

Report

	IDBA_UD	Ray	SOAPdenovo2	SPAdes
# contigs (>= 1000 bp)	81	32	26	83
# contigs (>= 5000 bp)	22	5	0	27
# contigs (>= 10000 bp)	14	3	0	15
# contigs (>= 25000 bp)	7	2	0	6
# contigs (>= 50000 bp)	2	0	0	1
Total length (>= 1000 bp)	600267	156495	54184	547110
Total length (>= 5000 bp)	478835	98367	0	425498
Total length (>= 10000 bp)	416549	83858	0	349639
Total length (>= 25000 bp)	325260	71644	0	232106
Total length (>= 50000 bp)	144000	0	0	57182
# contigs	154	60	96	188
Largest contig	93413	44072	4607	57182
Total length	652668	175674	101460	619513
Reference length	3757491	3757491	3757491	3757491
GC (%)	42.86	45.49	41.40	42.61
Reference GC (%)	42.49	42.49	42.49	42.49
N50	15997	7690	1102	11243
N75	4203	2119	696	3153
L50	8	4	23	12
L75	25	17	53	37
# misassemblies	5	0	1	1
# misassembled contigs	5	0	1	1
Misassembled contigs length	10559	0	1029	640
# local misassemblies	2	6	36	1
# structural variations	1	0	1	1
# unaligned contigs	0 + 72 part	0 + 25 part	0 + 44 part	0 + 126 part
Unaligned length	476132	120659	33351	443833
Genome fraction (%)	4.378	1.356	1.703	4.493
Duplication ratio	1.073	1.079	1.064	1.041
# N's per 100 kbp	89.94	4284.07	5178.40	700.39
# mismatches per 100 kbp	2173.69	2486.02	1942.49	2321.46
# indels per 100 kbp	80.84	33.36	29.69	65.75
Largest alignment	11731	6178	4307	11731
NA50	-	-	520	-
NGA50	-	-	-	-
LA50	-	-	51	-

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

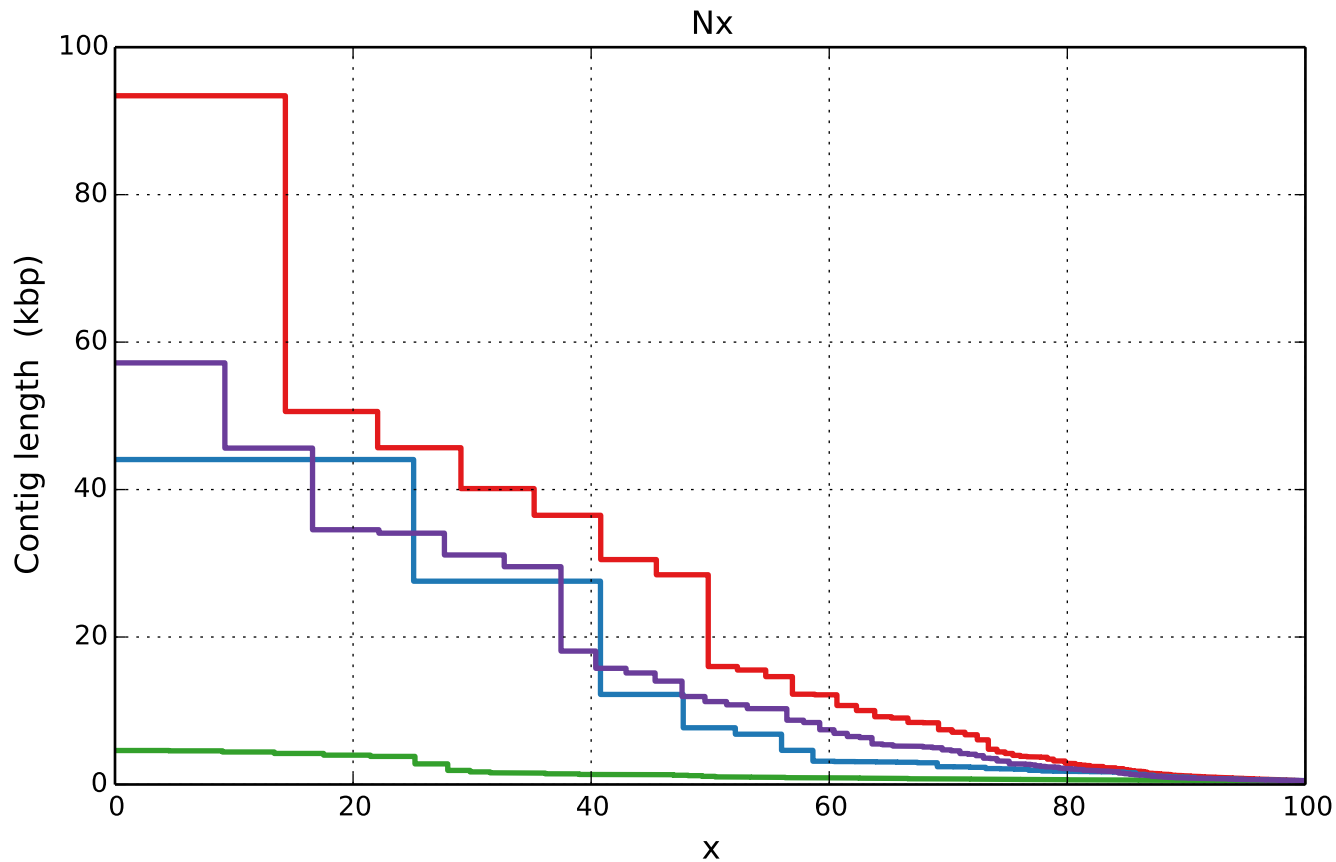
	IDBA_UD	Ray	SOAPdenovo2	SPAdes
# misassemblies	5	0	1	1
# relocations	5	0	1	1
# translocations	0	0	0	0
# inversions	0	0	0	0
# possibly misassembled contigs	28	9	7	26
# misassembled contigs	5	0	1	1
Misassembled contigs length	10559	0	1029	640
# local misassemblies	2	6	36	1
# structural variations	1	0	1	1
# mismatches	3576	1267	1243	3919
# indels	133	17	19	111
# short indels	127	17	19	98
# long indels	6	0	0	13
Indels length	221	20	22	303

