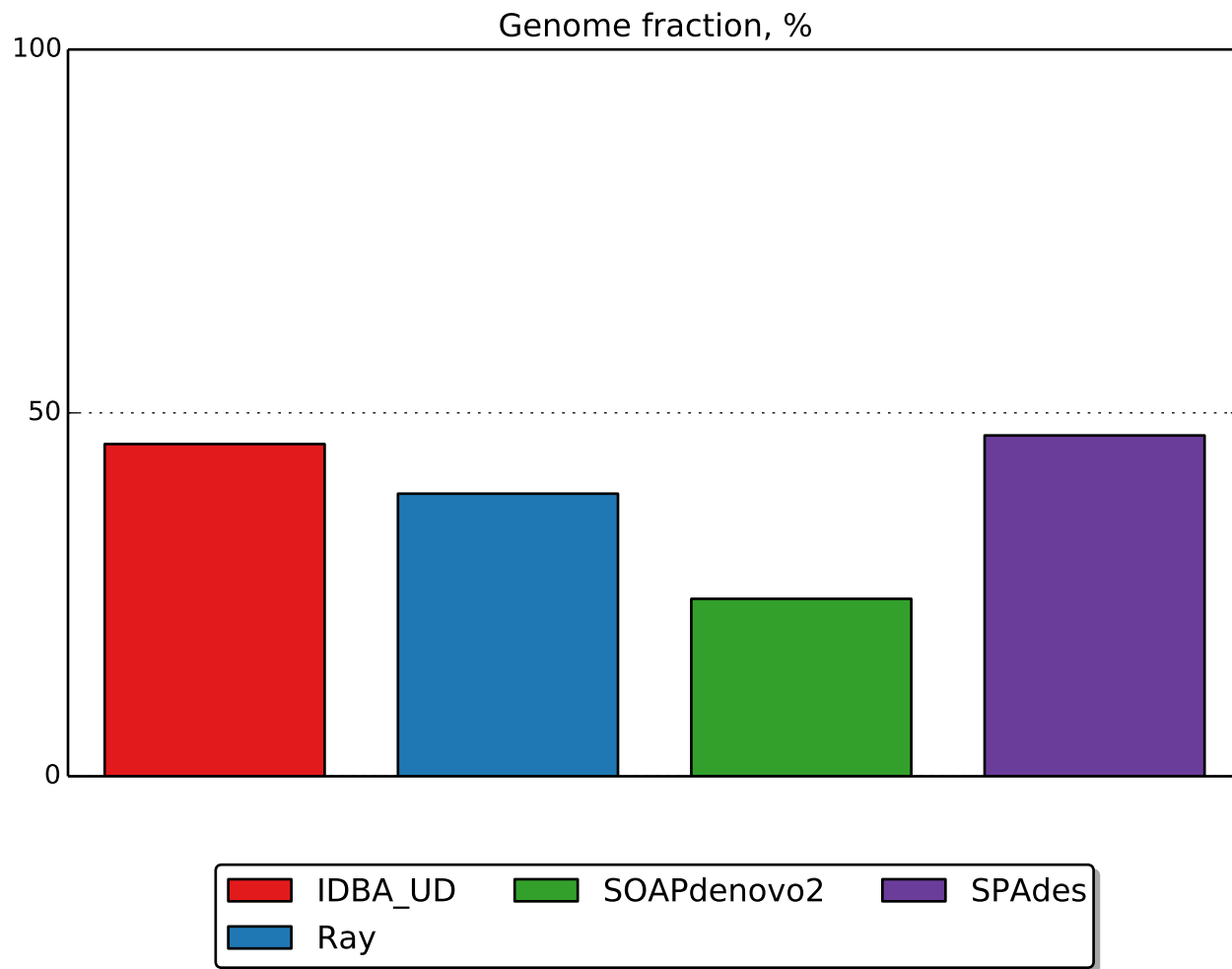


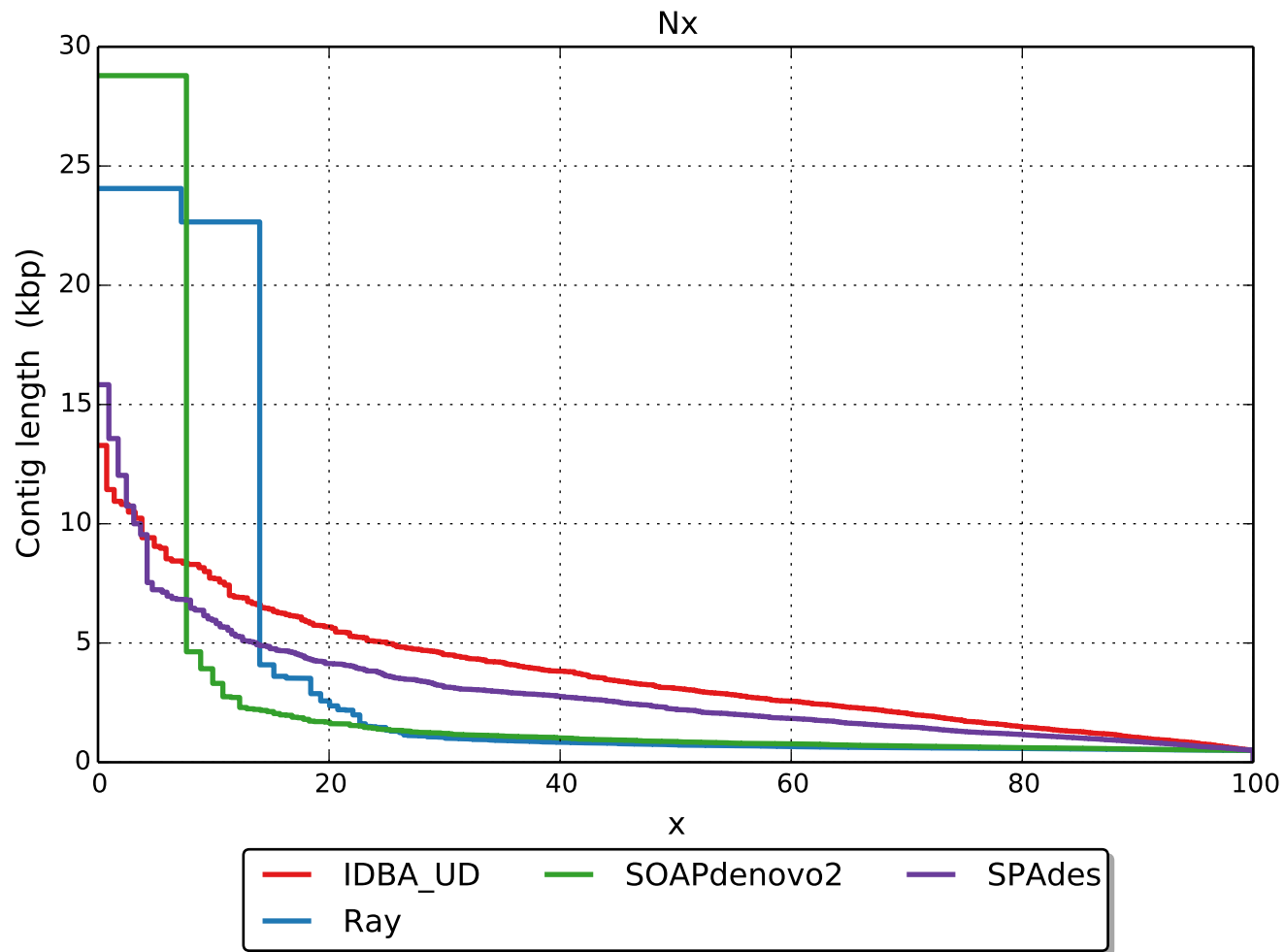
