Report

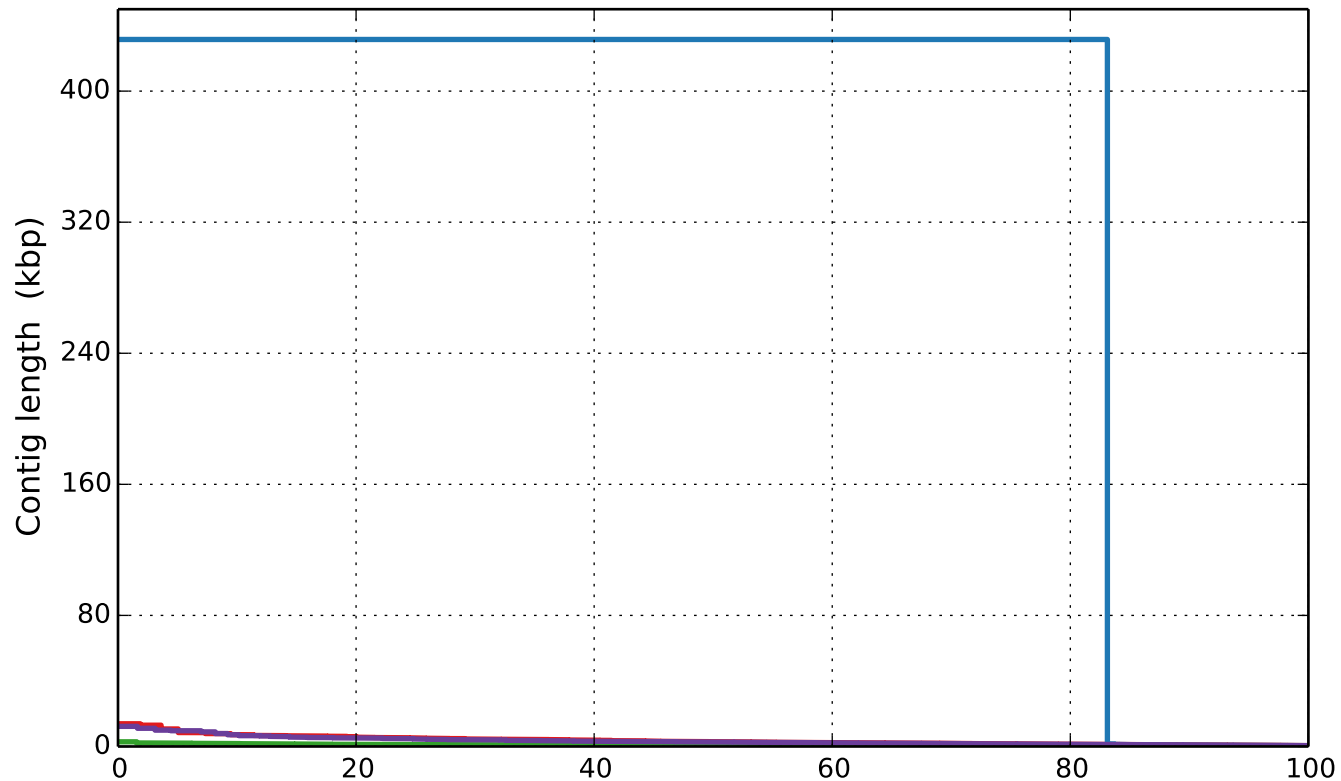|	IDBA_UD	Ray	SOAPdenovo2	SPAdes
# contigs (>= 1000 bp)	241	14	45	256
# contigs (>= 5000 bp)	28	1	0	24
# contigs (>= 10000 bp)	3	1	0	2
# contigs (>= 25000 bp)	0	1	0	0
# contigs (>= 50000 bp)	0	1	0	0
Total length (>= 1000 bp)	659000	446798	63309	665577
Total length (>= 5000 bp)	196622	431523	0	167159
Total length (>= 10000 bp)	37527	431523	0	23391
Total length (>= 25000 bp)	0	431523	0	0
Total length (>= 50000 bp)	0	431523	0	0
