

# Report

	IDBA_UD	Ray	SOAPdenovo2	SPAdes
# contigs (>= 1000 bp)	61	20	23	72
# contigs (>= 5000 bp)	12	5	0	19
# contigs (>= 10000 bp)	5	3	0	7
# contigs (>= 25000 bp)	4	0	0	1
# contigs (>= 50000 bp)	1	0	0	1
Total length (>= 1000 bp)	353052	83119	34457	360506
Total length (>= 5000 bp)	242346	52942	0	246015
Total length (>= 10000 bp)	193570	39970	0	161721
Total length (>= 25000 bp)	173537	0	0	57182
Total length (>= 50000 bp)	80507	0	0	57182
# contigs	108	25	60	150
Largest contig	80507	17800	2418	57182
Total length	386187	86538	59405	410876
Reference length	2915433	2915433	2915433	2915433
GC (%)	42.71	41.24	42.09	41.63
Reference GC (%)	41.44	41.44	41.44	41.44
N50	20033	7273	1111	6893
N75	2981	2678	723	2500
L50	5	4	19	13
L75	25	9	36	37
# misassemblies	2	0	1	1
# misassembled contigs	2	0	1	1
Misassembled contigs length	2267	0	2259	6538
# local misassemblies	0	0	34	1
# structural variations	0	0	0	0
# unaligned contigs	0 + 53 part	0 + 10 part	0 + 13 part	0 + 96 part
Unaligned length	256197	55854	8423	254036
Genome fraction (%)	4.411	1.009	1.643	5.254
Duplication ratio	1.011	1.043	1.064	1.024
# N's per 100 kbp	58.00	2115.83	4708.36	1298.45
# mismatches per 100 kbp	1567.04	1057.07	1056.17	2160.98
# indels per 100 kbp	48.99	23.79	22.96	71.16
Largest alignment	8007	3687	2295	12563
NA50	-	-	764	-
NGA50	-	-	-	-
NA75	-	-	438	-
LA50	-	-	25	-
LA75	-	-	50	-

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

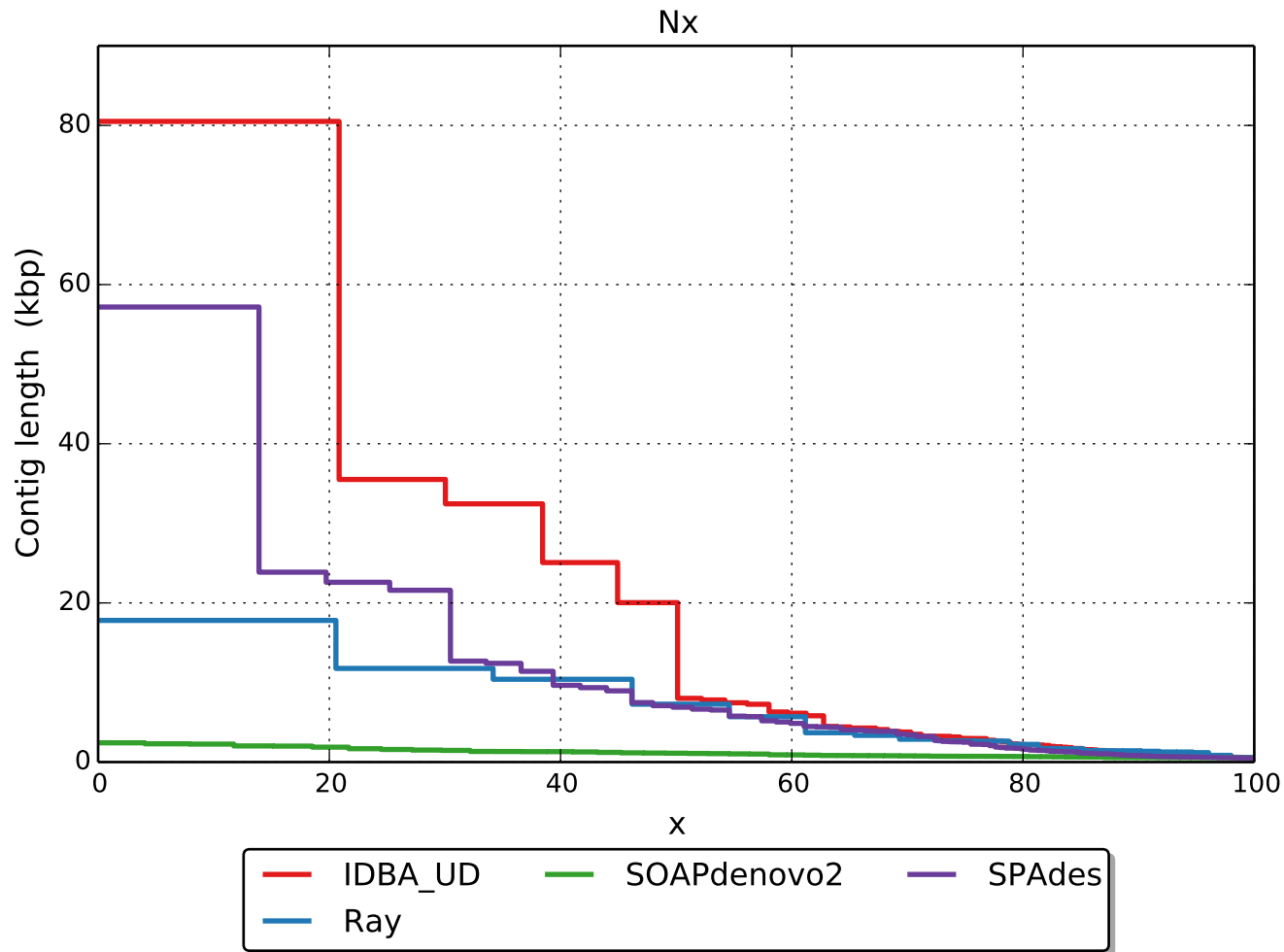
	IDBA_UD	Ray	SOAPdenovo2	SPAdes
# misassemblies	2	0	1	1
# relocations	1	0	0	0
# translocations	0	0	1	1
# inversions	1	0	0	0
# possibly misassembled contigs	8	4	2	14
# misassembled contigs	2	0	1	1
Misassembled contigs length	2267	0	2259	6538
# local misassemblies	0	0	34	1
# structural variations	0	0	0	0
# mismatches	2015	311	506	3310
# indels	63	7	11	109
# short indels	56	7	11	94
# long indels	7	0	0	15
Indels length	131	7	13	315

