Report

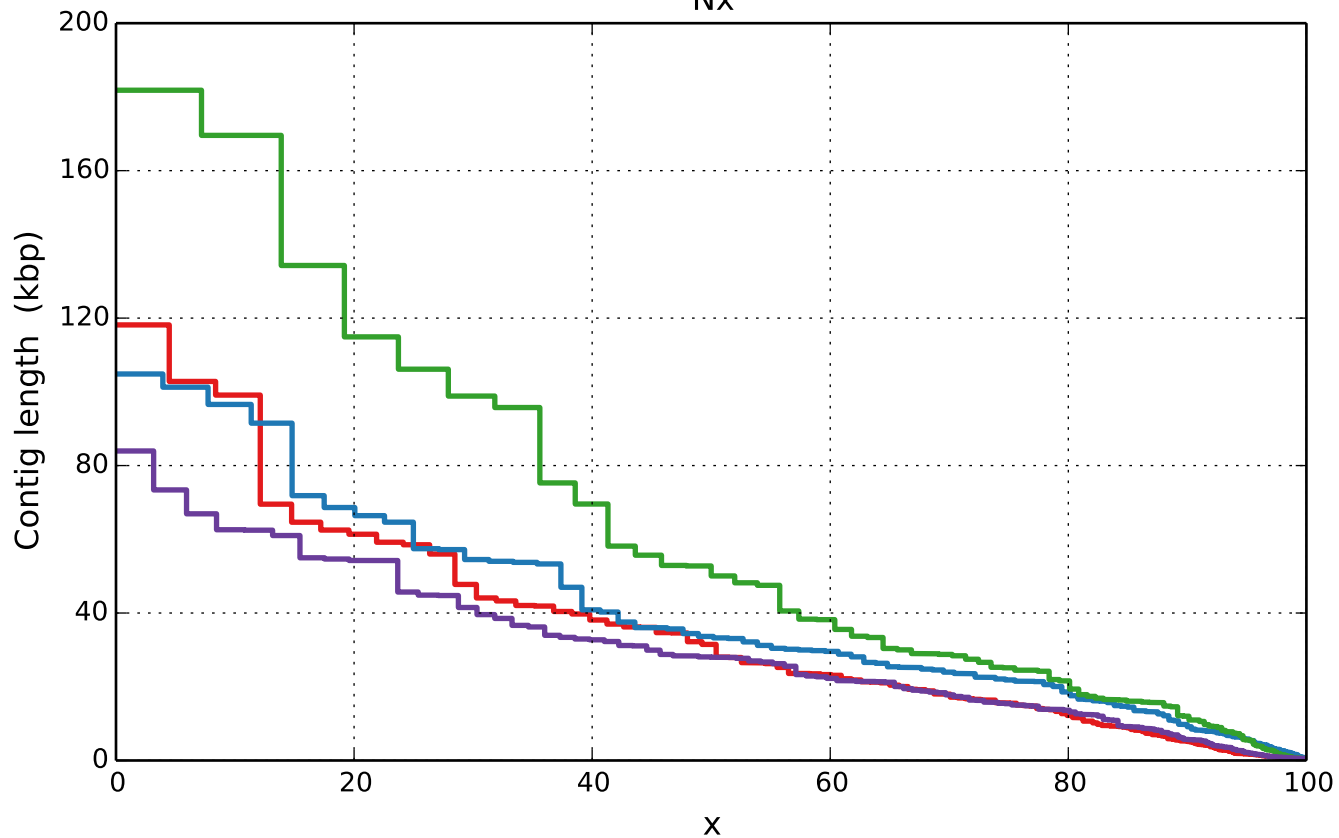|	IDBA_UD	Ray	SOAPdenovo2	SPAdes
# contigs (>= 1000 bp)	191	135	107	177
# contigs (>= 5000 bp)	100	94	70	107
# contigs (>= 10000 bp)	71	71	56	80
# contigs (>= 25000 bp)	31	39	32	37
# contigs (>= 50000 bp)	10	14	14	10
Total length (>= 1000 bp)	2573044	2652829	2498712	2585110
Total length (>= 5000 bp)	2387595	2547366	2418634	2431250
Total length (>= 10000 bp)	2177113	2378564	2314204	2235094
Total length (>= 25000 bp)	1491962	1802832	1911133	1516485
Total length (>= 50000 bp)	751844	995939	1315727	628457
# contigs	291	152	157	277
Largest contig	118154	104842	181817	83957
Total length	2640921	2664775	2531390	2655273
Reference length	2706954	2706954	2706954	2706954
GC (%)	42.98	43.16	43.10	43.20
Reference GC (%)	43.03	43.03	43.03	43.03
N50	31485	33646	50058	27997
NG50	28048	33249	48198	27997
N75	15601	21846	25139	15409
NG75	14771	21503	19365	14842
L50	25	23	14	31
LG50	26	24	15	31
L75	56	48	32	62
LG75	60	49	38	65
# misassemblies	36	45	11	43
# misassembled contigs	27	24	9	28
Misassembled contigs length	470099	642415	196771	628382
# local misassemblies	104	105	52	96
# structural variations	9	12	7	11
# unaligned contigs	0 + 138 part	0 + 61 part	0 + 89 part	0 + 118 part
Unaligned length	887400	803882	1432101	816968
Genome fraction (%)	56.186	55.225	34.961	57.064
Duplication ratio	1.153	1.245	1.162	1.190
# N's per 100 kbp	0.00	355.38	1813.19	54.19
# mismatches per 100 kbp	2690.70	2775.90	2366.72	2733.20
# indels per 100 kbp	105.26	100.74	95.63	107.92
Largest alignment	52482	66813	34451	58176
NA50	2433	3455	-	2873
NGA50	1918	3287	-	2531
LA50	121	116	-	126
LGA50	137	122	-	135

