Report

	IDBA_UD	Ray	SOAPdenovo2	SPAdes
# contigs (>= 1000 bp)	103	47	27	95
# contigs (>= 5000 bp)	8	16	5	5
# contigs (>= 10000 bp)	2	10	0	1
# contigs (>= 25000 bp)	0	1	0	0
# contigs (>= 50000 bp)	0	0	0	0
Total length (>= 1000 bp)	224360	297309	71977	171025
Total length (>= 5000 bp)	66636	214712	29546	32500
Total length (>= 10000 bp)	26903	177064	0	11384
Total length (>= 25000 bp)	0	31461	0	0
Total length (>= 50000 bp)	0	0	0	0
# contigs	590	67	67	558
Largest contig	15362	31461	7279	11384
Total length	553034	311984	99967	480701
Reference length	2002578	2002578	2002578	2002578
GC (%)	38.47	37.70	38.64	38.27
Reference GC (%)	38.99	38.99	38.99	38.99
N50	876	11323	2140	810
N75	649	3839	939	632
L50	159	9	12	174
L75	343	21	31	344
# misassemblies	8	1	1	4
# misassembled contigs	7	1	1	4
Misassembled contigs length	9340	502	1508	4970
# local misassemblies	7	1	3	2
# structural variations	1	0	0	0
# unaligned contigs	0 + 142 part	0 + 53 part	0 + 44 part	0 + 117 part
Unaligned length	148291	264067	67833	86310
Genome fraction (%)	19.764	2.122	1.523	19.539
Duplication ratio	1.023	1.128	1.054	1.008
# N's per 100 kbp	0.00	661.57	8281.73	0.00
# mismatches per 100 kbp	1865.10	