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).

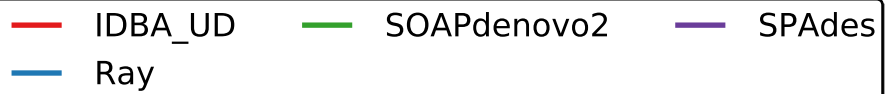
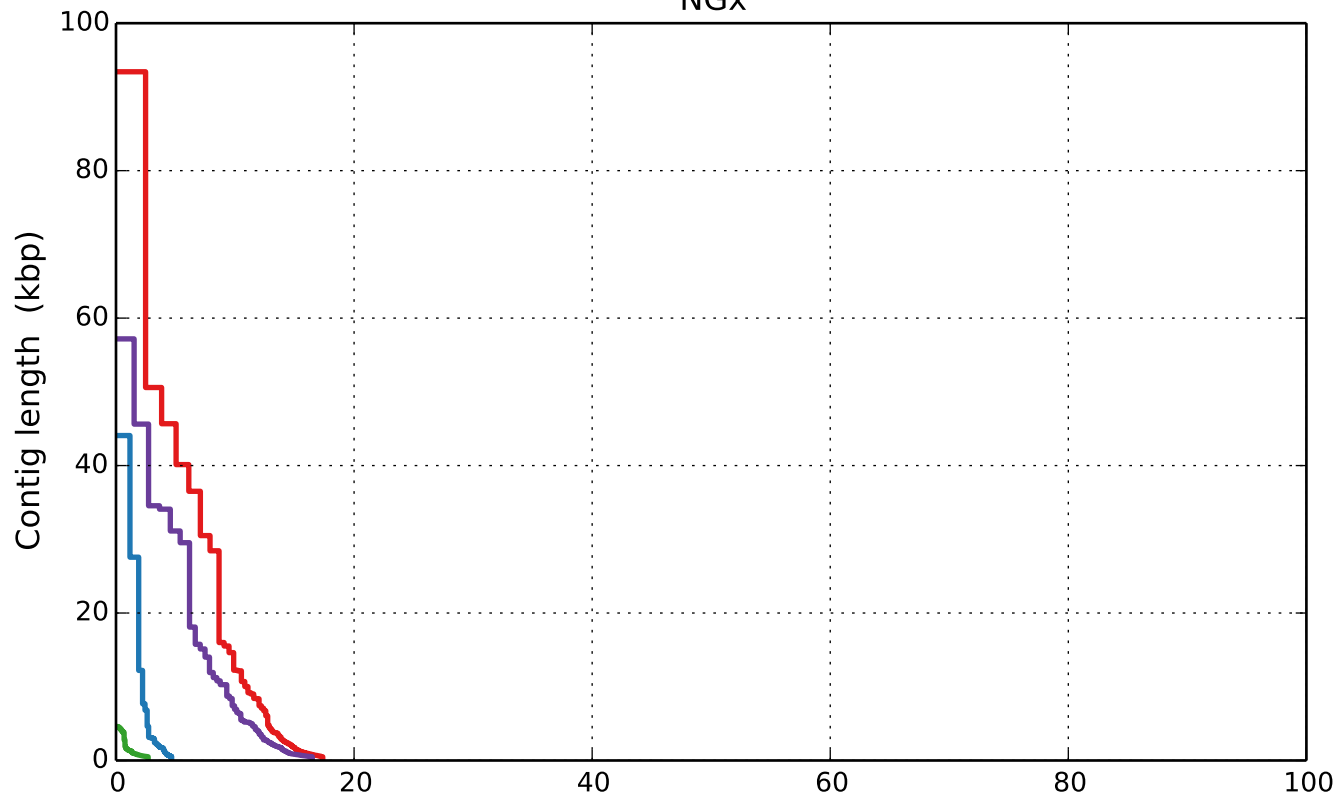
Unaligned report

