

Report

	IDBA_UD	Ray	SOAPdenovo2	SPAdes
# contigs (>= 1000 bp)	5	3	7	6
# contigs (>= 5000 bp)	1	0	0	2
# contigs (>= 10000 bp)	0	0	0	0
# contigs (>= 25000 bp)	0	0	0	0
# contigs (>= 50000 bp)	0	0	0	0
Total length (>= 1000 bp)	18373	7379	13305	21238
Total length (>= 5000 bp)	8007	0	0	10584
Total length (>= 10000 bp)	0	0	0	0
Total length (>= 25000 bp)	0	0	0	0
Total length (>= 50000 bp)	0	0	0	0
# contigs	9	6	12	7
Largest contig	8007	3687	3441	5319
Total length	20985	9815	16806	21783
Reference length	2664035	2664035	2664035	2664035
GC (%)	44.63	45.57	44.71	42.68
Reference GC (%)	44.97	44.97	44.97	44.97
N50	4081	2427	2005	4859
N75	1772	1265	1061	2289
L50	2	2	3	3
L75	4	3	7	4
# misassemblies	0	0	0	0
# misassembled contigs	0	0	0	0
Misassembled contigs length	0	0	0	0
# local misassemblies	0	0	3	0
# structural variations	0	0	0	0
# unaligned contigs	0 + 6 part	0 + 1 part	0 + 3 part	0 + 5 part
Unaligned length	4365	502	5876	15570
Genome fraction (%)	0.550	0.350	0.406	0.231
Duplication ratio	1.134	1.000	1.010	1.010
# N's per 100 kbp	481.30	0.00	1100.80	913.56
# mismatches per 100 kbp	586.91	848.46	859.44	1235.17
# indels per 100 kbp	61.42	10.74	9.24	48.76
Largest alignment	8007	3687	2005	2289
NA50	1772	2427	797	-
NGA50	-	-	-	-
NA75	-	1265	-	-
LA50	3	2	7	-
LA75	-	3	-	-

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

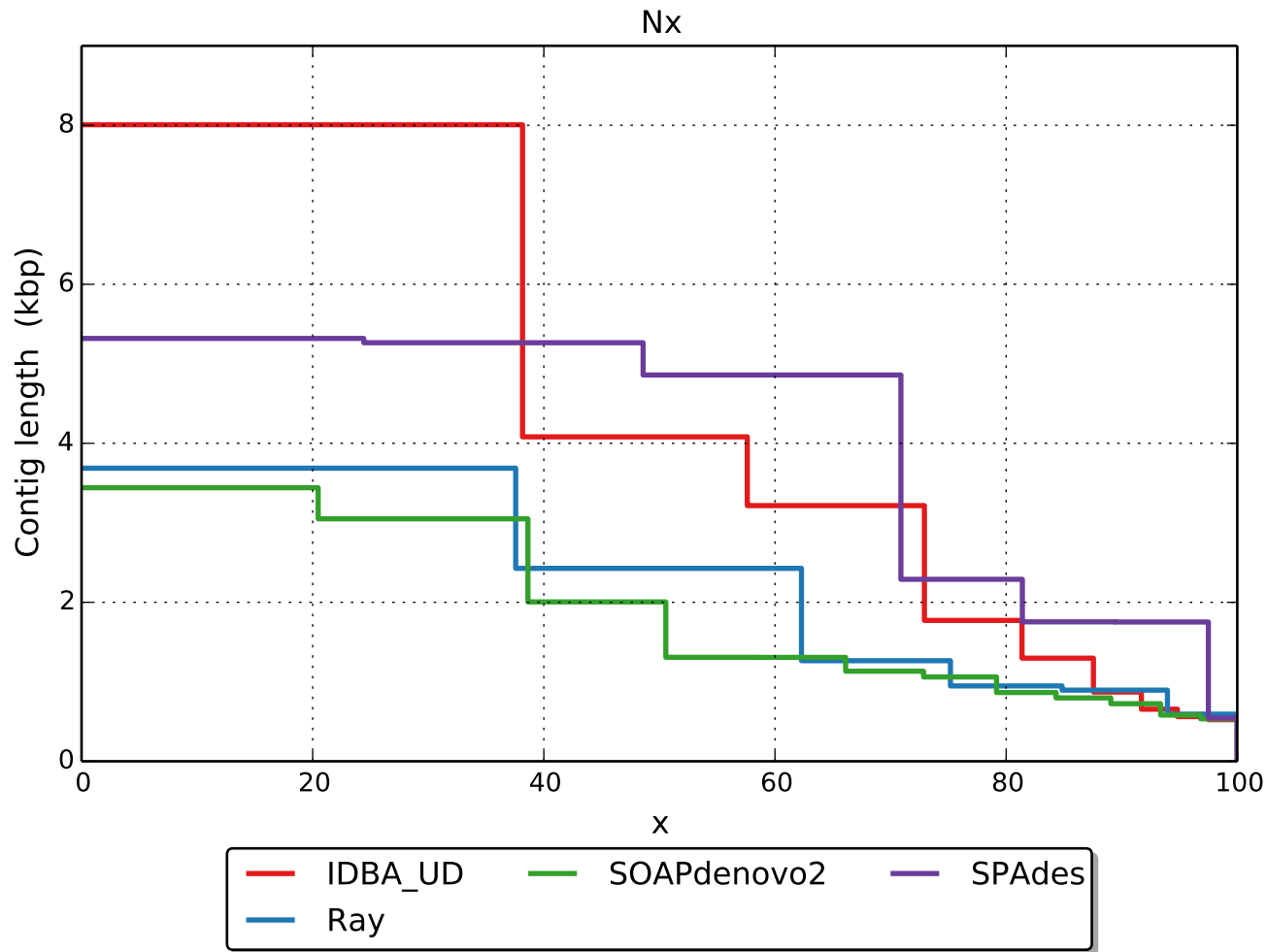
	IDBA_UD	Ray	SOAPdenovo2	SPAdes
# misassemblies	0	0	0	0
# relocations	0	0	0	0
# translocations	0	0	0	0
# inversions	0	0	0	0
# possibly misassembled contigs	2	0	1	3
# misassembled contigs	0	0	0	0
Misassembled contigs length	0	0	0	0
# local misassemblies	0	0	3	0
# structural variations	0	0	0	0
# mismatches	86	79	93	76
# indels	9	1	1	3
# short indels	8	1	1	3
# long indels	1	0	0	0
Indels length	20	2	4	5

