

Report

	IDBA_UD	Ray	SOAPdenovo2	SPAdes
# contigs (>= 1000 bp)	93	46	29	67
# contigs (>= 5000 bp)	27	10	2	21
# contigs (>= 10000 bp)	15	4	1	10
# contigs (>= 25000 bp)	11	0	0	6
# contigs (>= 50000 bp)	6	0	0	1
Total length (>= 1000 bp)	1020115	183368	70027	469253
Total length (>= 5000 bp)	877293	101764	18314	365905
Total length (>= 10000 bp)	789045	56753	12707	282592
Total length (>= 25000 bp)	729582	0	0	225465
Total length (>= 50000 bp)	566464	0	0	57182
# contigs	126	62	78	101
Largest contig	182993	21544	12707	57182
Total length	1045093	194449	103677	494317
Reference length	3843583	3843583	3843583	3843583
GC (%)	42.38	40.81	38.44	39.91
Reference GC (%)	40.34	40.34	40.34	40.34
N50	50587	5615	1583	14985
N75	10002	2577	806	4848
L50	6	10	16	8
L75	15	23	38	22
# misassemblies	6	6	1	3
# misassembled contigs	6	5	1	3
Misassembled contigs length	16640	14651	1583	8744
# local misassemblies	2	10	15	1
# structural variations	1	0	1	1
# unaligned contigs	0 + 80 part	0 + 25 part	0 + 32 part	0 + 78 part
Unaligned length	883472	90065	30197	360407
Genome fraction (%)	3.805	2.232	1.844	3.006
Duplication ratio	1.105	1.217	1.037	1.159
# N's per 100 kbp	53.87	2351.26	2829.94	595.77
# mismatches per 100 kbp	2196.92	2304.46	1895.34	2048.43
# indels per 100 kbp	78.63	59.45	38.10	70.10
Largest alignment	18100	9474	11864	18091
NA50	-	-	692	-
NGA50	-	-	-	-
LA50	-	-	32	-

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	6	1	3
# relocations	1	1	0	0
# translocations	5	5	1	3
# inversions	0	0	0	0
# possibly misassembled contigs	31	16	5	31
# misassembled contigs	6	5	1	3
Misassembled contigs length	16640	14651	1583	8744
# local misassemblies	2	10	15	1
# structural variations	1	0	1	1
# mismatches	3213	1977	1343	2367
# indels	115	51	27	81
# short indels	104	46	27	72
# long indels	11	5	0	9
Indels length	270	109	32	190

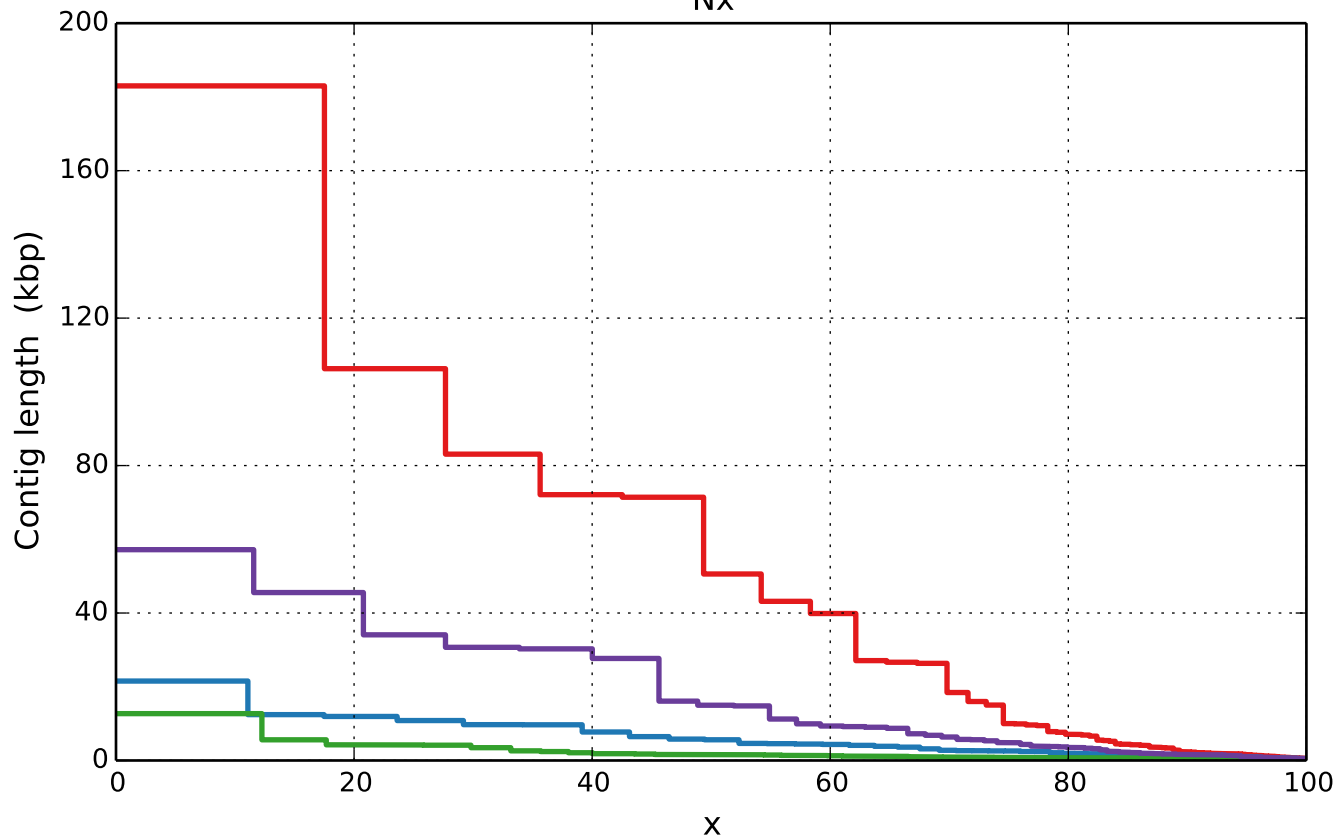
All statistics are based on contigs of size ≥ 500 bp, unless otherwise noted (e.g., "# contigs (≥ 0 bp)" and "Total length (≥ 0 bp)" include all contigs).