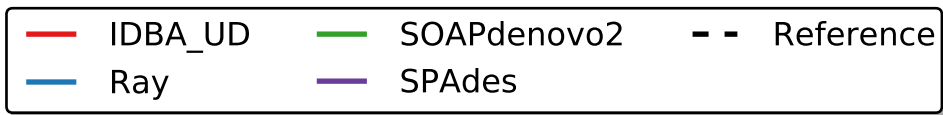
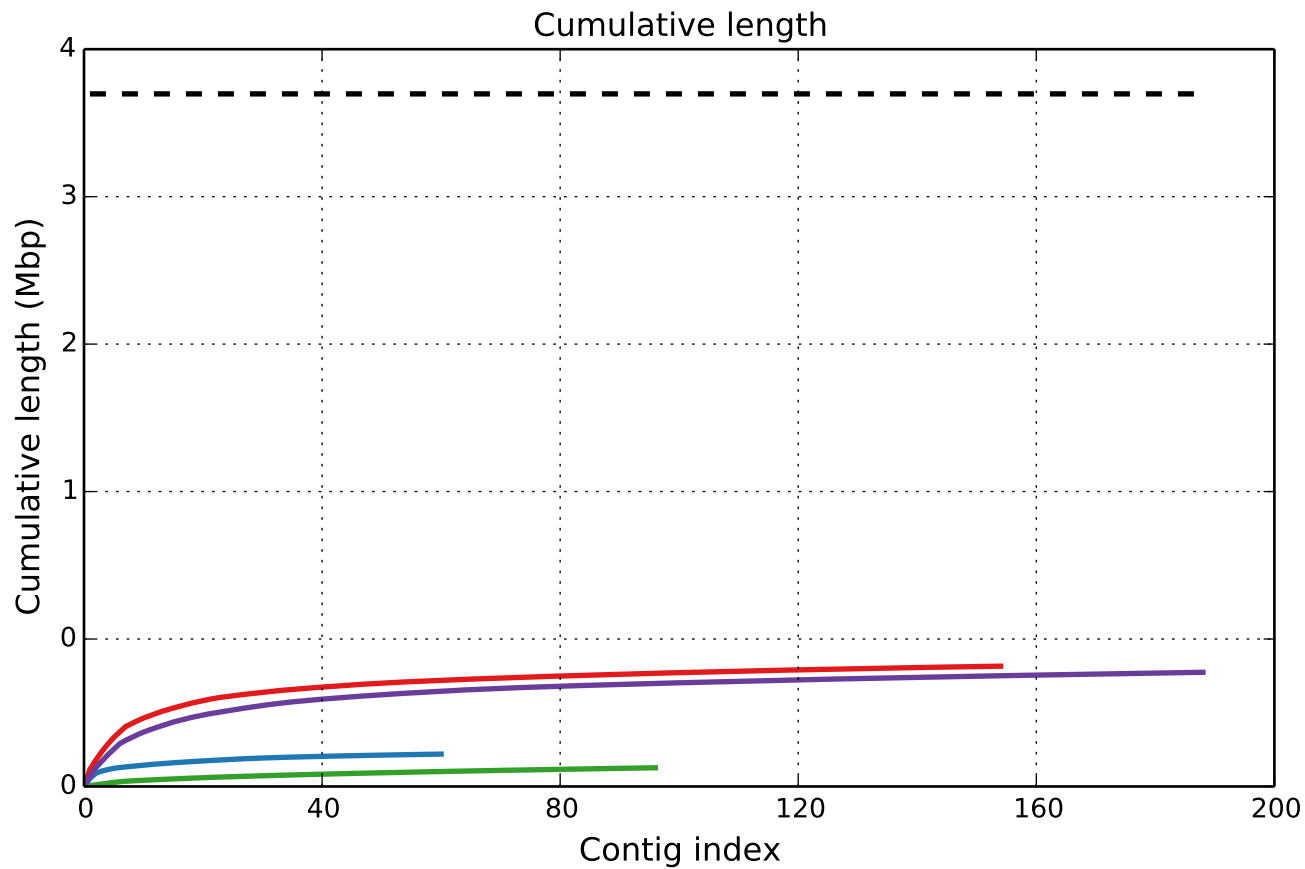
	IDBA_UD	Ray	SOAPdenovo2	SPAdes
# fully unaligned contigs	0	0	0	0
Fully unaligned length	0	0	0	0
# partially unaligned contigs	72	25	44	126
# with misassembly	4	2	6	8
# both parts are significant	24	8	6	25
Partially unaligned length	476132	120659	33351	443833
# N's	587	7526	5254	4339