IDBA_UD

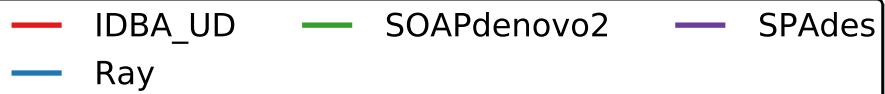
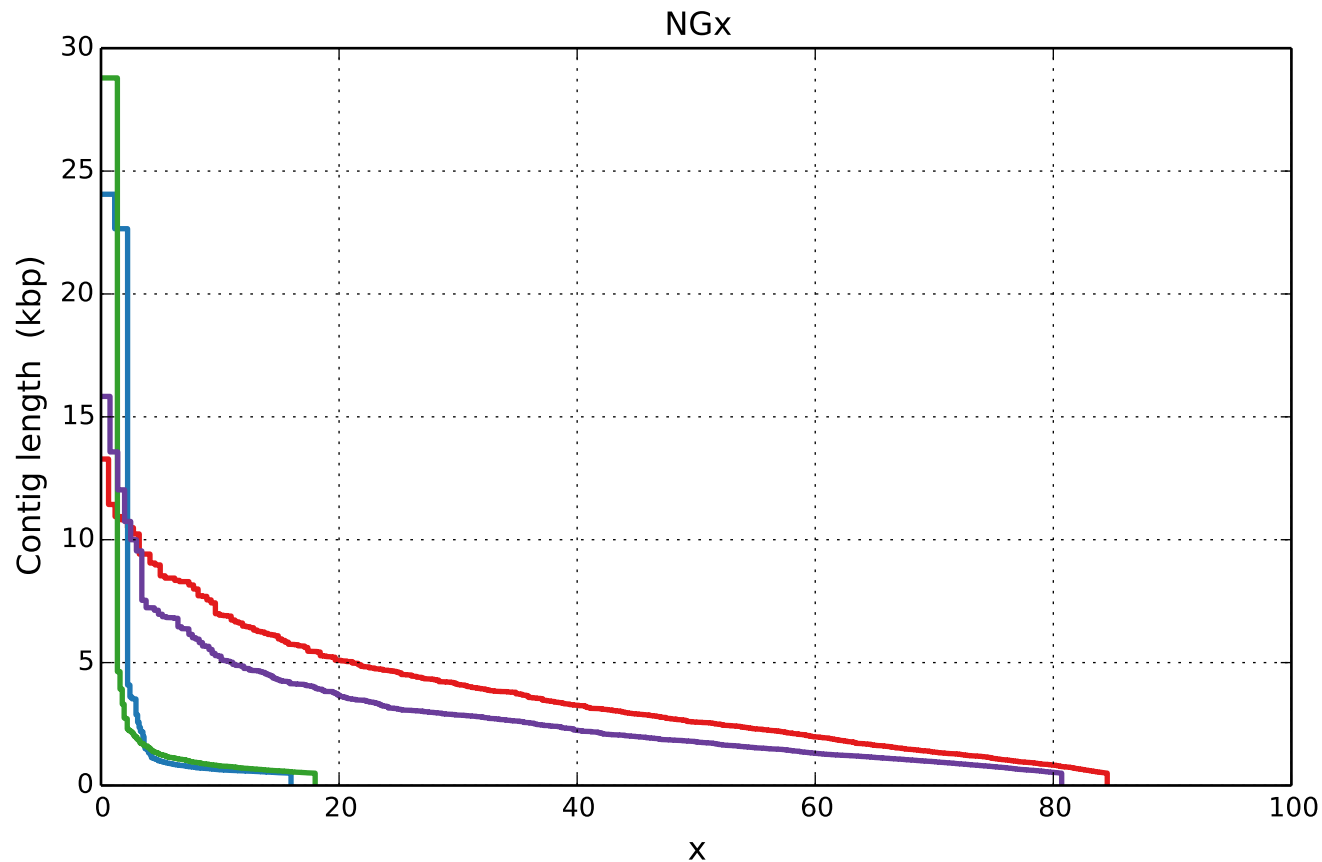
SOAPdenovo2