# contigs	354	127	224	375
Largest contig	13857	431523	2845	12284
Total length	741572	519190	180546	752264
Reference length	1527867	1527867	1527867	1527867
GC (%)	47.85	57.31	47.01	48.29
Reference GC (%)	48.43	48.43	48.43	48.43
N50	2922	431523	783	2746
N75	1584	431523	612	1535
L50	74	1	76	84
L75	160	1	143	175
# misassemblies	6	2	2	7
# misassembled contigs	6	2	2	7
Misassembled contigs length	20651	2624	2143	23258
# local misassemblies	3	0	5	1
# structural variations	0	0	0	0
# unaligned contigs	0 + 95 part	0 + 9 part	0 + 78 part	0 + 89 part
Unaligned length	91665	429857	37907	77295
Genome fraction (%)	41.800	5.810	9.225	43.663
Duplication ratio	1.018	1.006	1.012	1.012
# N's per 100 kbp	0.00	220.73	3132.17	13.29
# mismatches per 100 kbp	3189.58	2078.45	2300.85	3179.99
# indels per 100 kbp	52.77	27.04	49.66	47.97
Largest alignment	10680	4250	2845	9968
NA50	2150	-	591	2184
NGA50	-	-	-	-
NA75	952	-	266	1073
LA50	94	-	105	100
LA75	222	-	198	222

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	6	2	2	7