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

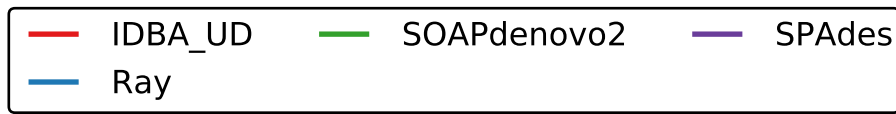
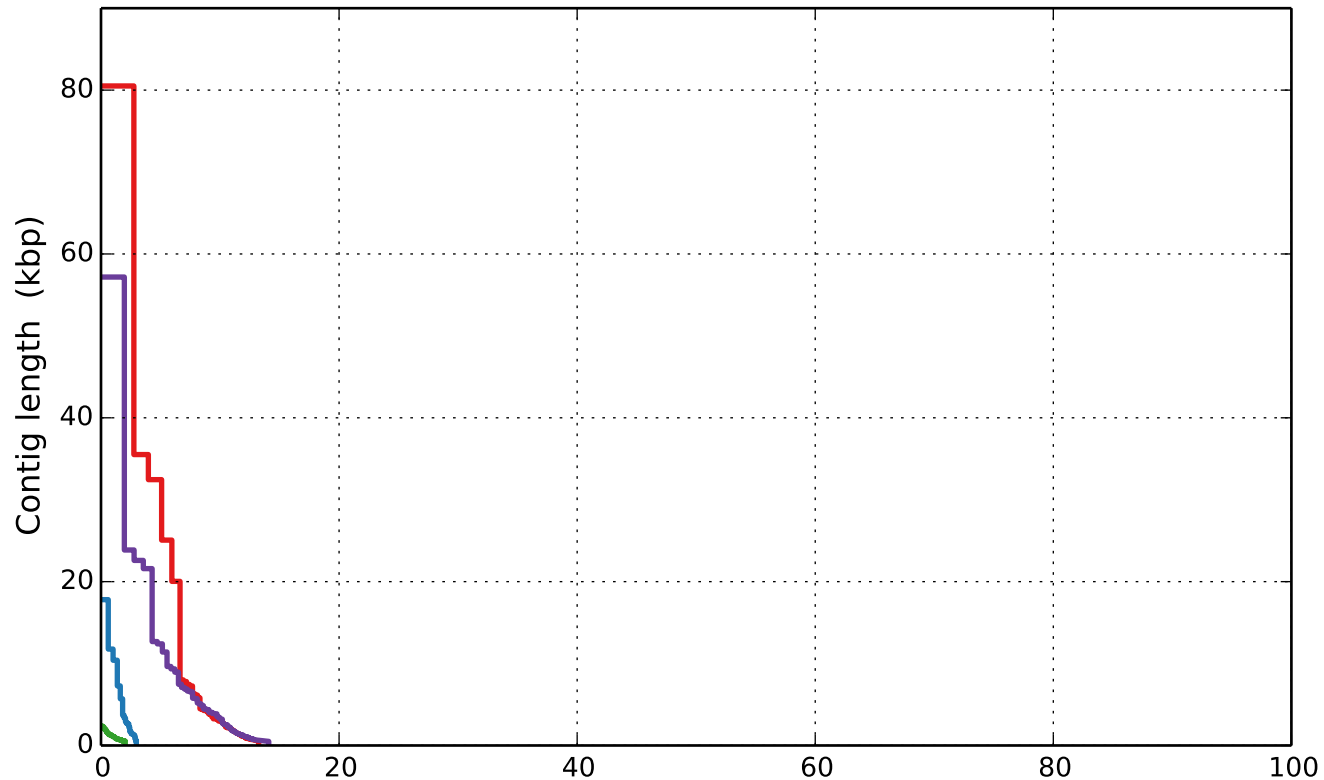
## Unaligned report