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

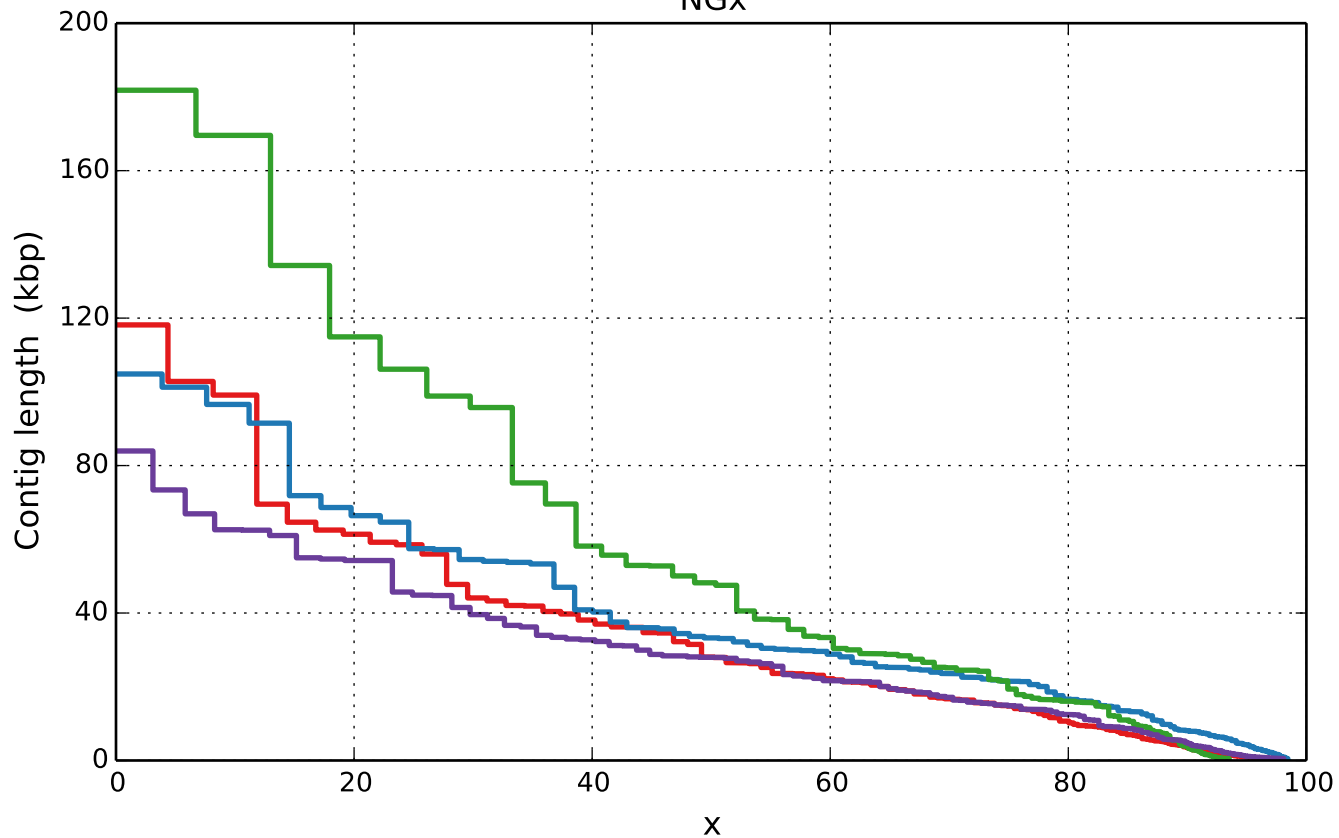|	IDBA_UD	Ray	SOAPdenovo2	SPAdes
# misassemblies	36	45	11	43
# relocations	13	22	7	19
# translocations	18	22	4	24
# inversions	5	1	0	0
# possibly misassembled contigs	92	84	72	100
# misassembled contigs	27	24	9	28
Misassembled contigs length	470099	642415	196771	628382
# local misassemblies	104	105	52	96
# structural variations	9	12	7	11
# mismatches	40924	41497	22398	42220
# indels	1601	1506	905	1667
# short indels	1314	1243	560	1376
# long indels	287	263	345	291
Indels length	7249	6273	8650	7131