Unaligned report

	IDBA_UD	Ray	SOAPdenovo2	SPAdes
# fully unaligned contigs	0	0	0	0
Fully unaligned length	0	0	0	0
# partially unaligned contigs	80	25	32	78
# with misassembly	18	3	6	11
# both parts are significant	27	9	4	26
Partially unaligned length	883472	90065	30197	360407
# N's	563	4572	2934	2945

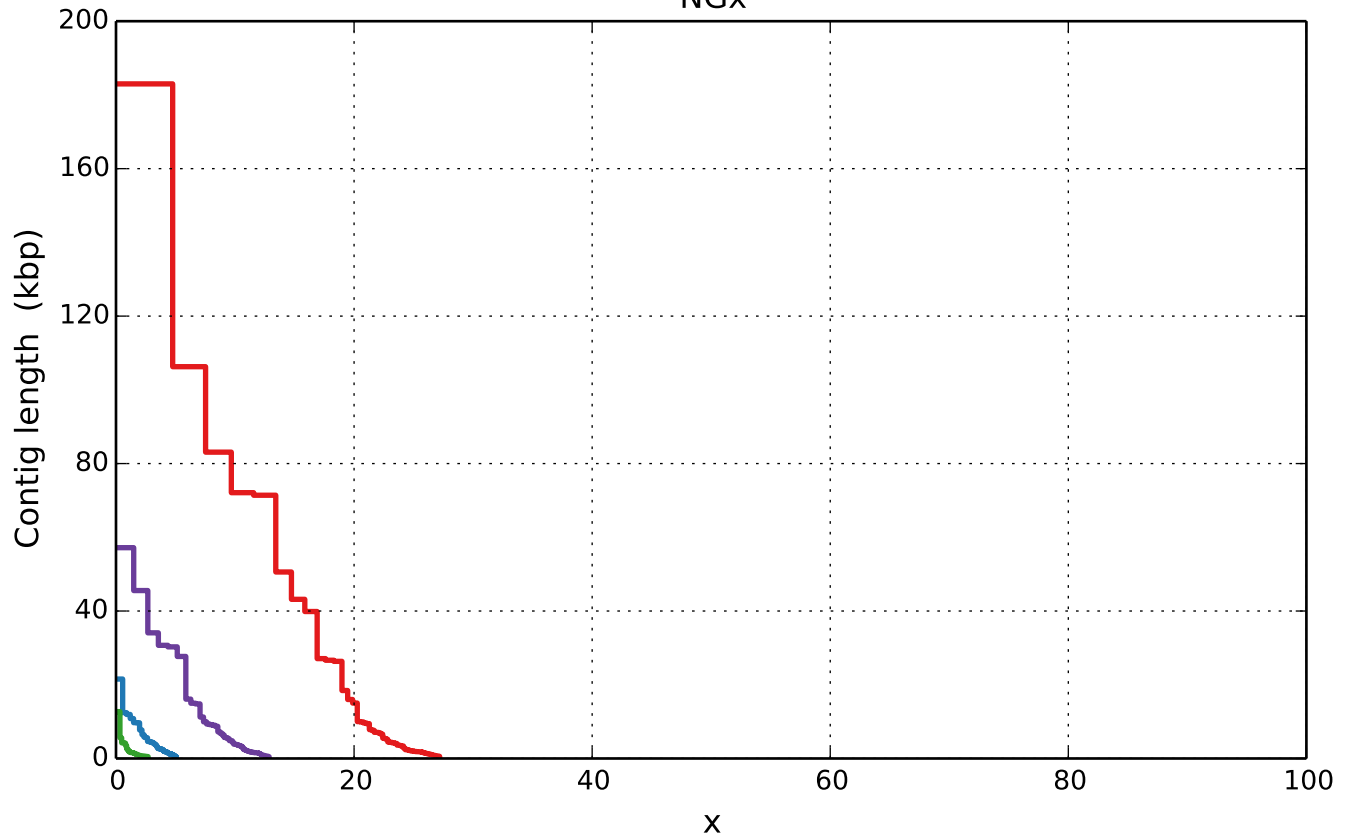
All statistics are based on contigs of size ≥ 500 bp, unless otherwise noted (e.g., "# contigs (≥ 0 bp)" and "Total length (≥ 0 bp)" include all contigs).