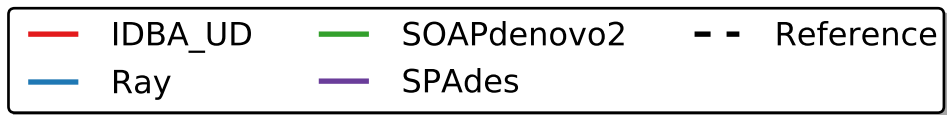
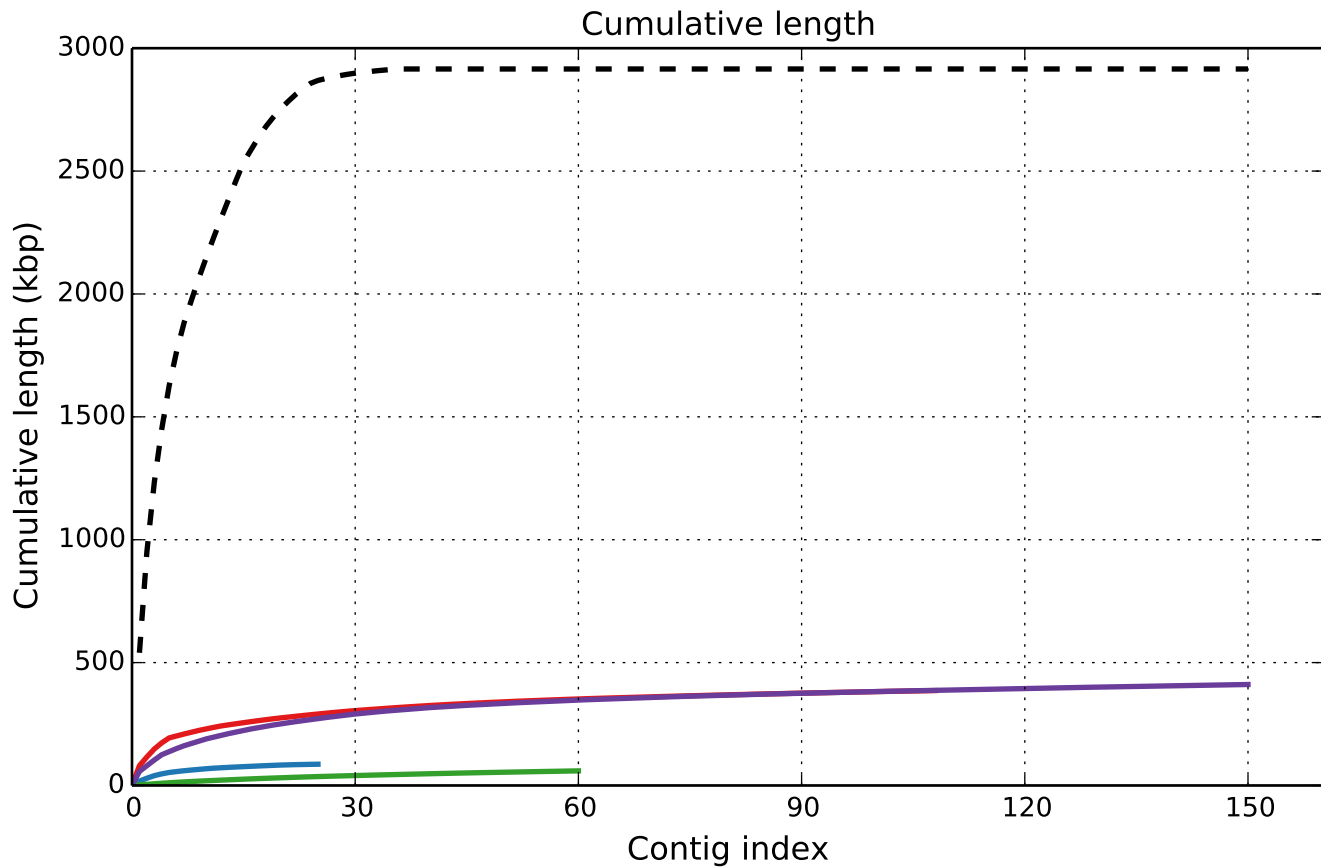
	IDBA_UD	Ray	SOAPdenovo2	SPAdes
# fully unaligned contigs	0	0	0	0
Fully unaligned length	0	0	0	0
# partially unaligned contigs	53	10	13	96
# with misassembly	2	1	2	6
# both parts are significant	8	4	1	13
Partially unaligned length	256197	55854	8423	254036
# N's	224	1831	2797	5335