# relocations	0	0	0	2
# translocations	6	2	2	5
# inversions	0	0	0	0
# possibly misassembled contigs	31	1	12	22
# misassembled contigs	6	2	2	7
Misassembled contigs length	20651	2624	2143	23258
# local misassemblies	3	0	5	1
# structural variations	0	0	0	0
# mismatches	20370	1845	3243	21214
# indels	337	24	70	320
# short indels	317	23	47	300
# long indels	20	1	23	20
Indels length	763	38	674	607

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).
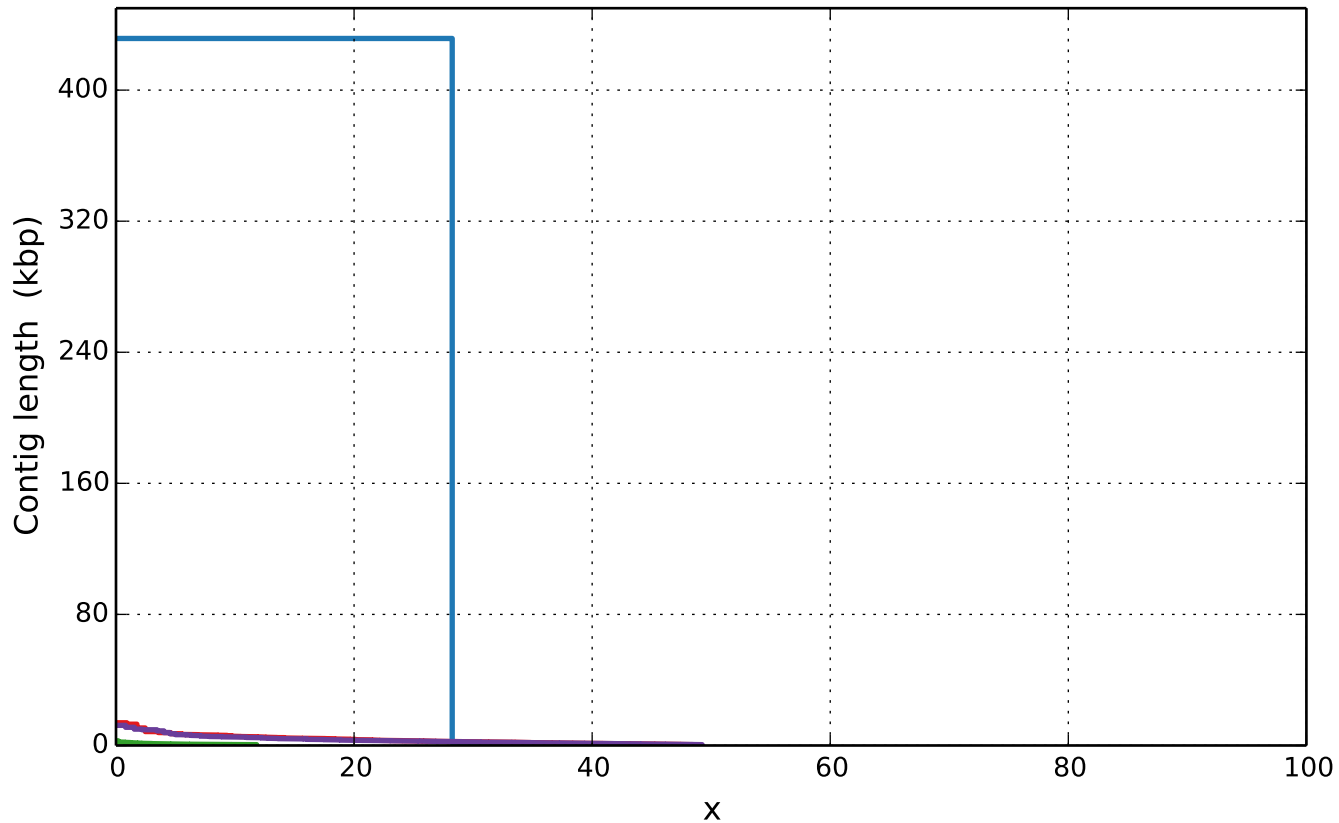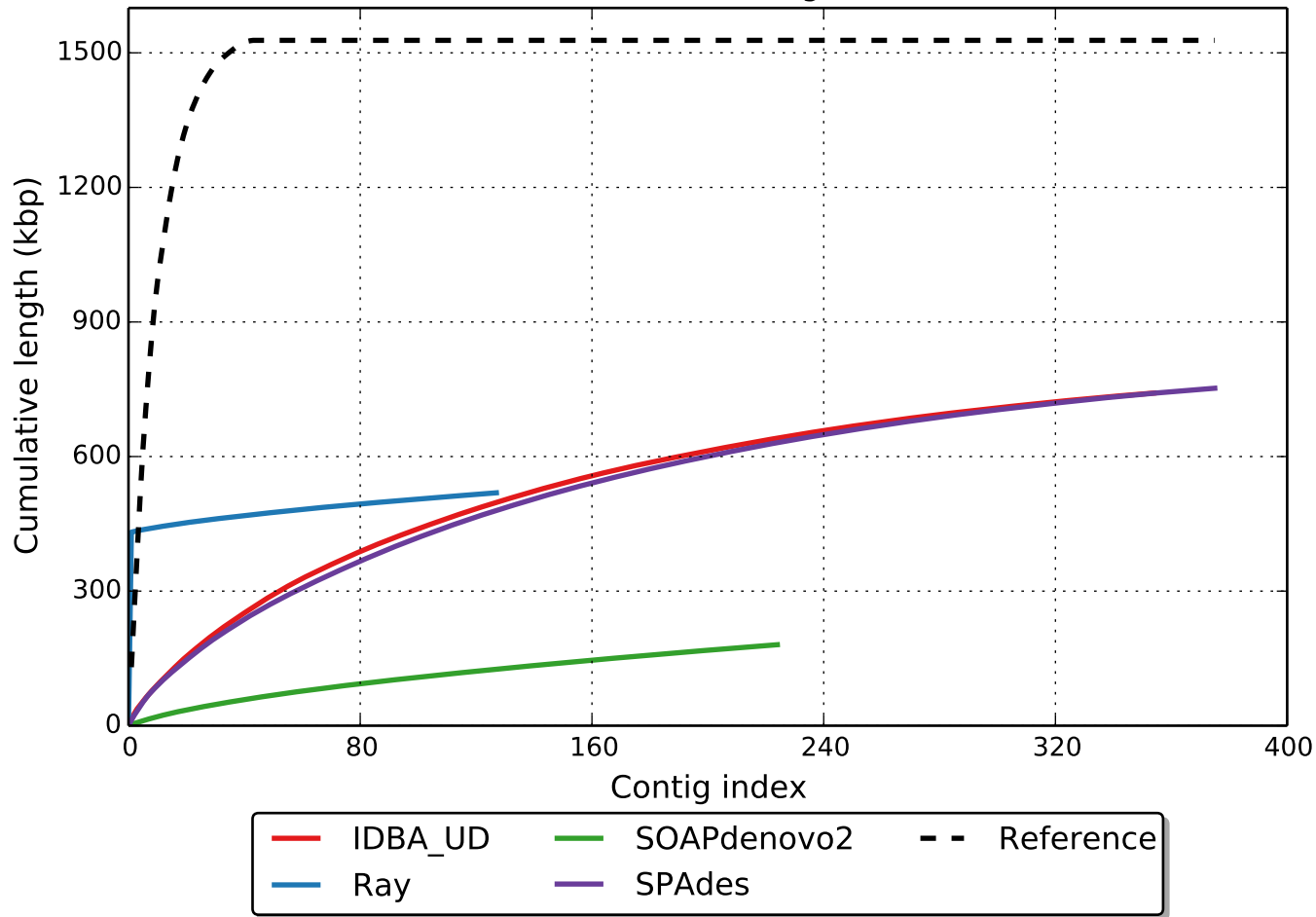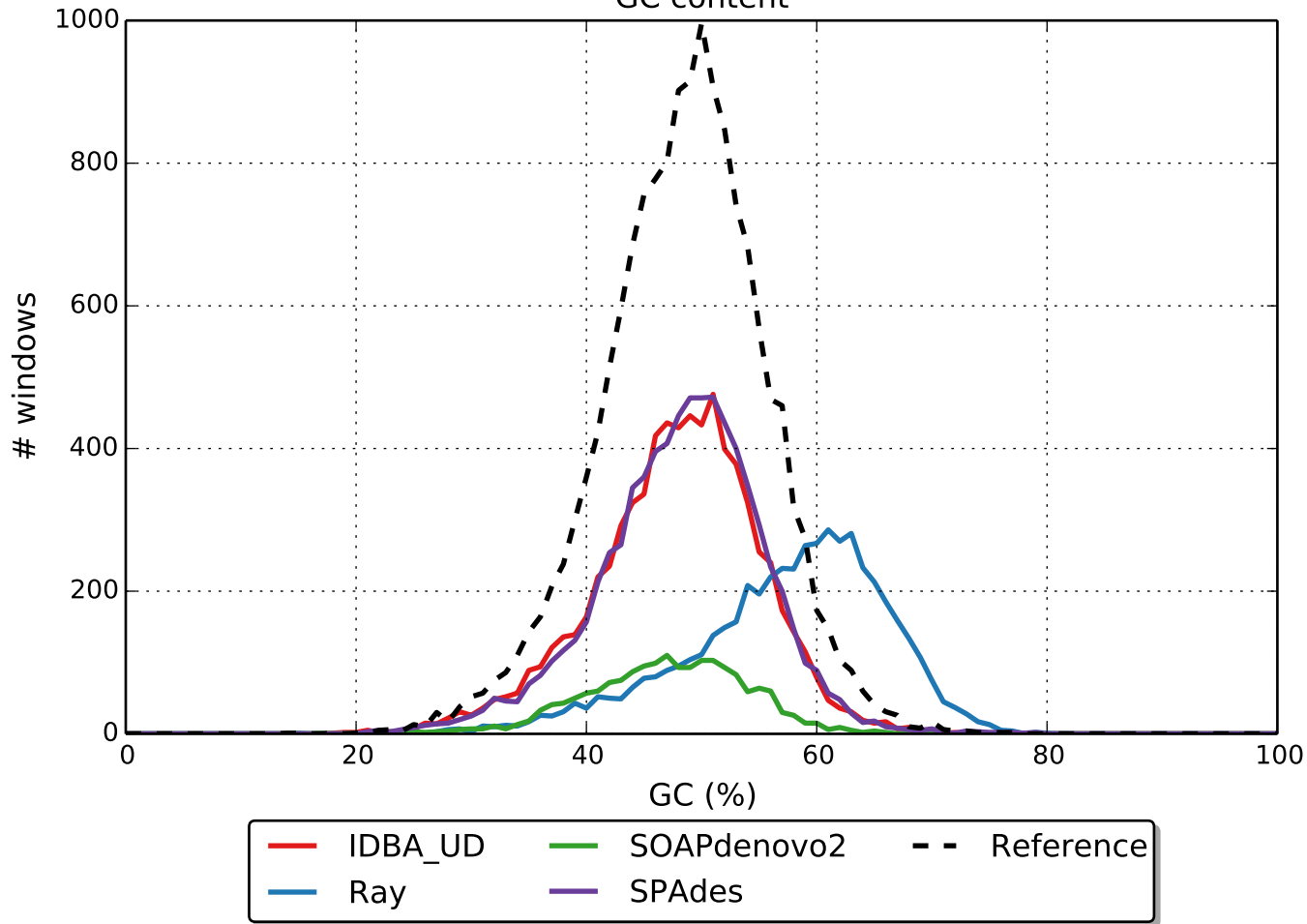