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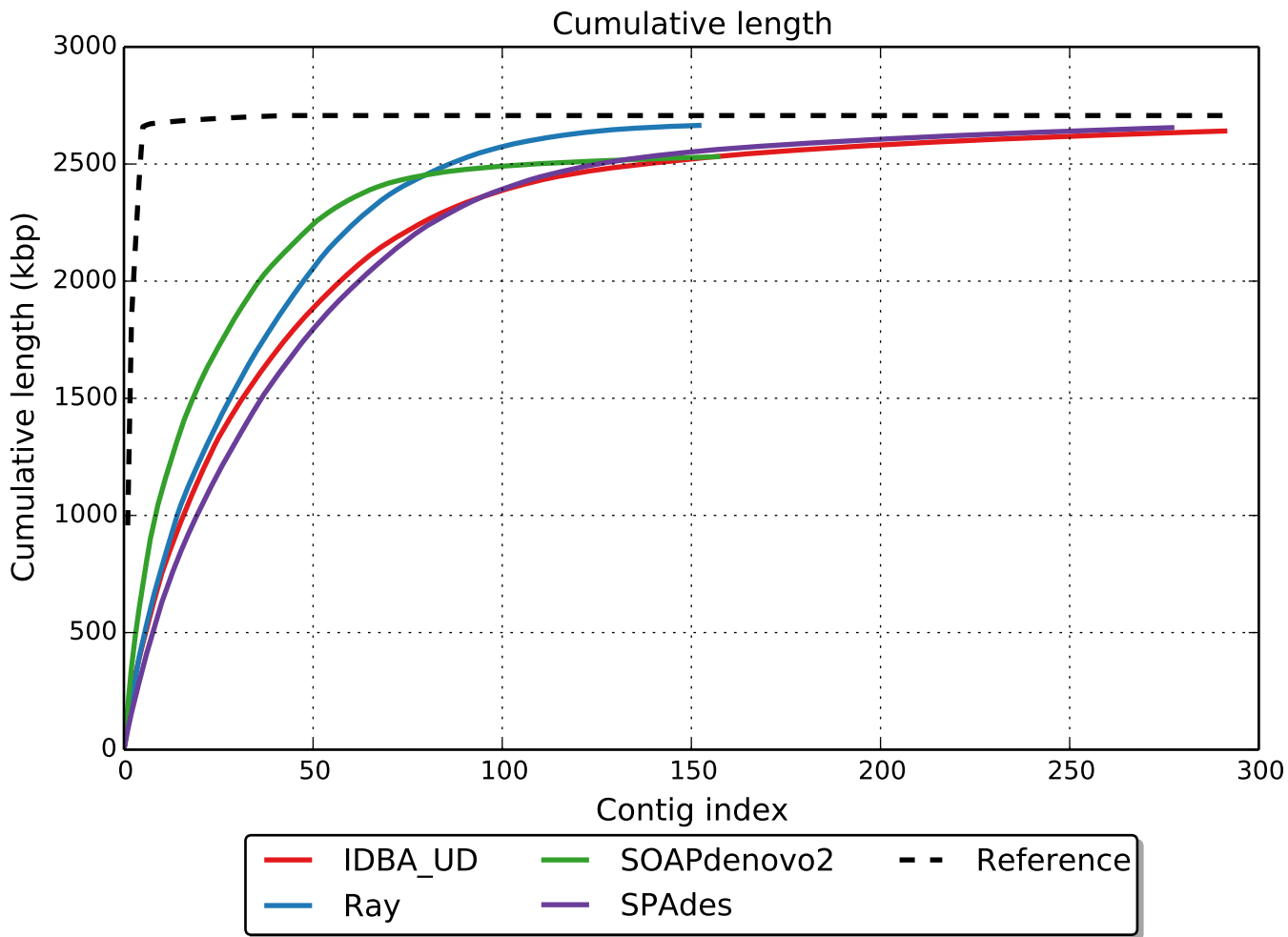