Nx



— IDBA_UD — SOAPdenovo2 — SPAdes
— Ray

NGx

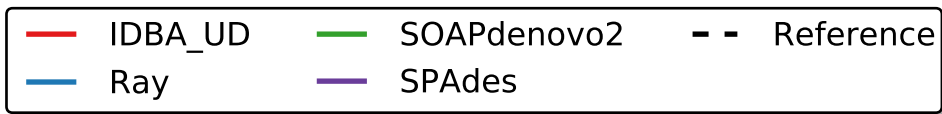
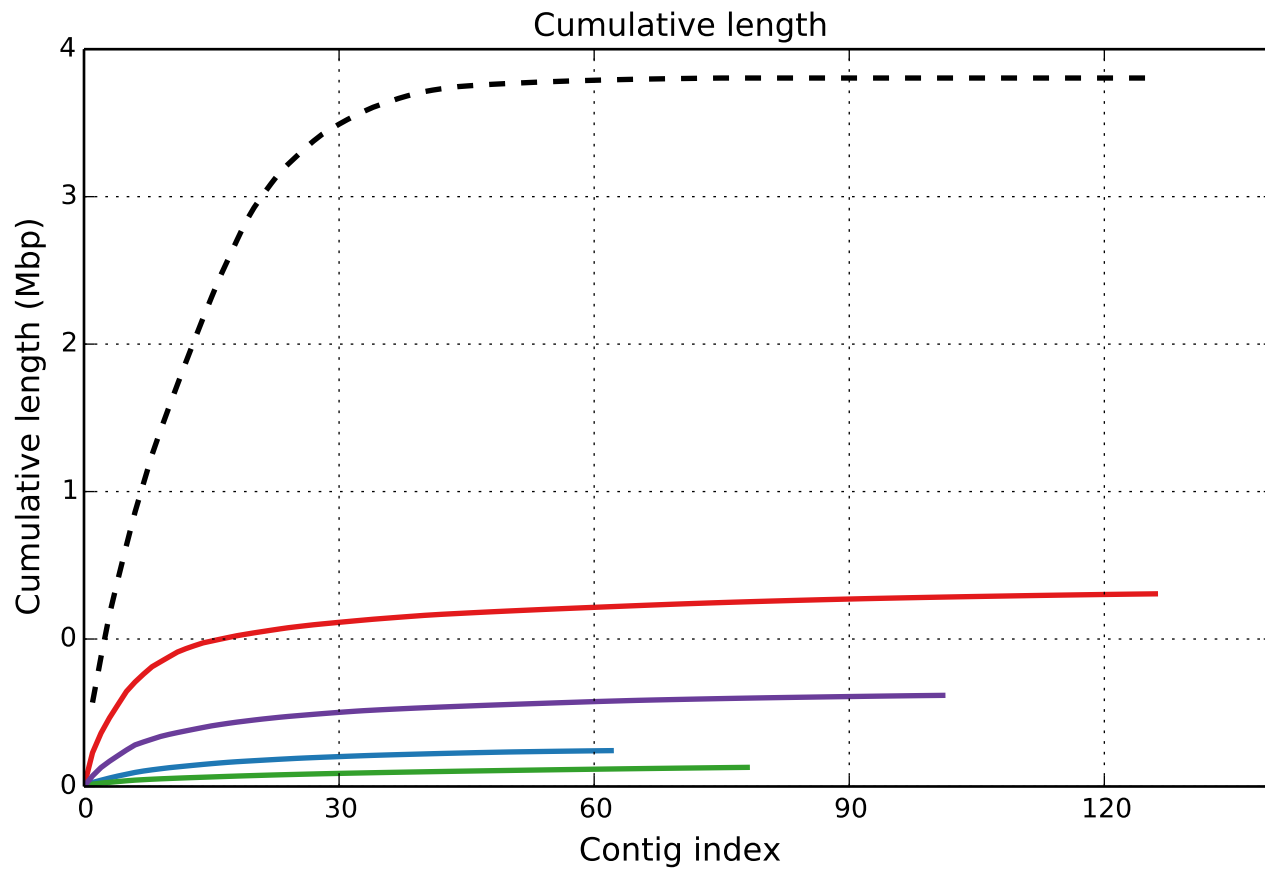