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

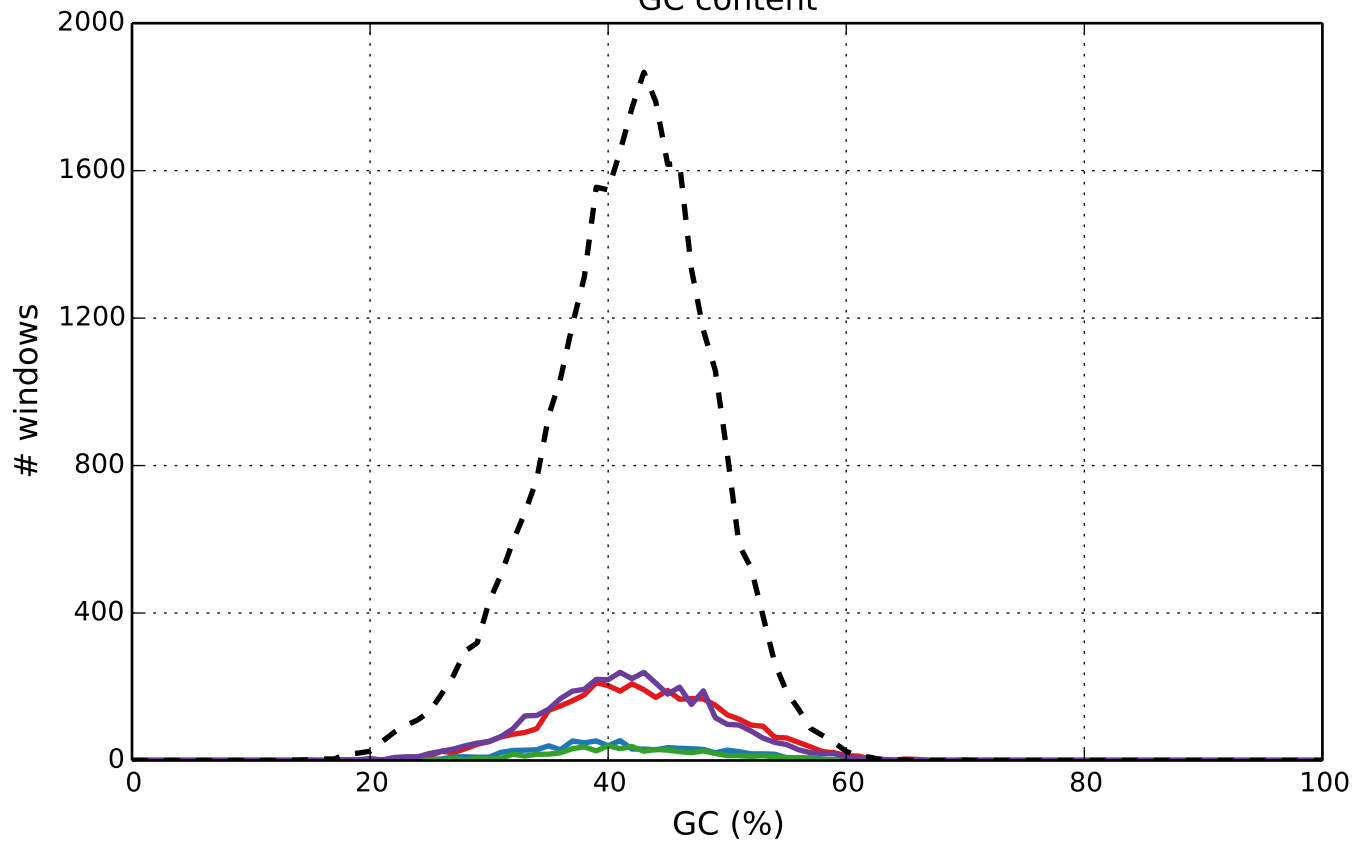