Unaligned report

	IDBA_UD	Ray	SOAPdenovo2	SPAdes
# fully unaligned contigs	0	0	0	0
Fully unaligned length	0	0	0	0
# partially unaligned contigs	95	9	78	89
# with misassembly	2	0	3	3
# both parts are significant	29	1	12	21
Partially unaligned length	91665	429857	37907	77295
# N's	0	1146	5655	100

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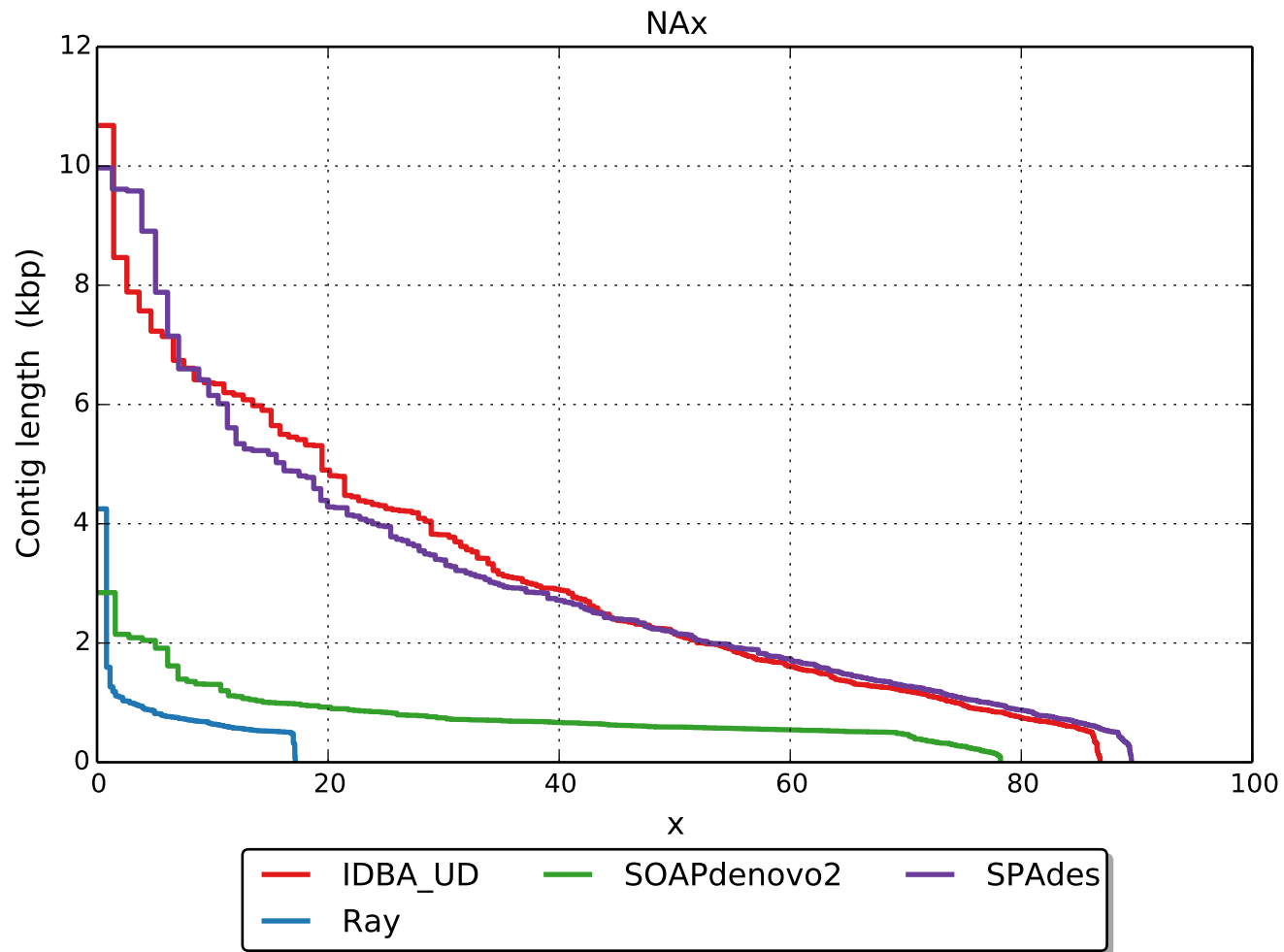(e.g., "# contigs (>= 0 bp)" and "Total length (>= 0 bp)" include all contigs).