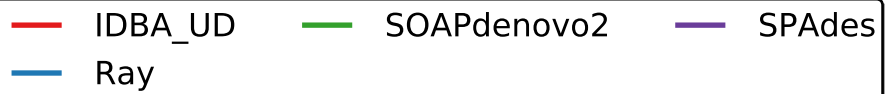
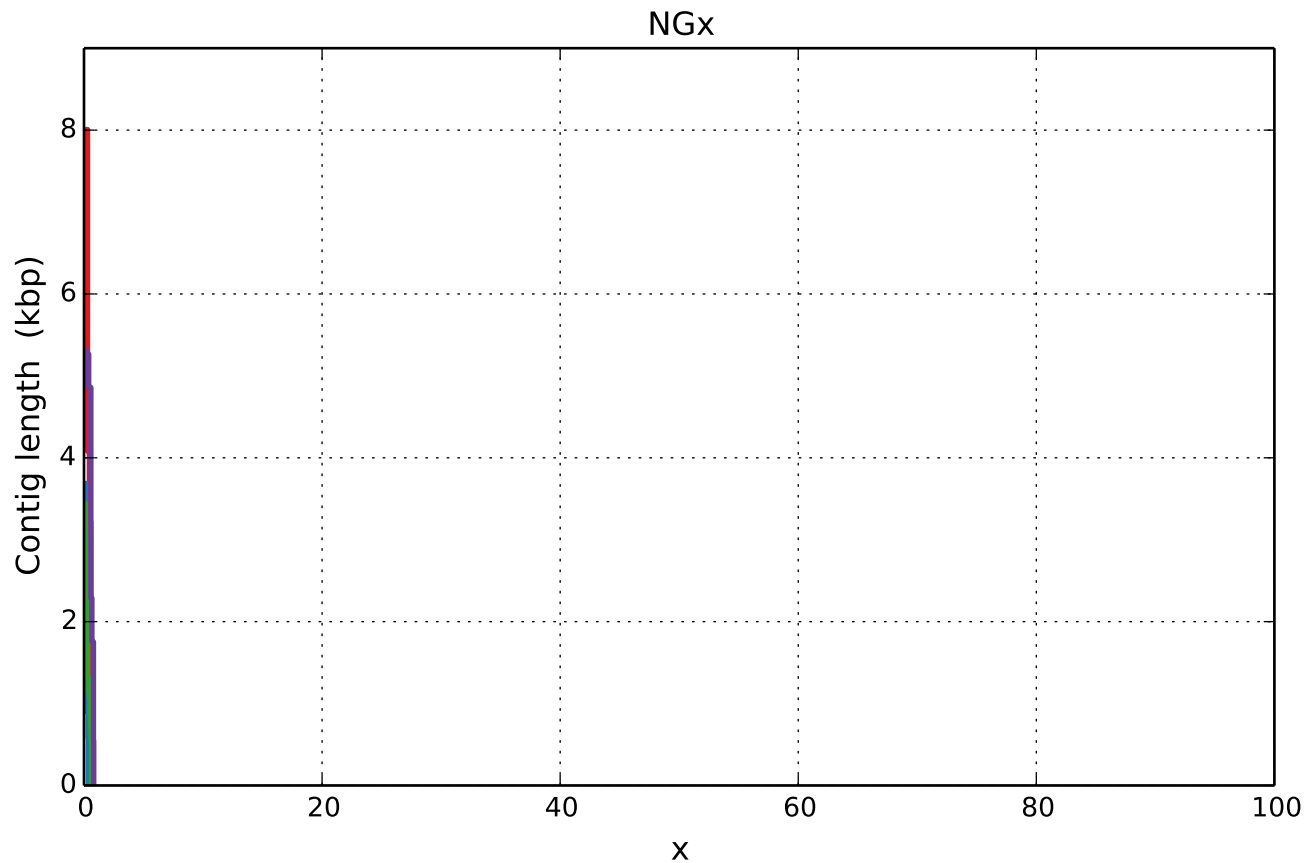
All statistics are based on contigs of size ≥ 500 bp, unless otherwise noted (e.g., "# contigs (≥ 0 bp)" and "Total length (≥ 0 bp)" include all contigs).