NGx



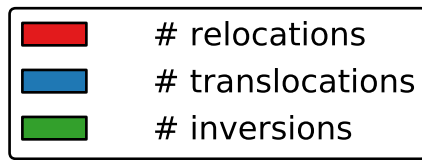
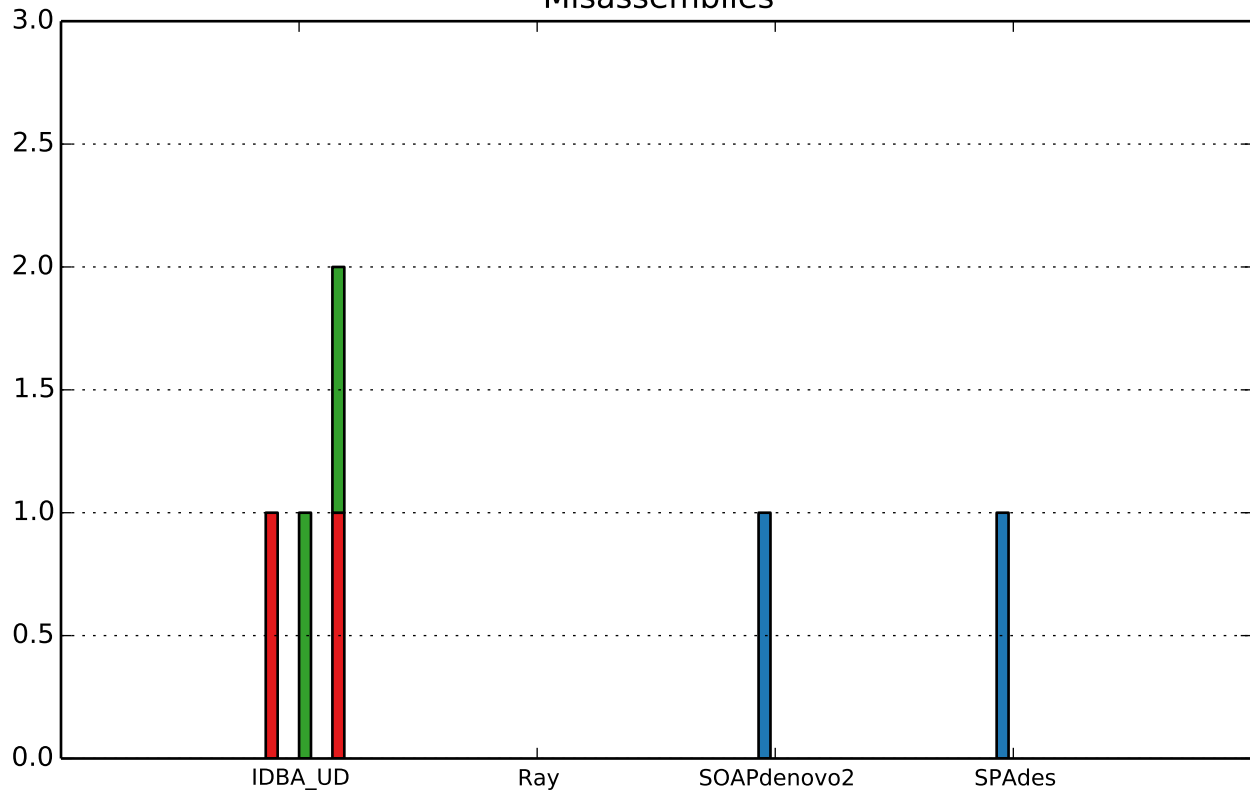