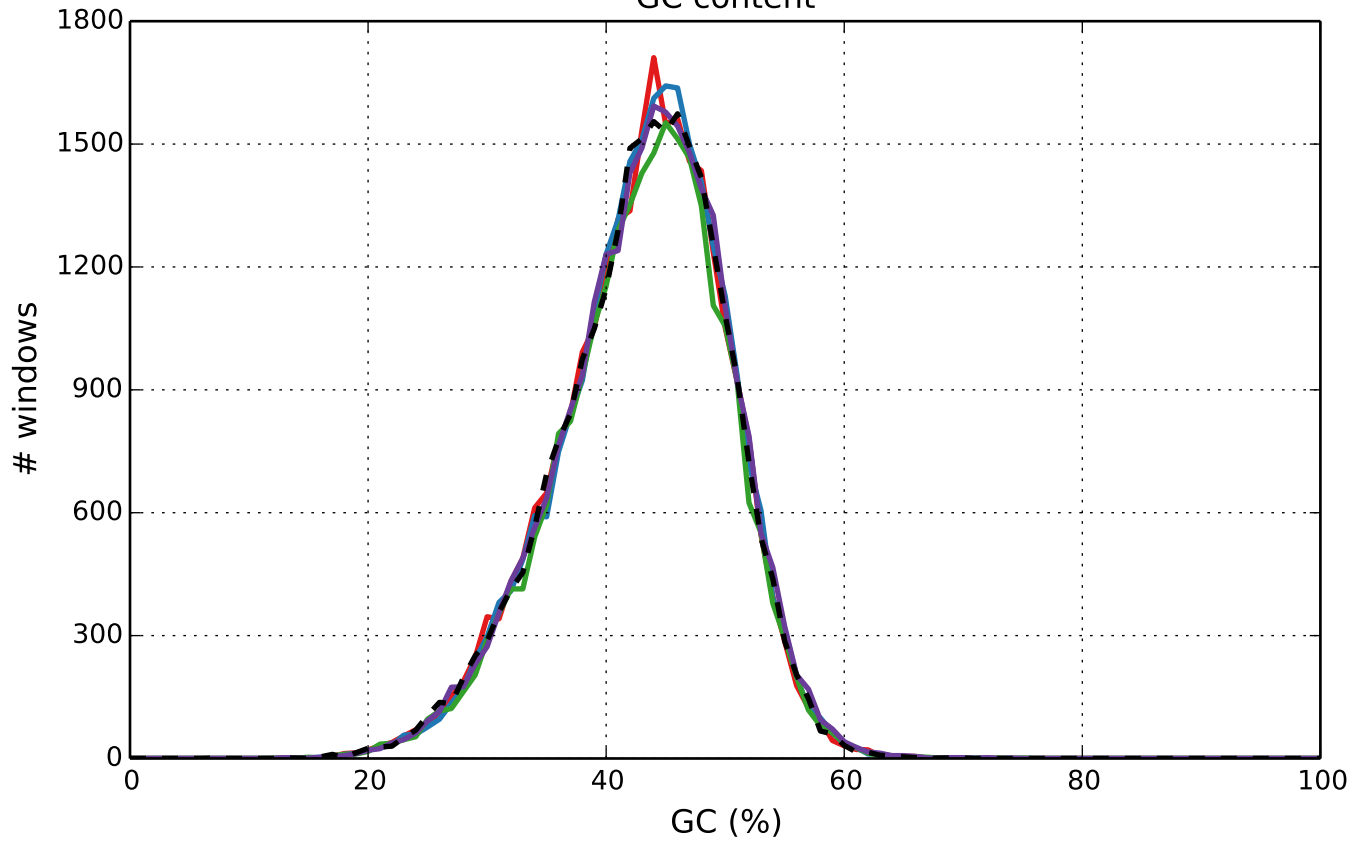(e.g., "# contigs (>= 0 bp)" and "Total length (>= 0 bp)" include all contigs).