3033.51	2170.71	1846.78
# indels per 100 kbp	33.10	103.55	16.40	27.60
Largest alignment	7233	3434	2791	4269
NA50	591	-	-	654
NGA50	-	-	-	-
NA75	-	-	-	517
LA50	313	-	-	263
LA75	-	-	-	471

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).
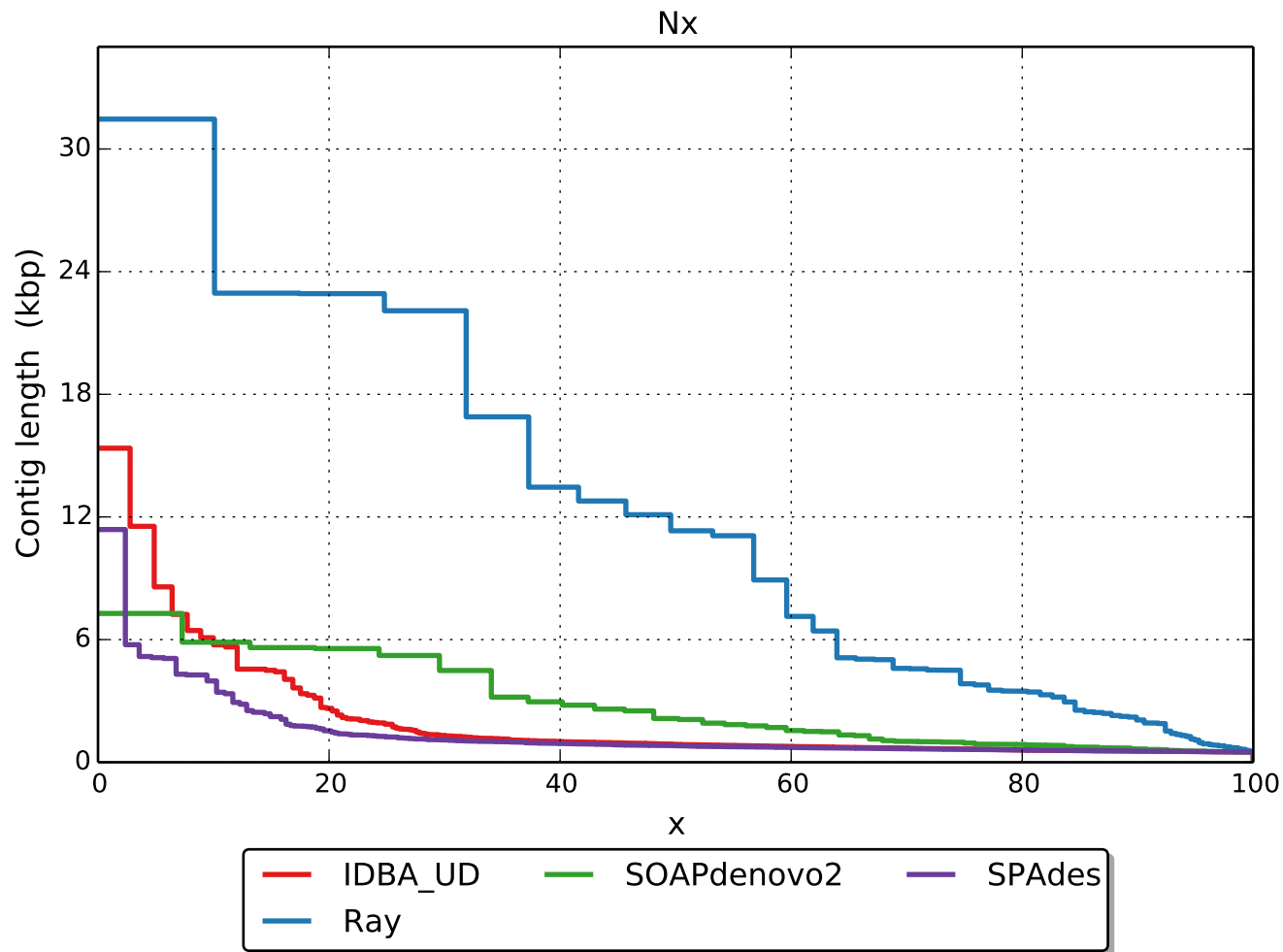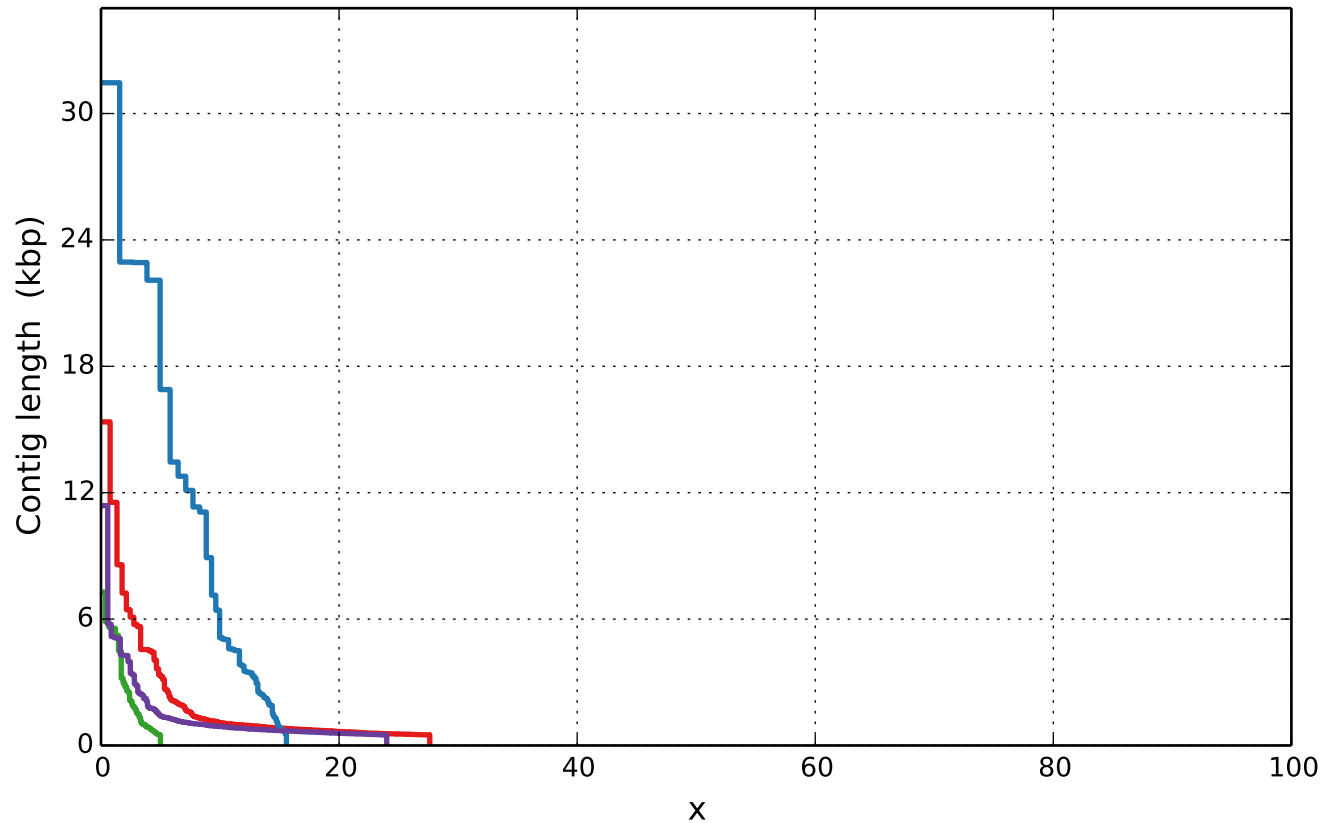
Misassemblies report

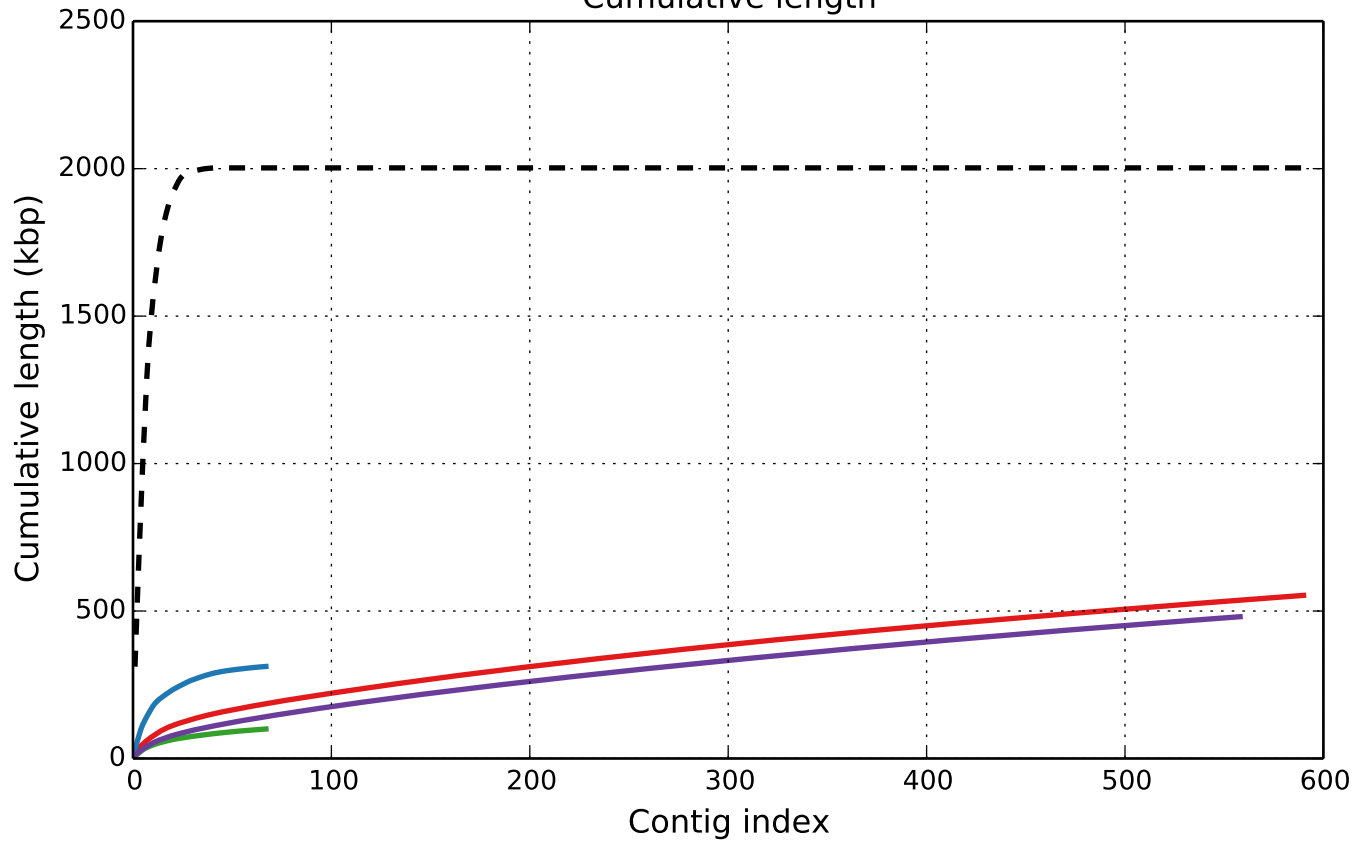|	IDBA_UD	Ray	SOAPdenovo2	SPAdes