GC content



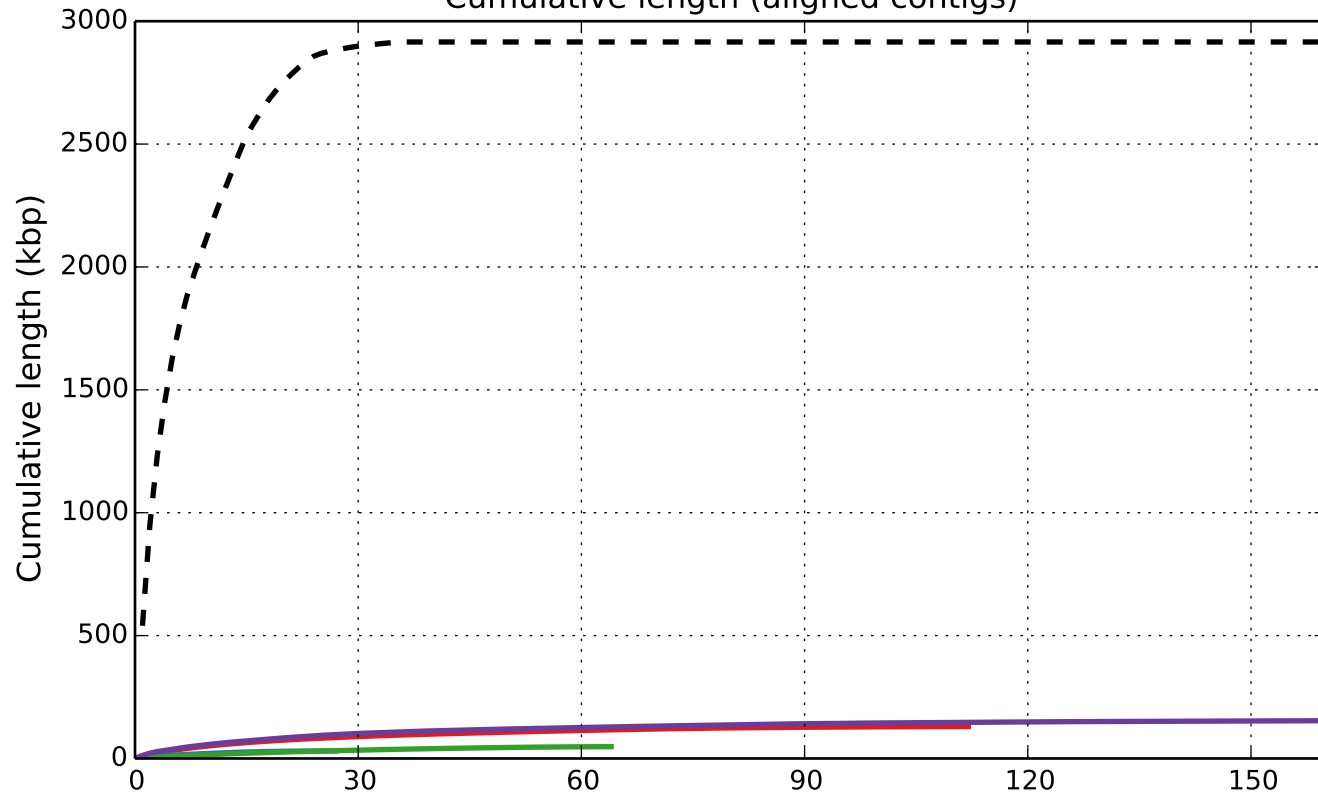
— IDBA\_UD    — SOAPdenovo2    - - Reference  
— Ray    — SPAdes