Unaligned report

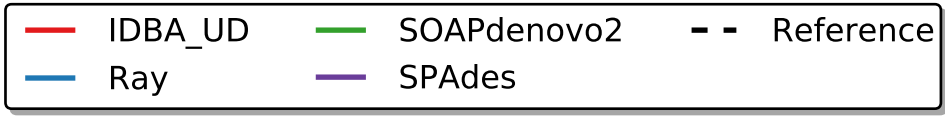
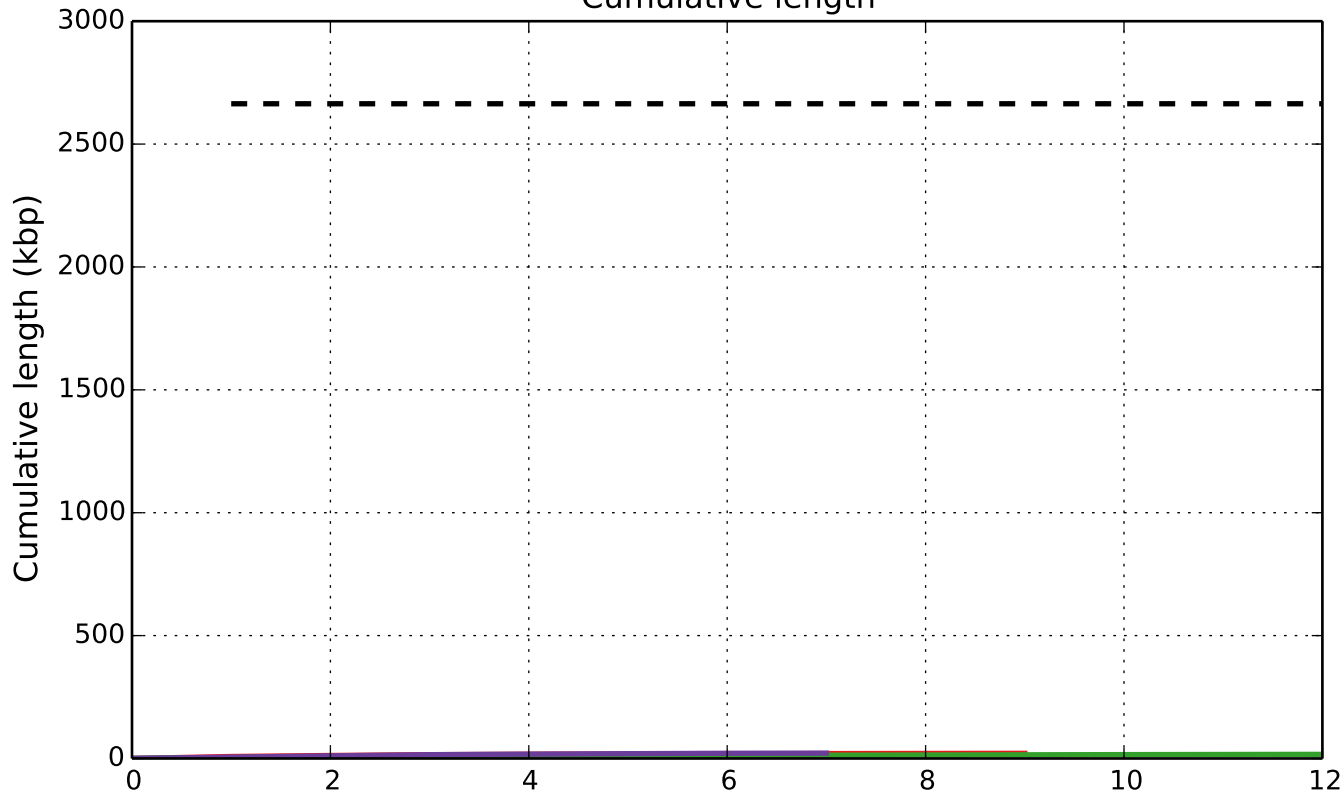
	IDBA_UD	Ray	SOAPdenovo2	SPAdes
# fully unaligned contigs	0	0	0	0
Fully unaligned length	0	0	0	0
# partially unaligned contigs	6	1	3	5
# with misassembly	0	0	0	0
# both parts are significant	1	0	1	3
Partially unaligned length	4365	502	5876	15570
# N's	101	0	185	199