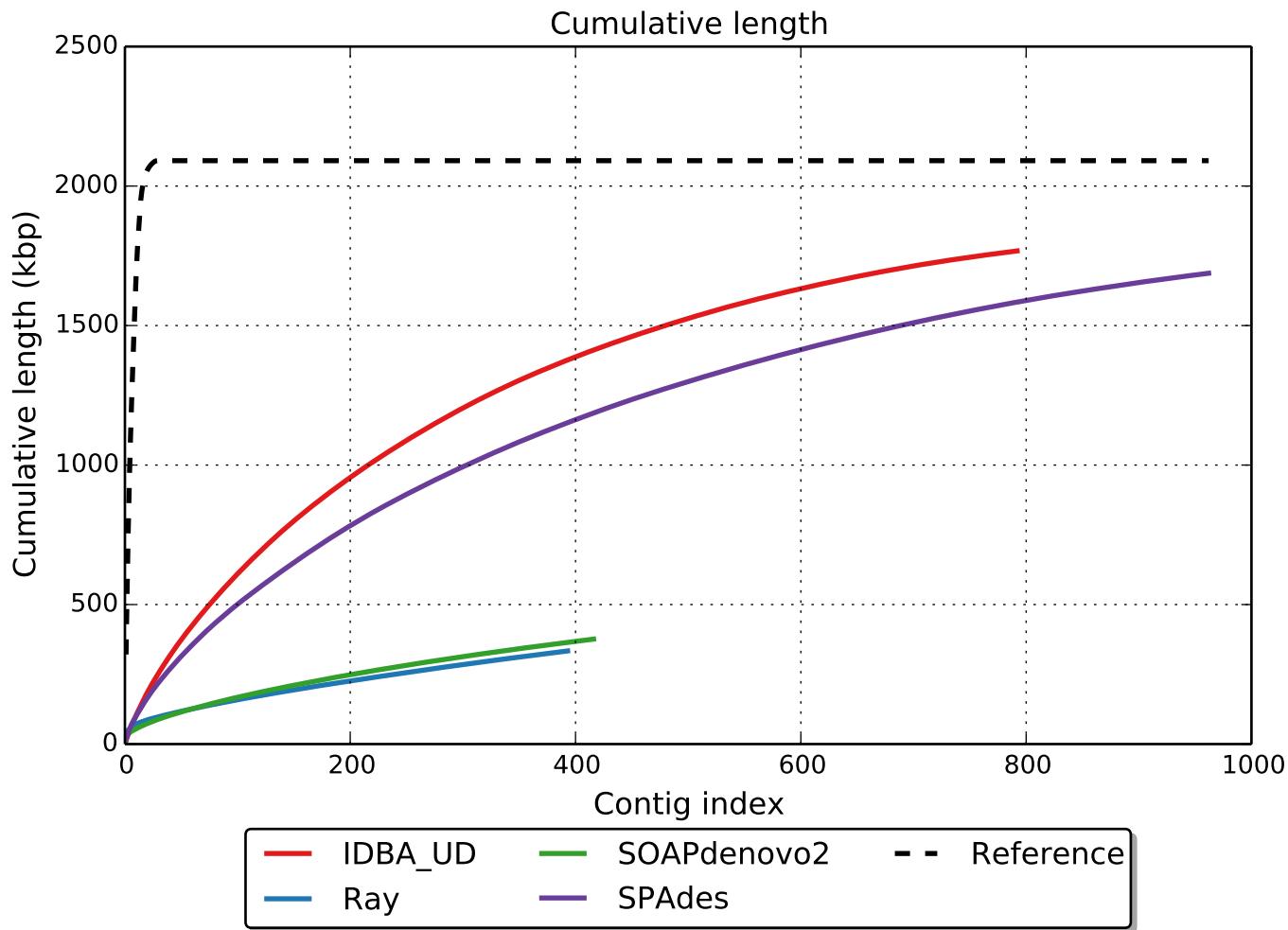
SPAdes

Ray

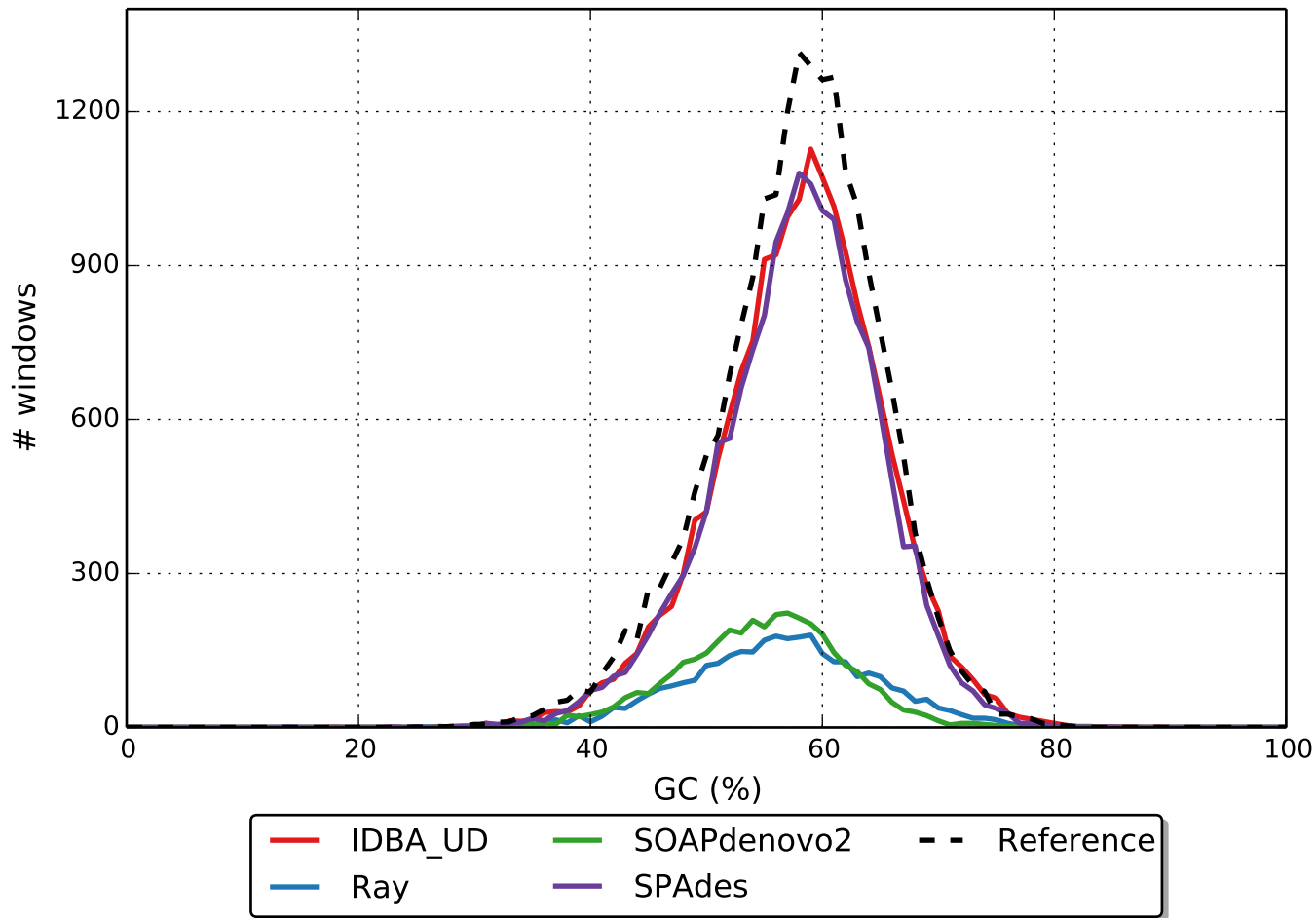