# misassemblies	8	1	1	4
# relocations	1	1	0	1
# translocations	6	0	1	3
# inversions	1	0	0	0
# possibly misassembled contigs	14	14	5	8
# misassembled contigs	7	1	1	4
Misassembled contigs length	9340	502	1508	4970
# local misassemblies	7	1	3	2
# structural variations	1	0	0	0
# mismatches	7382	1289	662	7226
# indels	131	44	5	108
# short indels	126	44	2	105
# long indels	5	0	3	3
Indels length	242	50	128	149

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).
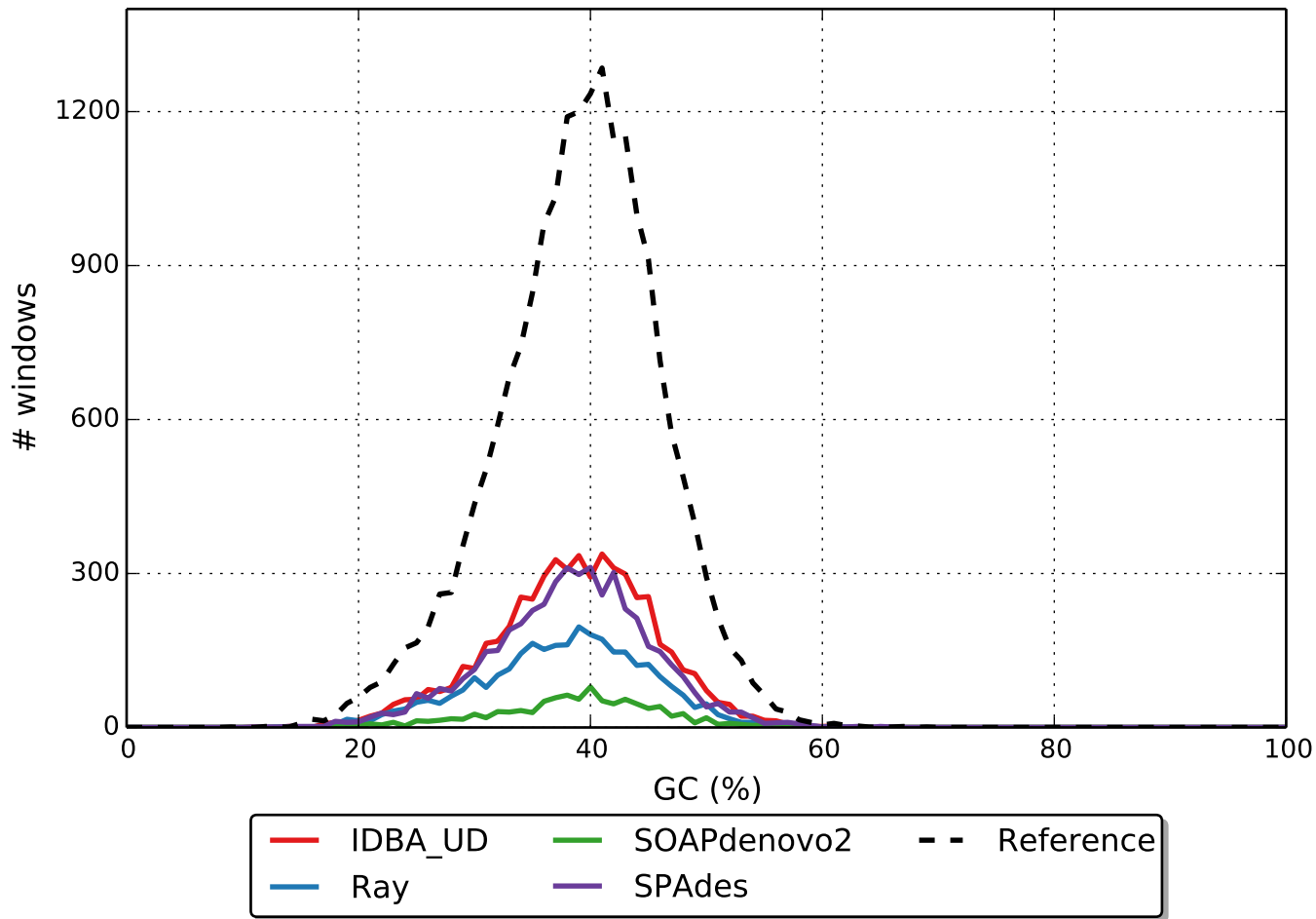
Unaligned report

	IDBA_UD	Ray	SOAPdenovo2	SPAdes
# fully unaligned contigs	0	0	0	0
Fully unaligned length	0	0	0	0
# partially unaligned contigs	142	53	44	117
# with misassembly	5	9	5	2
# both parts are significant	14	14	4	8
Partially unaligned length	148291	264067	67833	86310