IDBA_UD

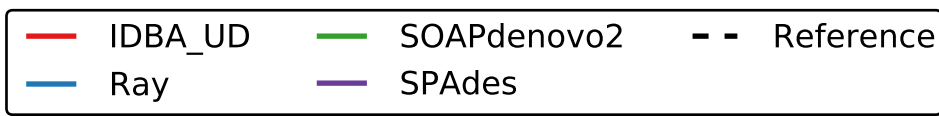
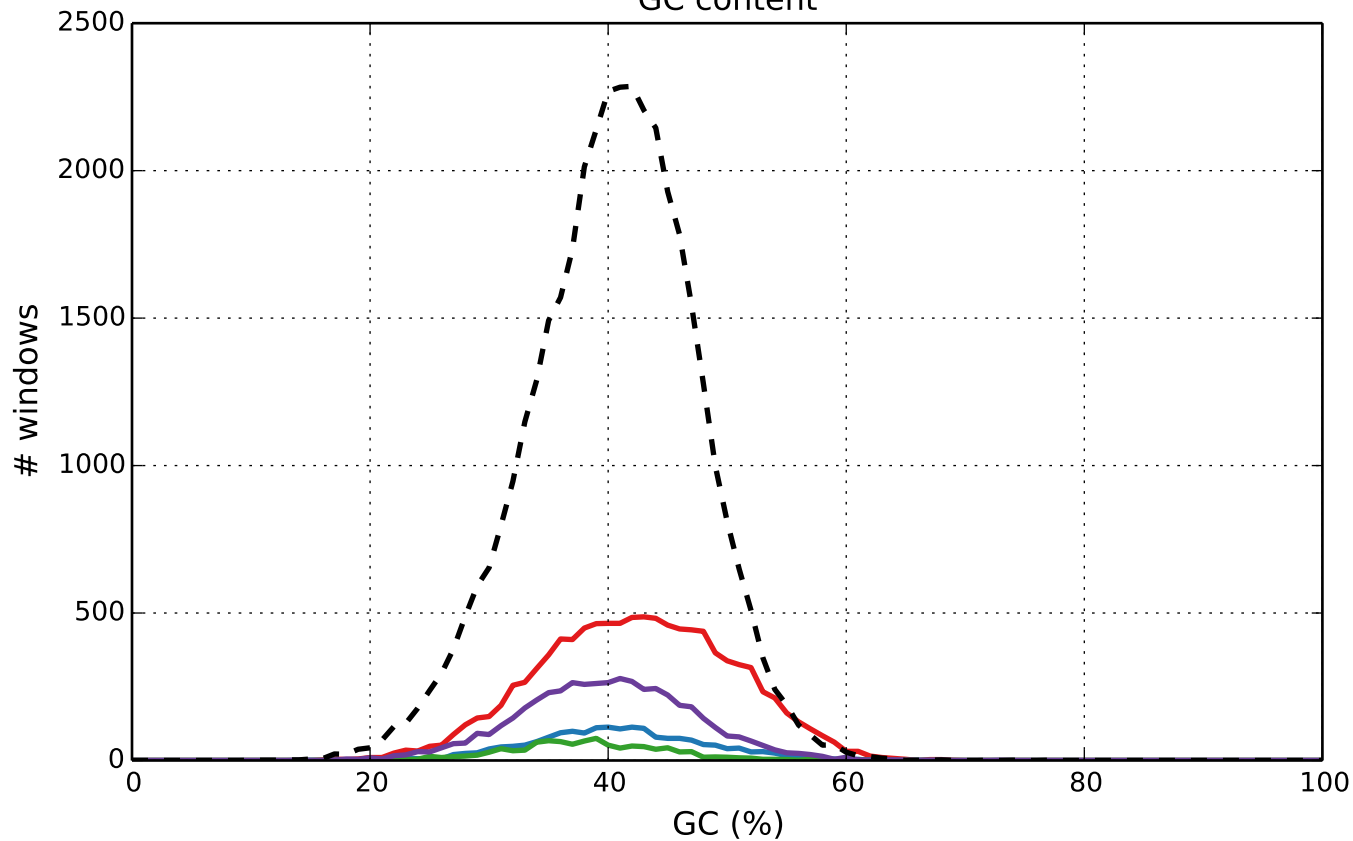
SOAPdenovo2