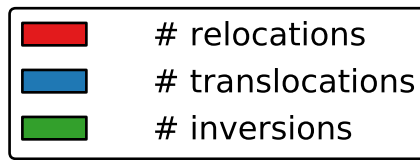
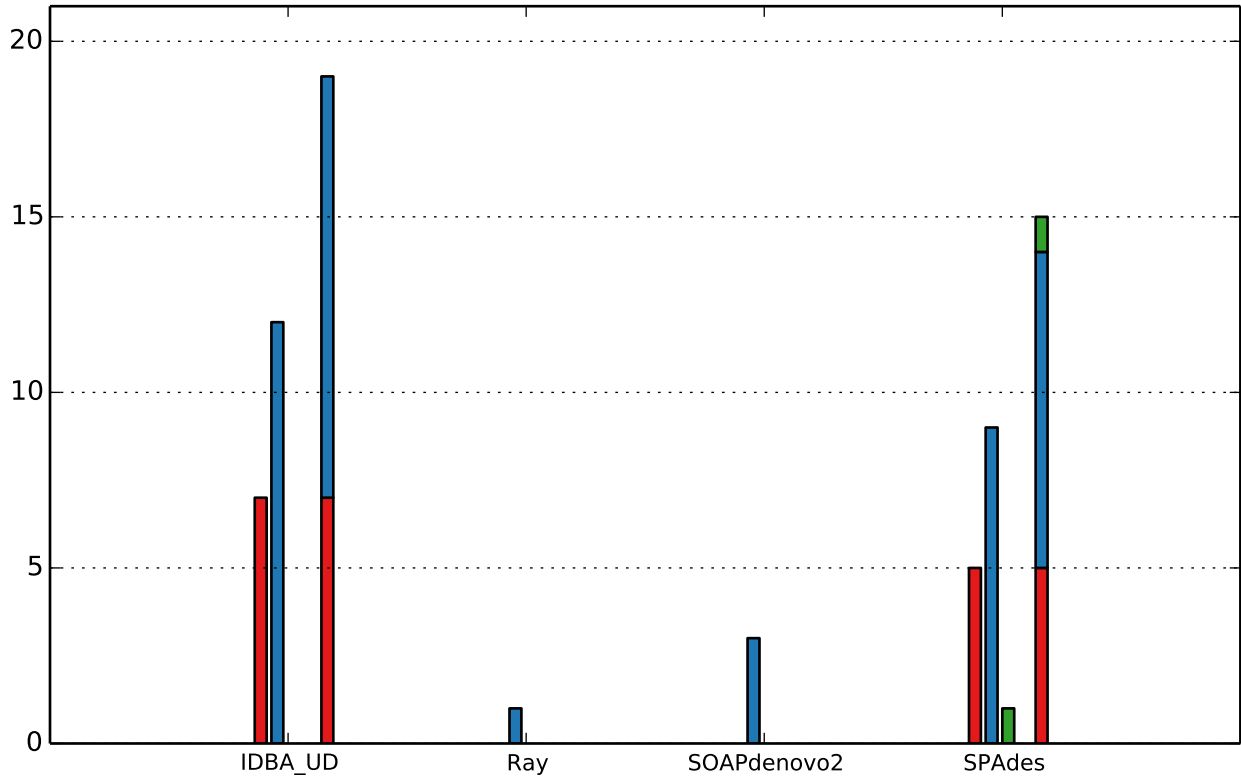




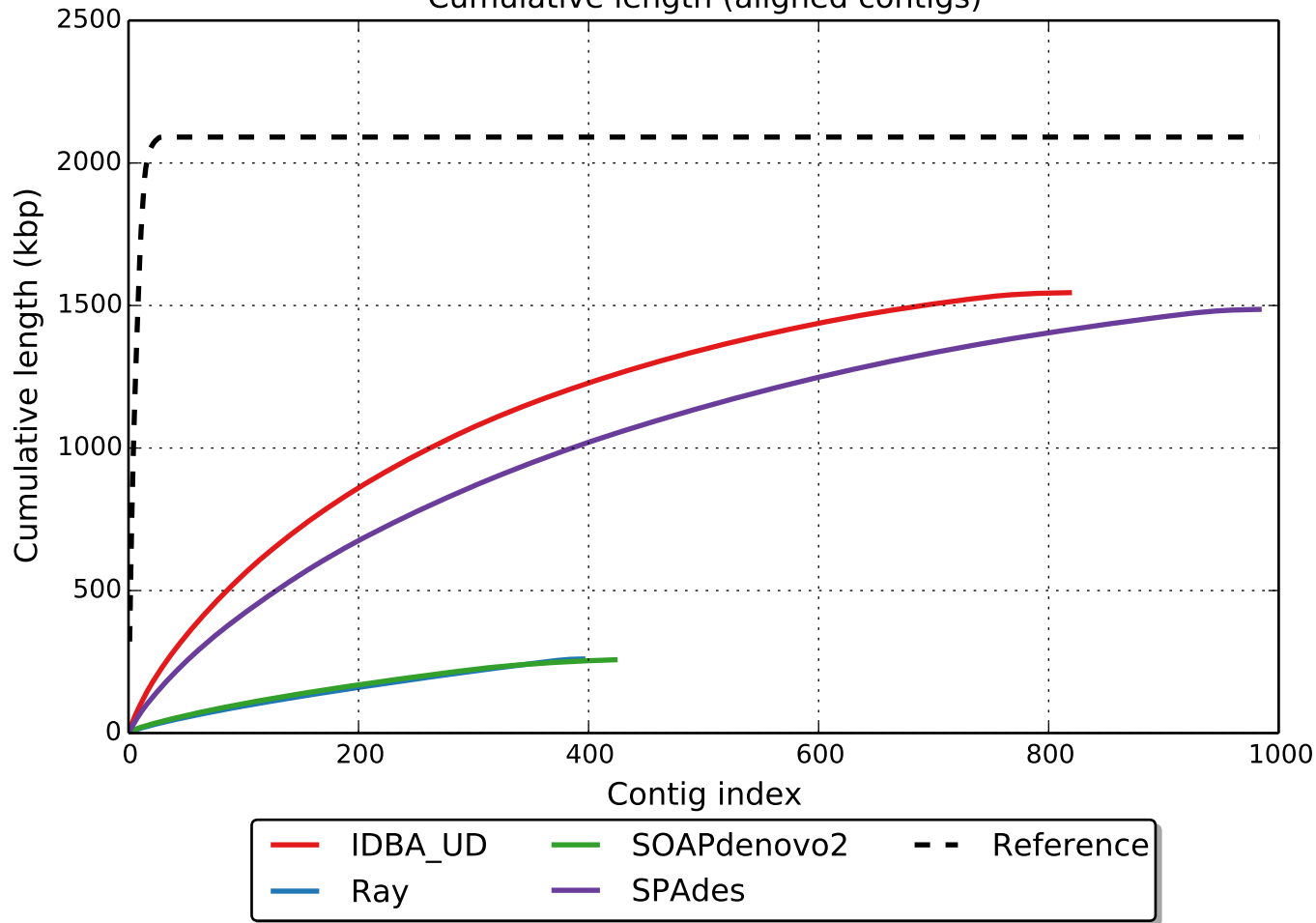