Cumulative length

Misassemblies
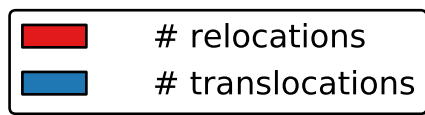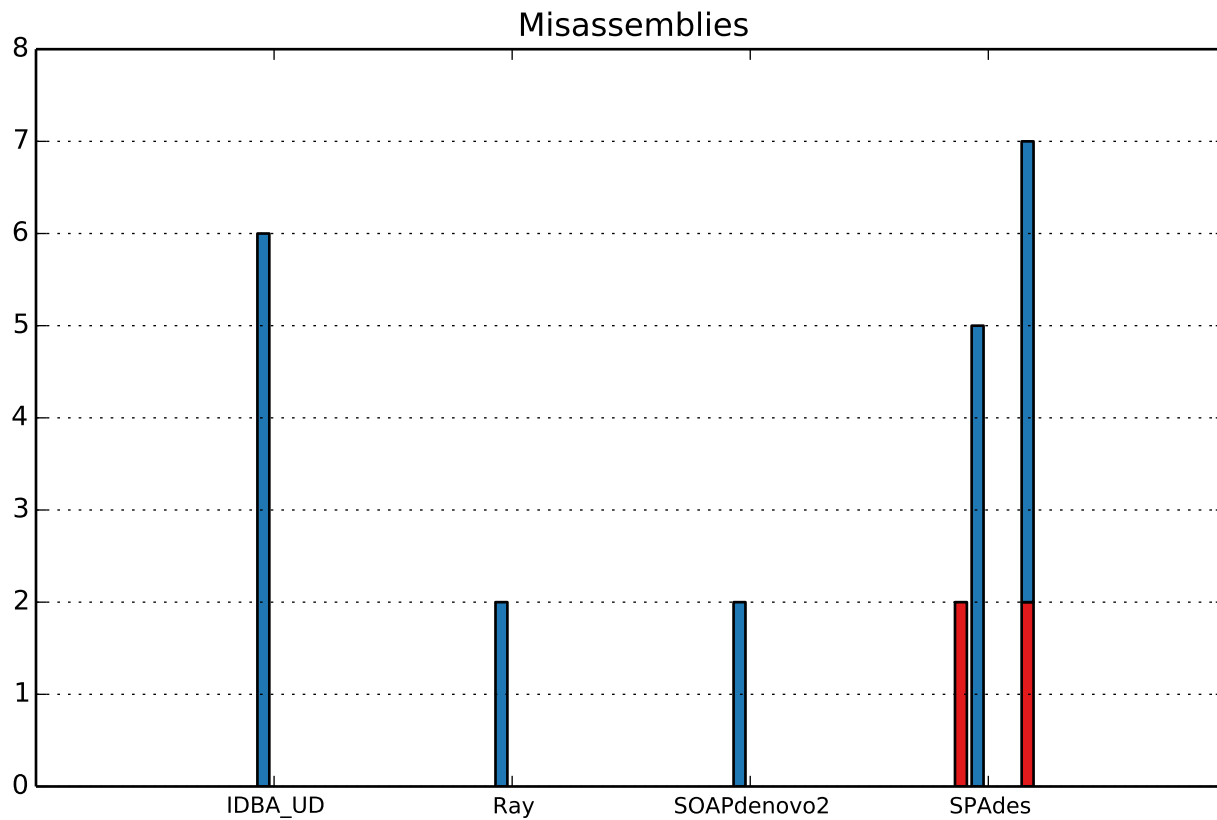
Cumulative length (aligned contigs)

Genome fraction, %

IDBA_UD
Ray
SOAPdenovo2
SPAdes