Unaligned report

	IDBA_UD	Ray	SOAPdenovo2	SPAdes
# fully unaligned contigs	0	0	0	0
Fully unaligned length	0	0	0	0
# partially unaligned contigs	138	61	89	118
# with misassembly	28	30	38	25
# both parts are significant	59	47	53	60
Partially unaligned length	887400	803882	1432101	816968
# N's	0	9470	45899	1439

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

Contig length (kbp)

x

IDBA_UD
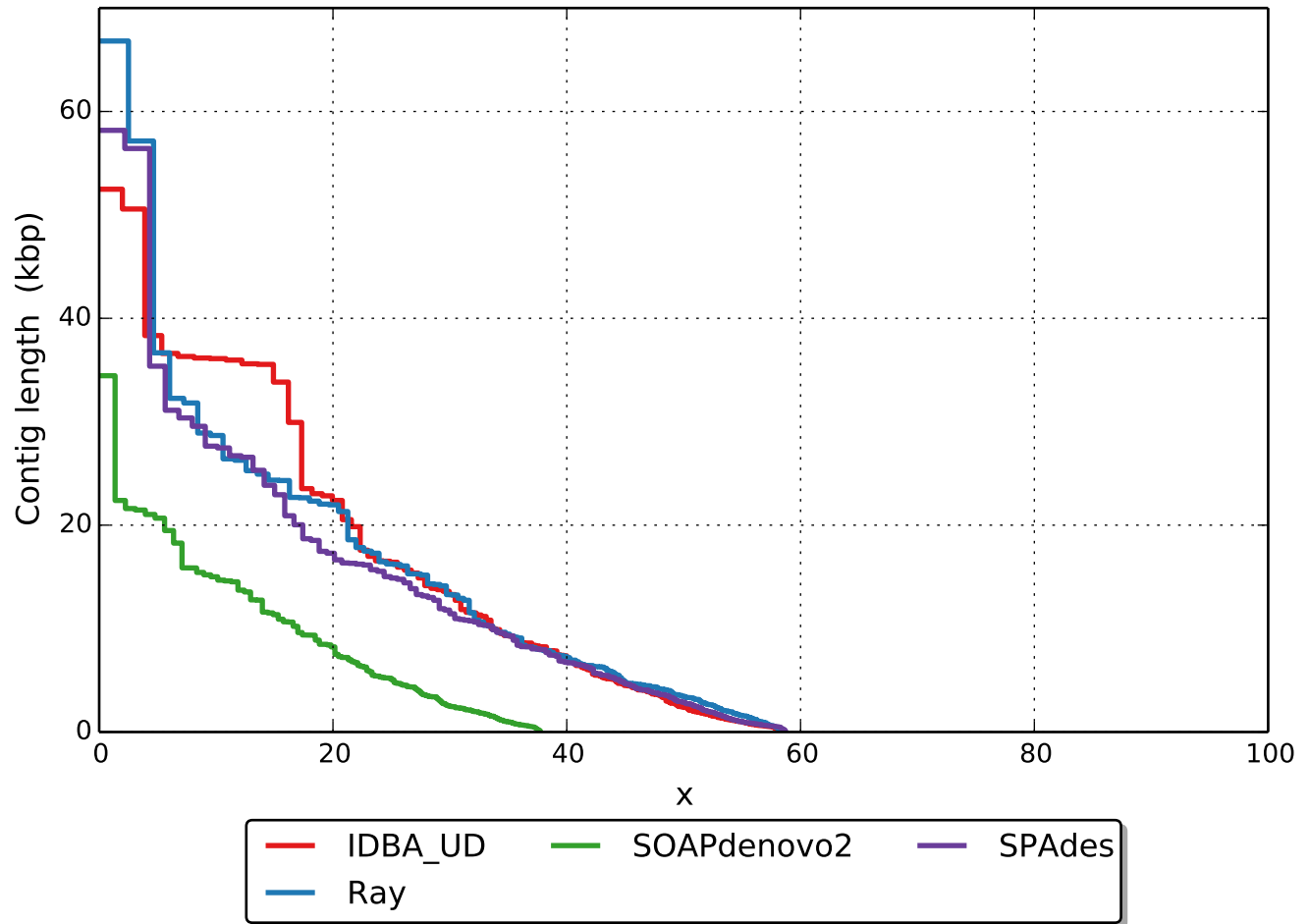SOAPdenovo2
SPAdes
Ray

Cumulative length

GC content

Misassemblies
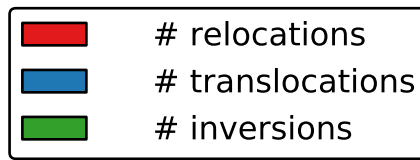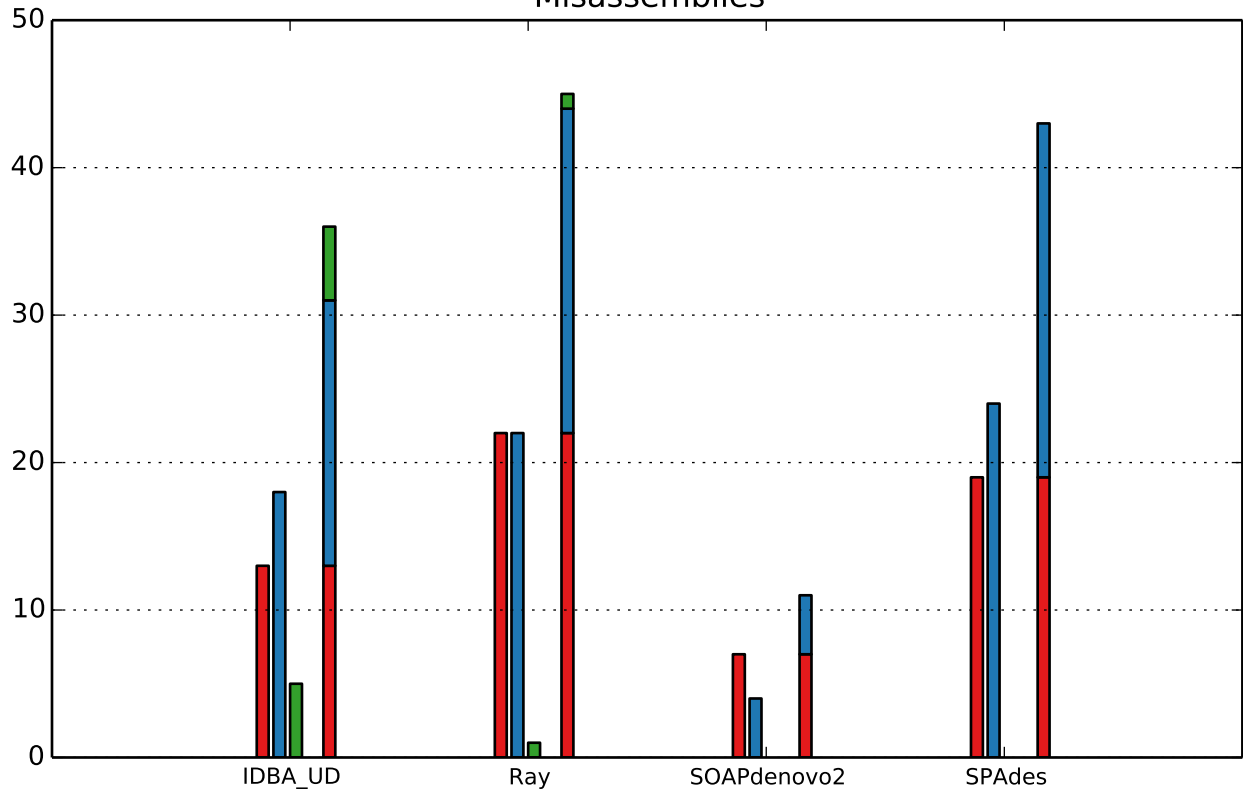
Cumulative length (aligned contigs)

NAx

Contig length (kbp)

x

IDBA_UD
SOAPdenovo2
SPAdes
Ray

NGAx

Genome fraction, %

IDBA_UD
Ray
SOAPdenovo2
SPAdes