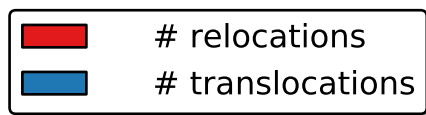
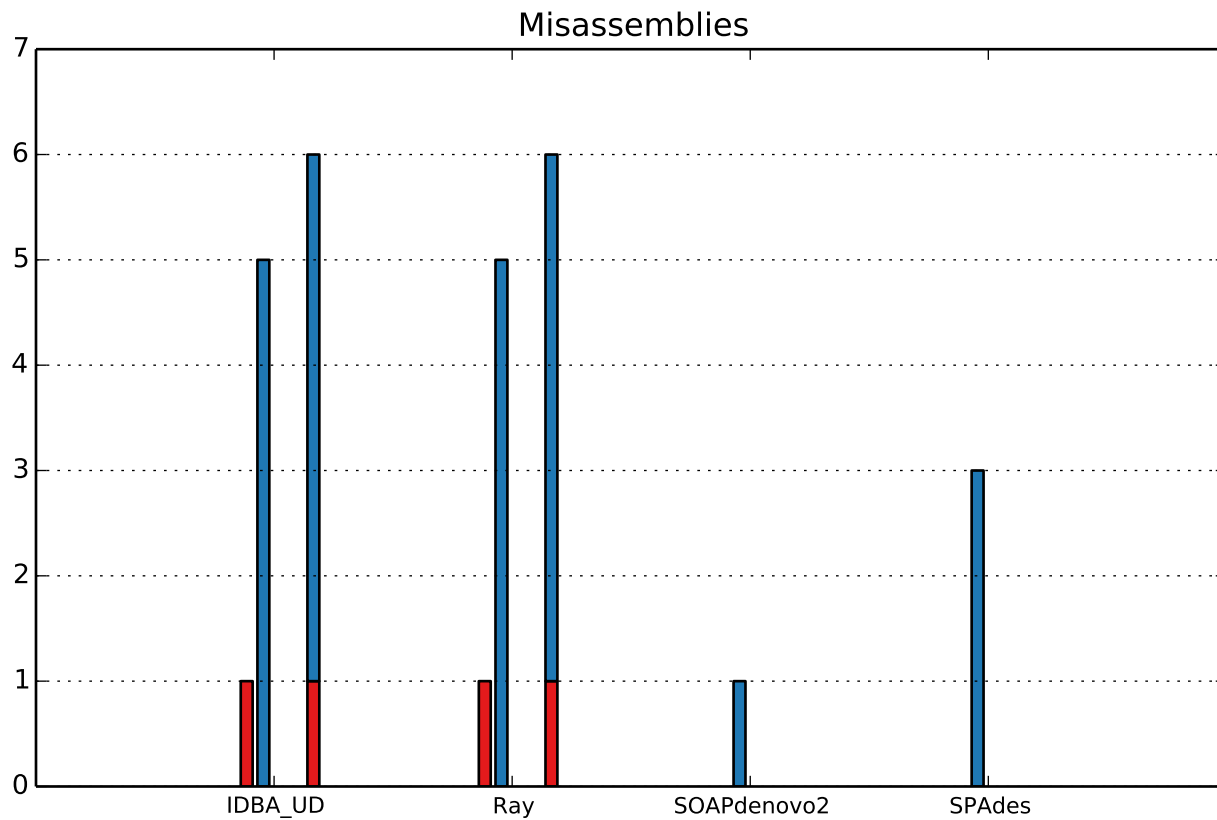
SPAdes