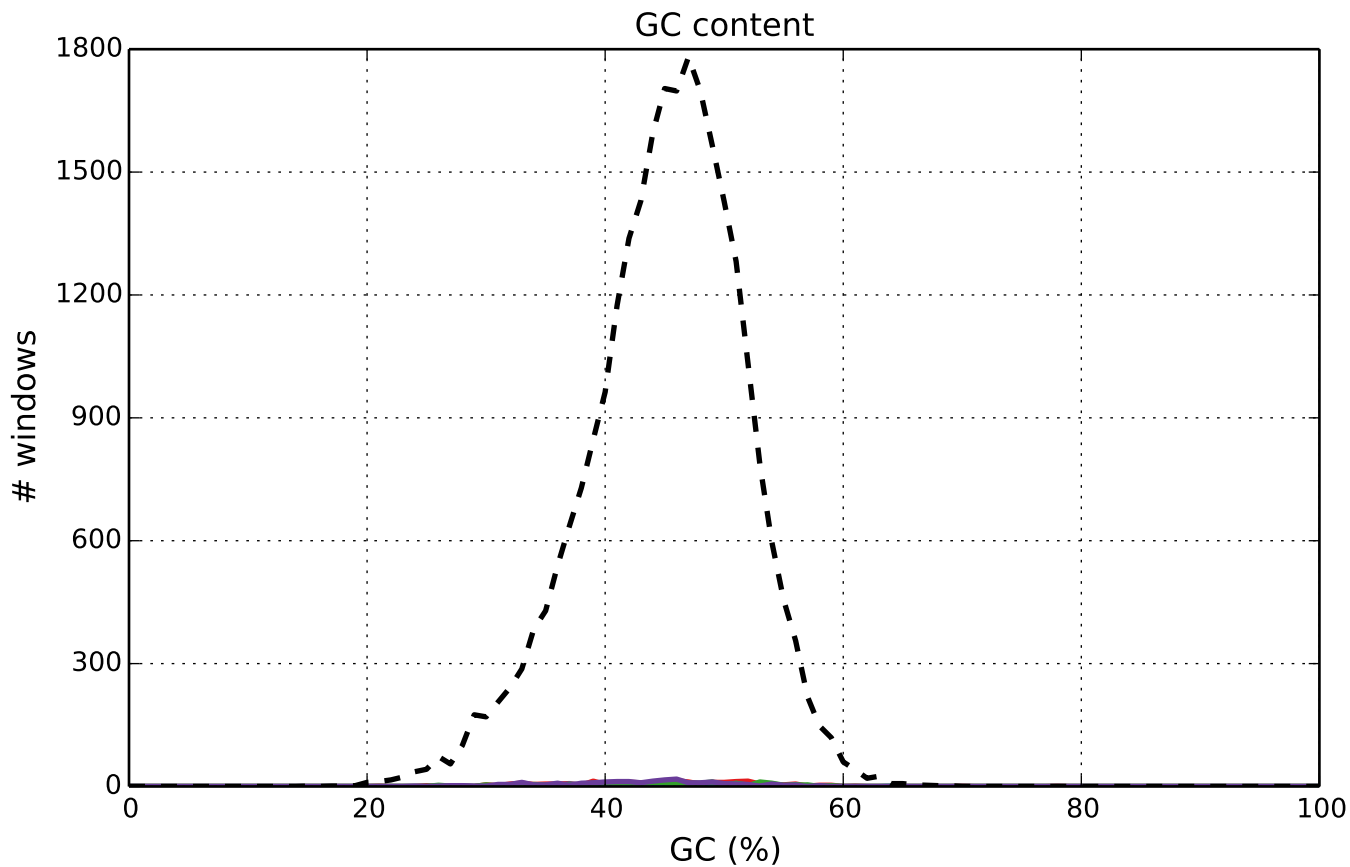
All statistics are based on contigs of size ≥ 500 bp, unless otherwise noted (e.g., "# contigs (≥ 0 bp)" and "Total length (≥ 0 bp)" include all contigs).