# N's	0	2064	8279	0

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).
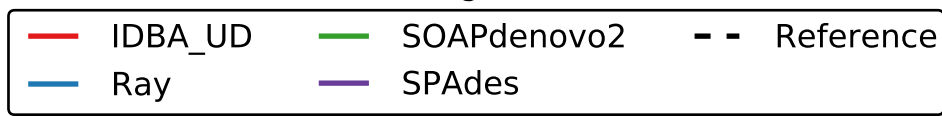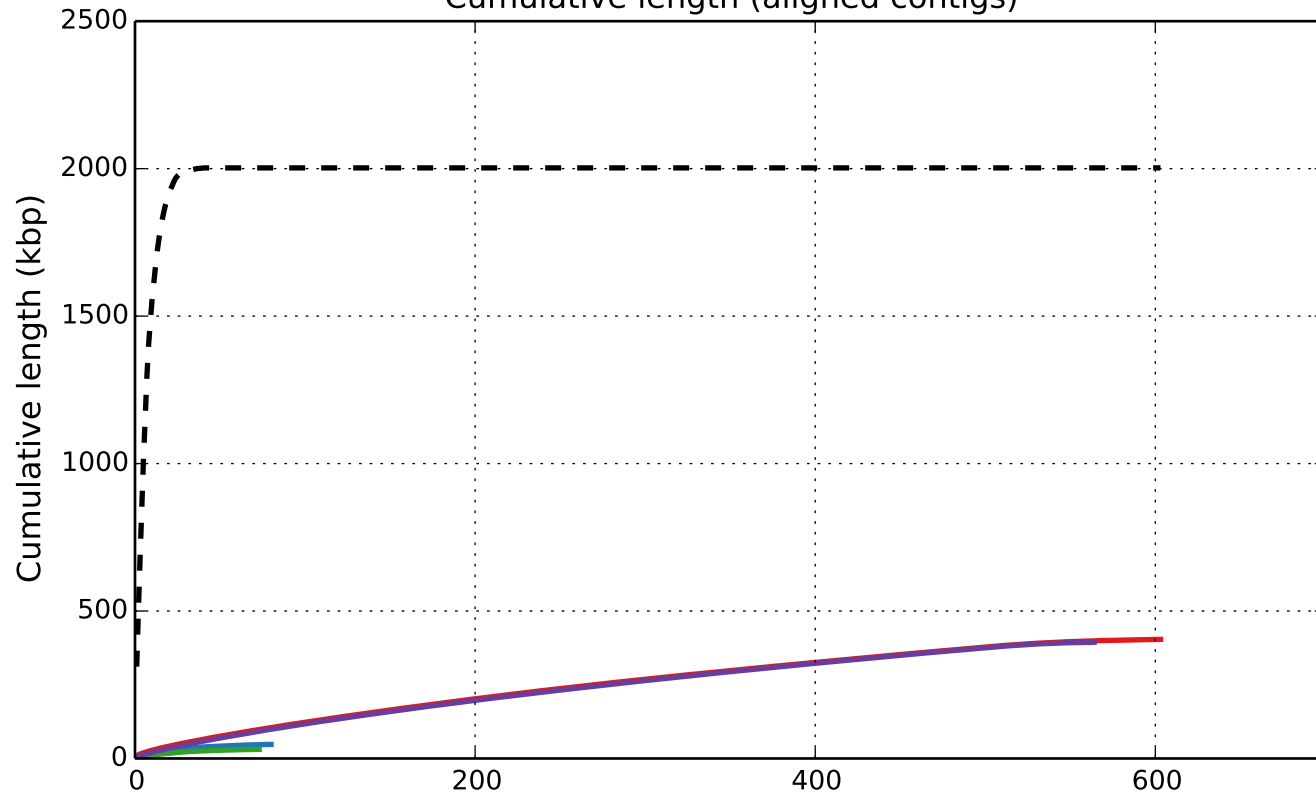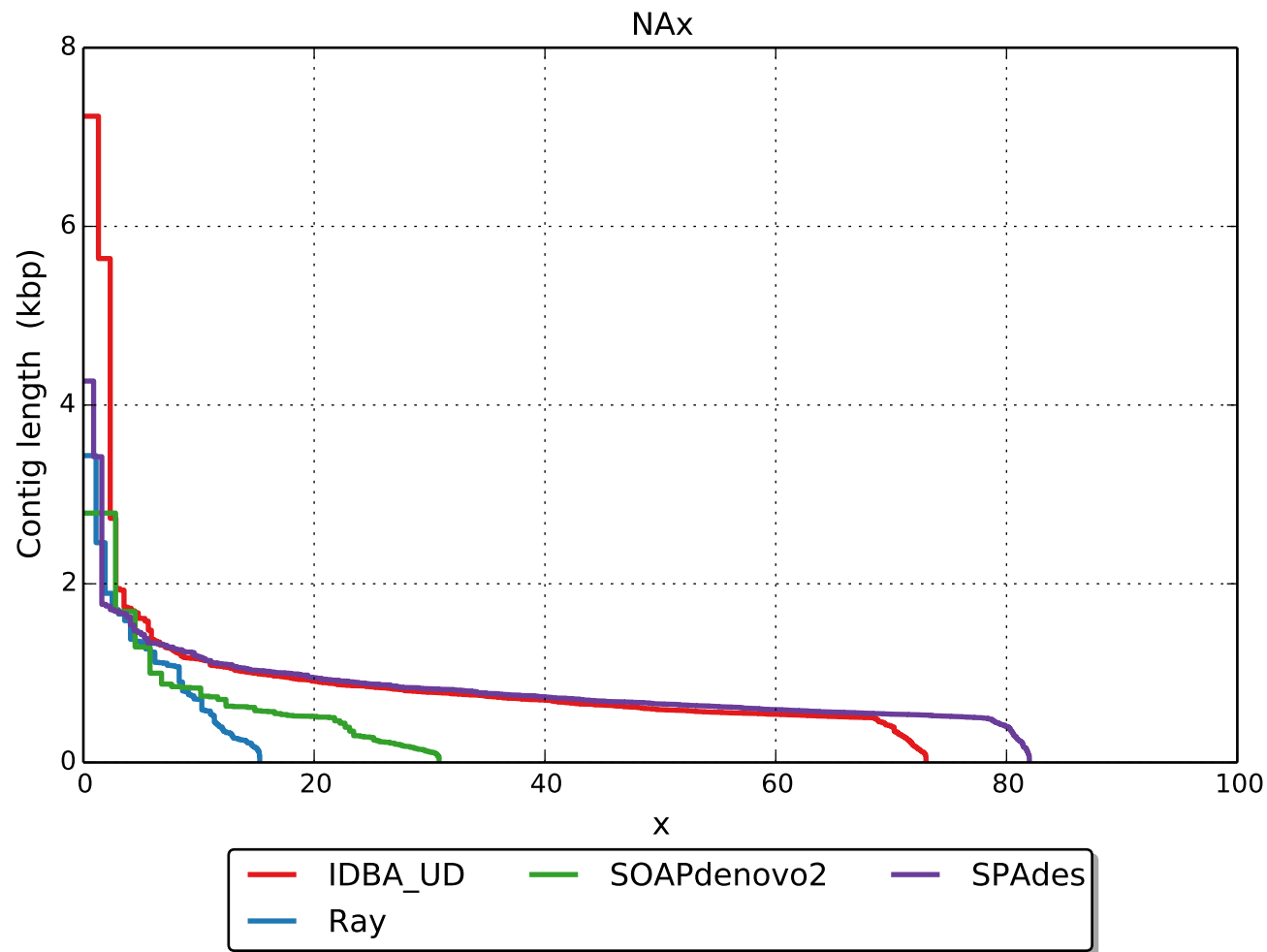
GC content

Misassemblies
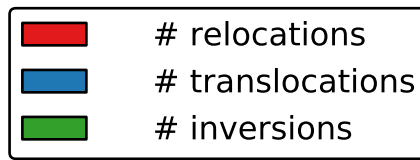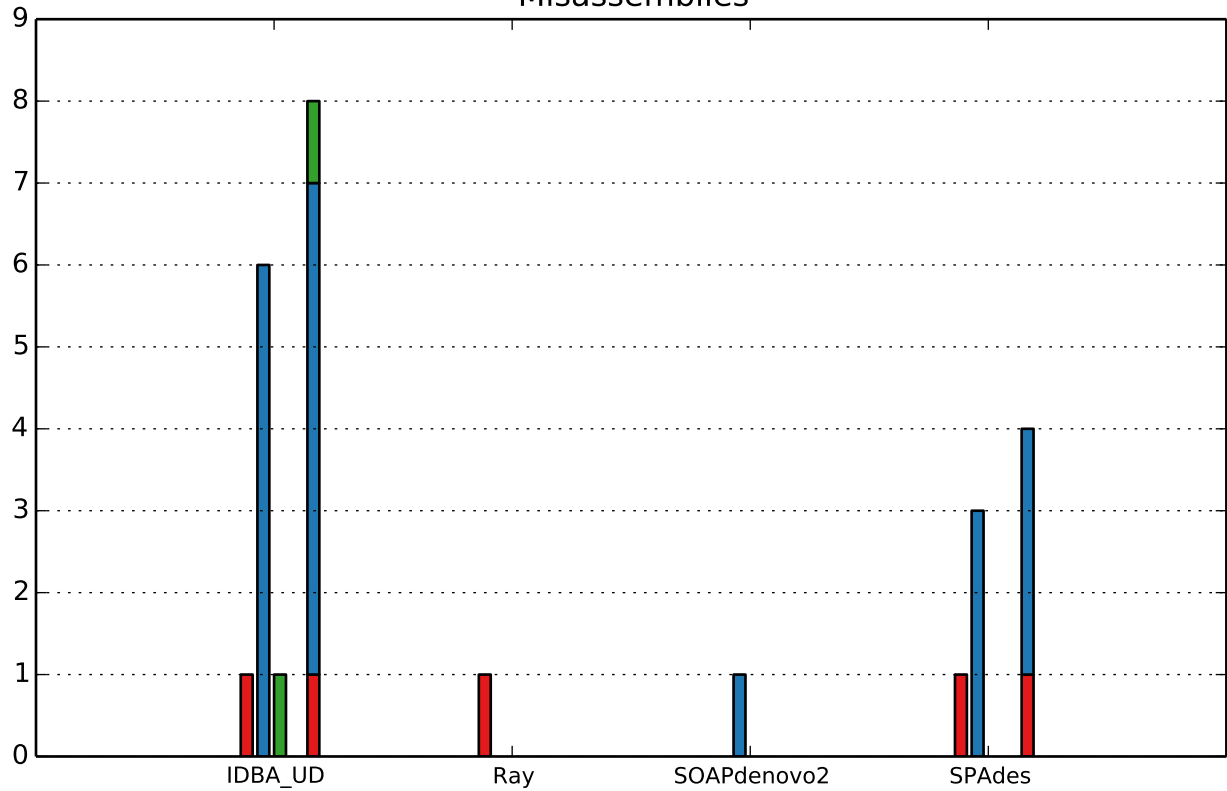
Cumulative length (aligned contigs)

NGAx

Genome fraction, %