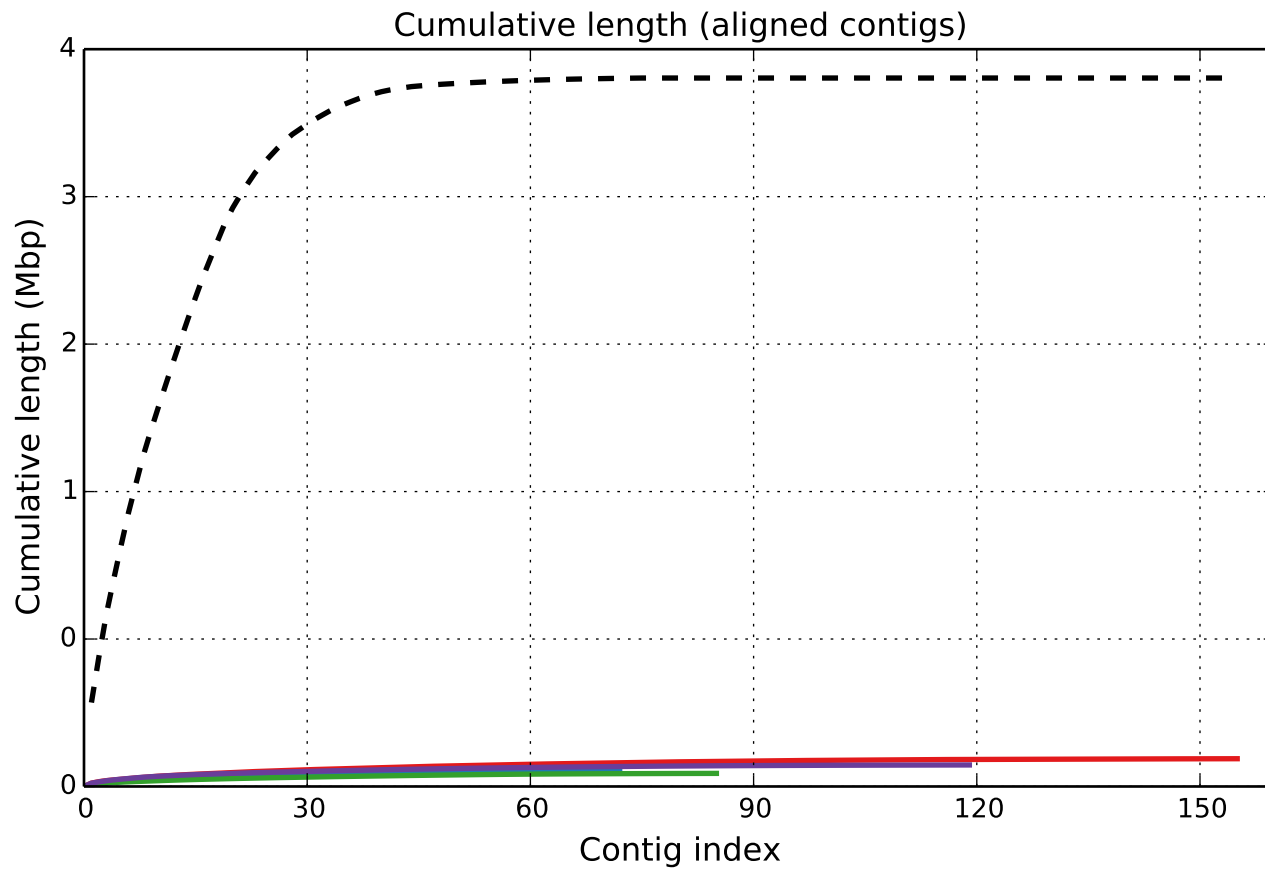
Ray



GC content







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