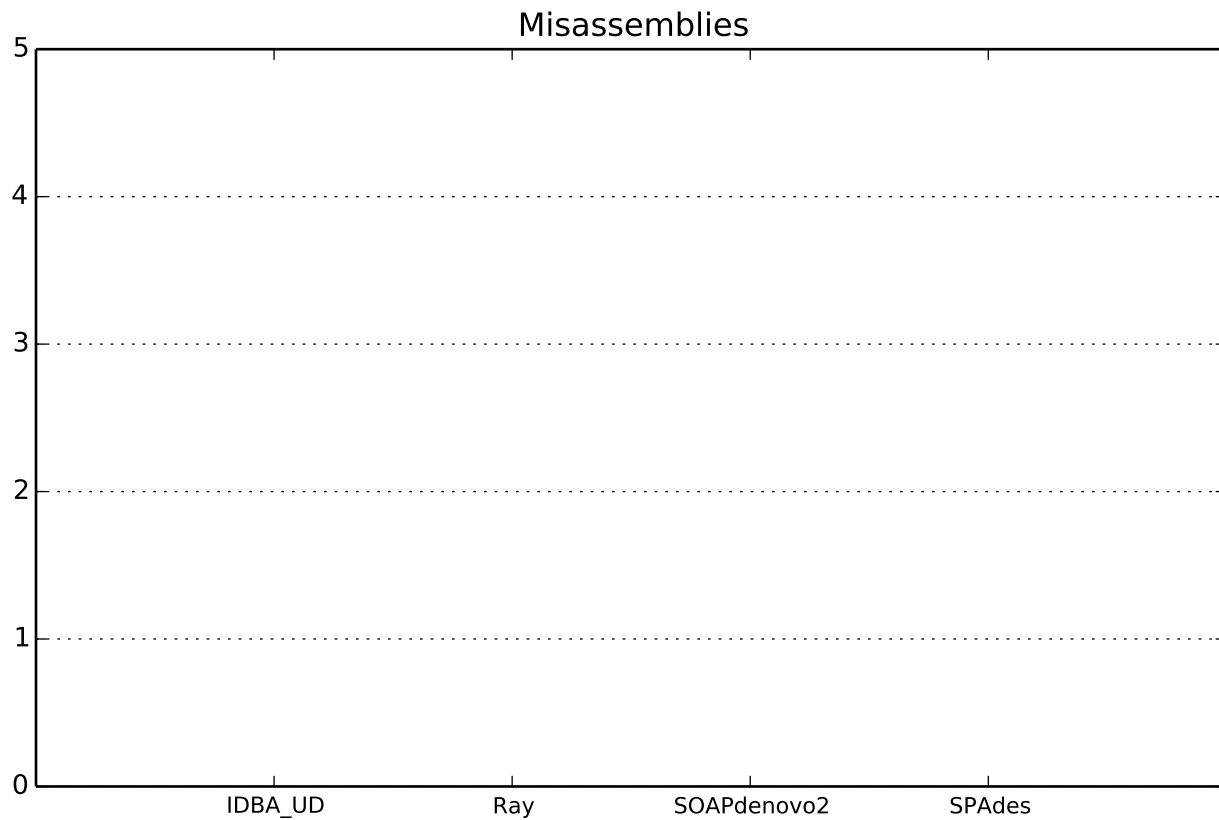




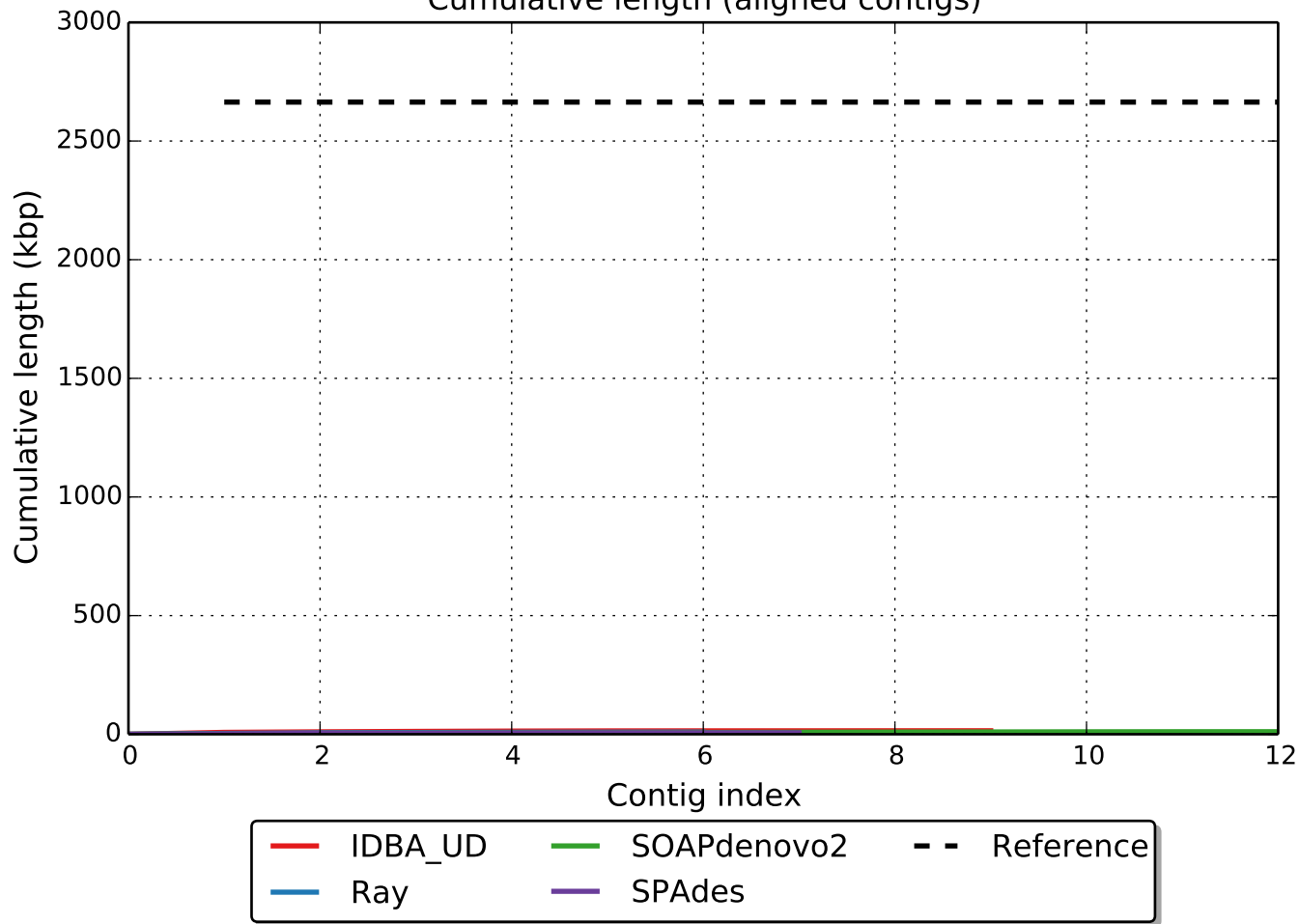
Cumulative length







Cumulative length (aligned contigs)



NAx