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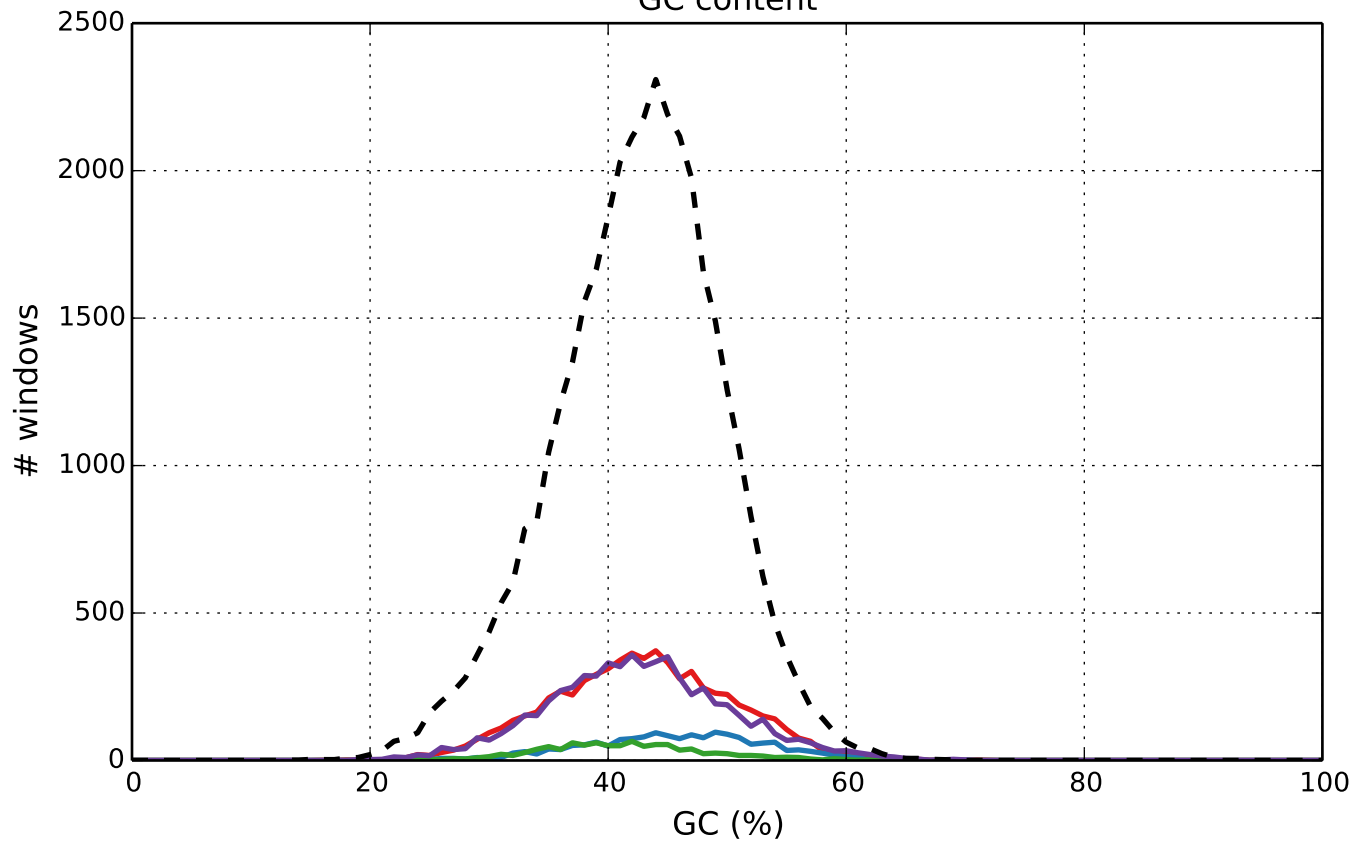