# Misassemblies

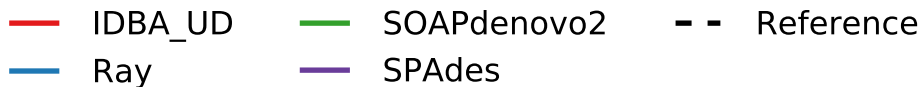


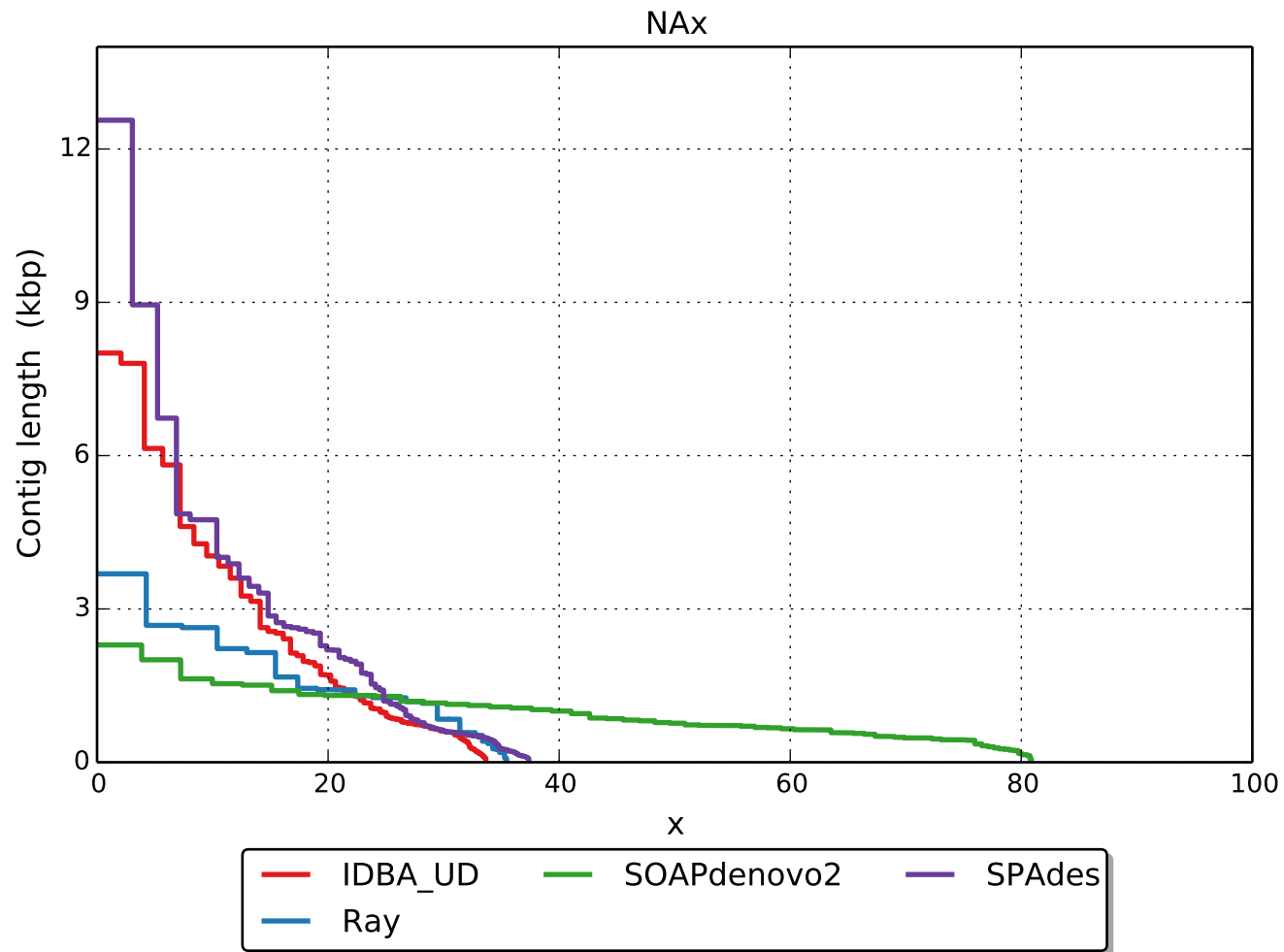


Cumulative length (aligned contigs)



Contig index





# NGAx