GC content



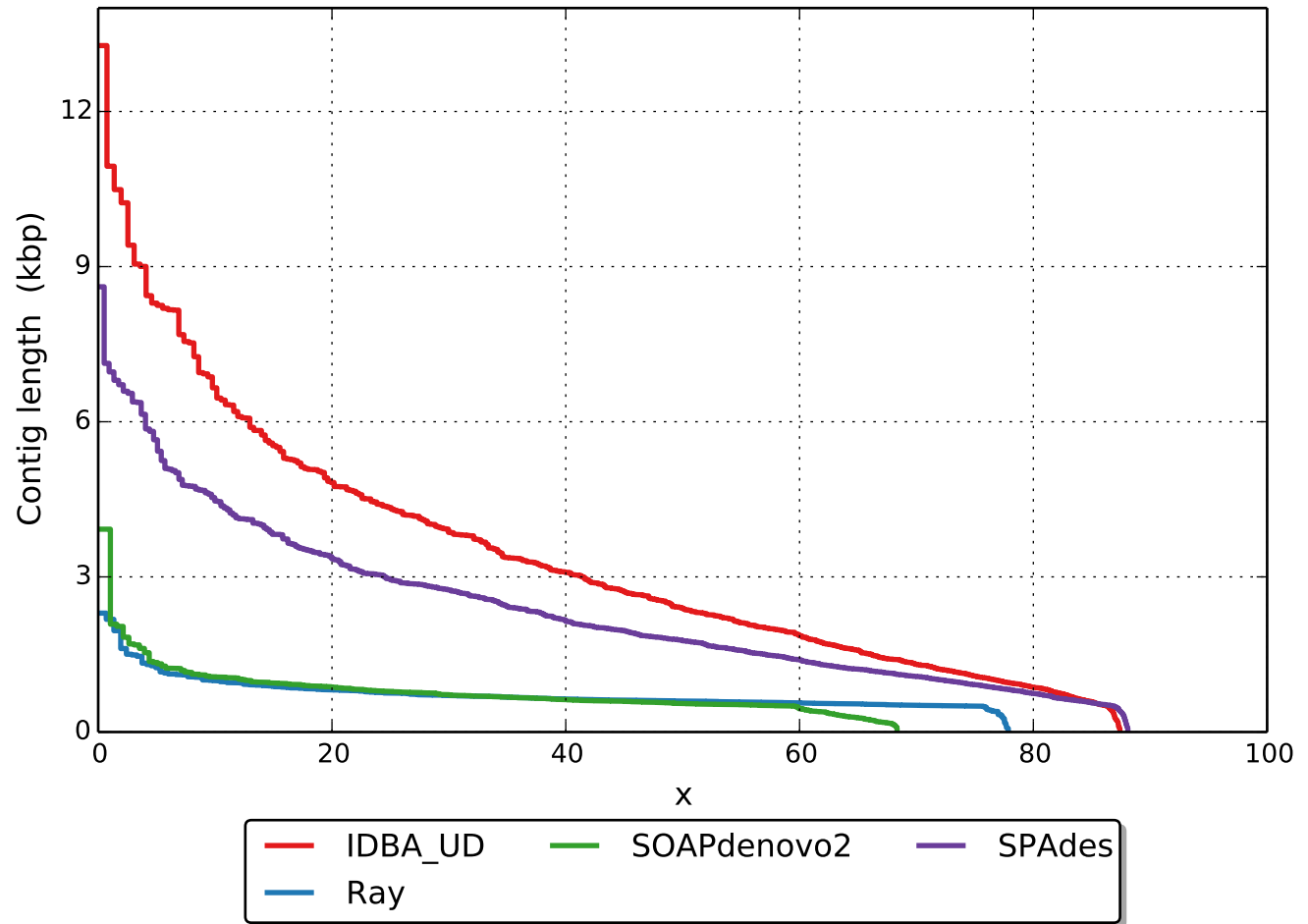
Misassemblies



Cumulative length (aligned contigs)



NAx



NGAx