NGx

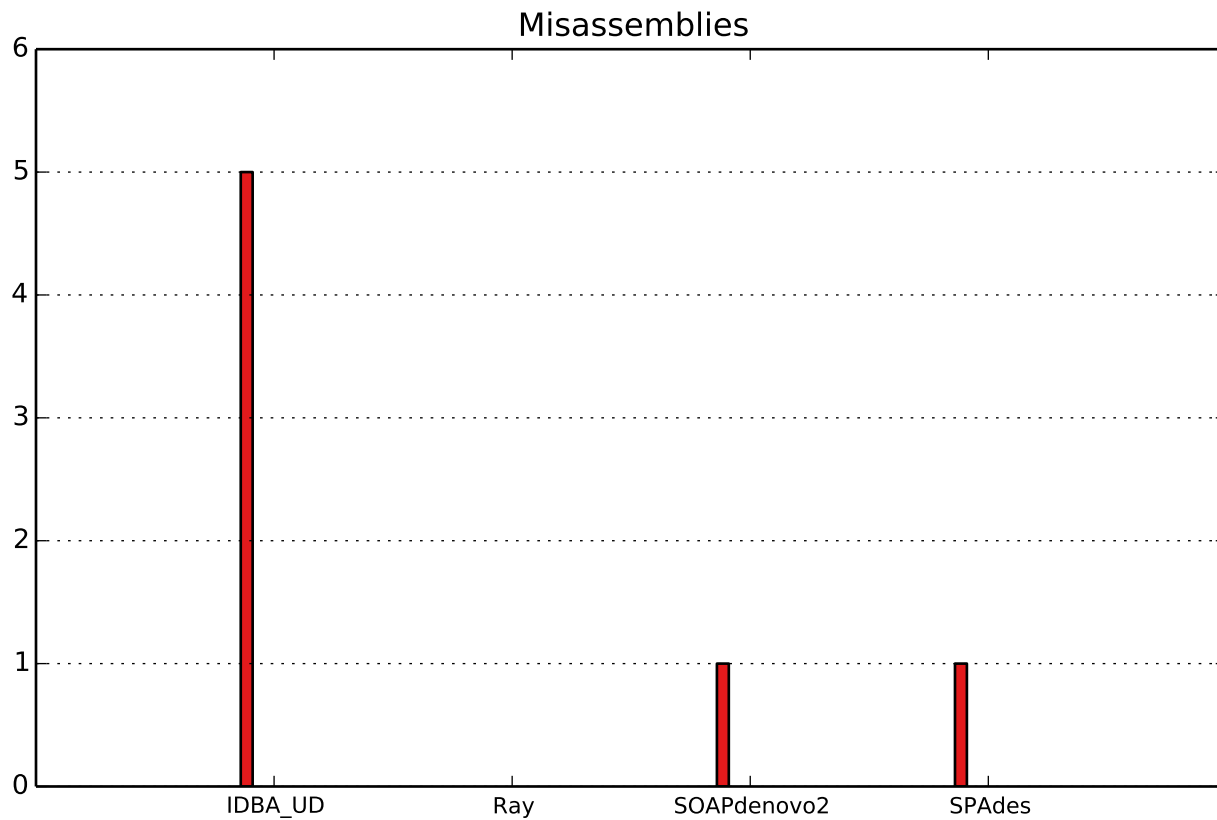




GC content



— IDBA_UD — SOAPdenovo2 - - Reference
— Ray — SPAdes



 # relocations

