

# Report

	Gold_Assembly	IDBA_UD	Ray	SOAPdenovo2	SPAdes
# contigs (>= 1000 bp)	792	1059	9	286	1169
# contigs (>= 5000 bp)	217	33	0	0	31
# contigs (>= 10000 bp)	38	8	0	0	17
# contigs (>= 25000 bp)	1	1	0	0	5
# contigs (>= 50000 bp)	0	0	0	0	1
Total length (>= 1000 bp)	3248528	1978680	10670	359911	2348817
Total length (>= 5000 bp)	1775826	304150	0	0	545609
Total length (>= 10000 bp)	535154	127756	0	0	453819
Total length (>= 25000 bp)	28158	32390	0	0	261535
Total length (>= 50000 bp)	0	0	0	0	112862
# contigs	965	2519	517	2007	2735
Largest contig	28158	32390	1574	3284	112862
Total length	3379716	3022403	319827	1528500	3463323
Reference length	7235897	7235897	7235897	7235897	7235897
GC (%)	68.50	68.18	68.67	68.05	68.64
Reference GC (%)	68.13	68.13	68.13	68.13	68.13
N50	5313	1306	599	761	1345
N75	3026	852	544	613	871
L50	201	648	224	752	635
L75	415	1372	364	1313	1435
# misassemblies	55	38	0	0	13
# misassembled contigs	28	35	0	0	12
Misassembled contigs length	202757	48560	0	0	18893
# local misassemblies	12	4	0	2	4
# structural variations	0	0	0	0	0
# unaligned contigs	0 + 1 part	0 + 243 part	0 + 1 part	0 + 8 part	0 + 221 part
Unaligned length	682	437128	42	513	616430
Genome fraction (%)	45.771	35.362	4.418	21.132	38.974
Duplication ratio	1.020	1.010	1.000	0.999	1.009
# N's per 100 kbp	1.51	0.00	0.00	102.98	12.13
# mismatches per 100 kbp	365.07	531.54	305.92	613.95	944.64
# indels per 100 kbp	35.57	21.42	11.57	59.45	26.98
Largest alignment	22427	5970	1573	3284	6227
NA50	5059	980	599	759	988
NGA50	-	-	-	-	-
NA75	2845	620	544	611	585
LA50	209	971	224	752	1121
LA75	433	1935	364	1314	2253

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

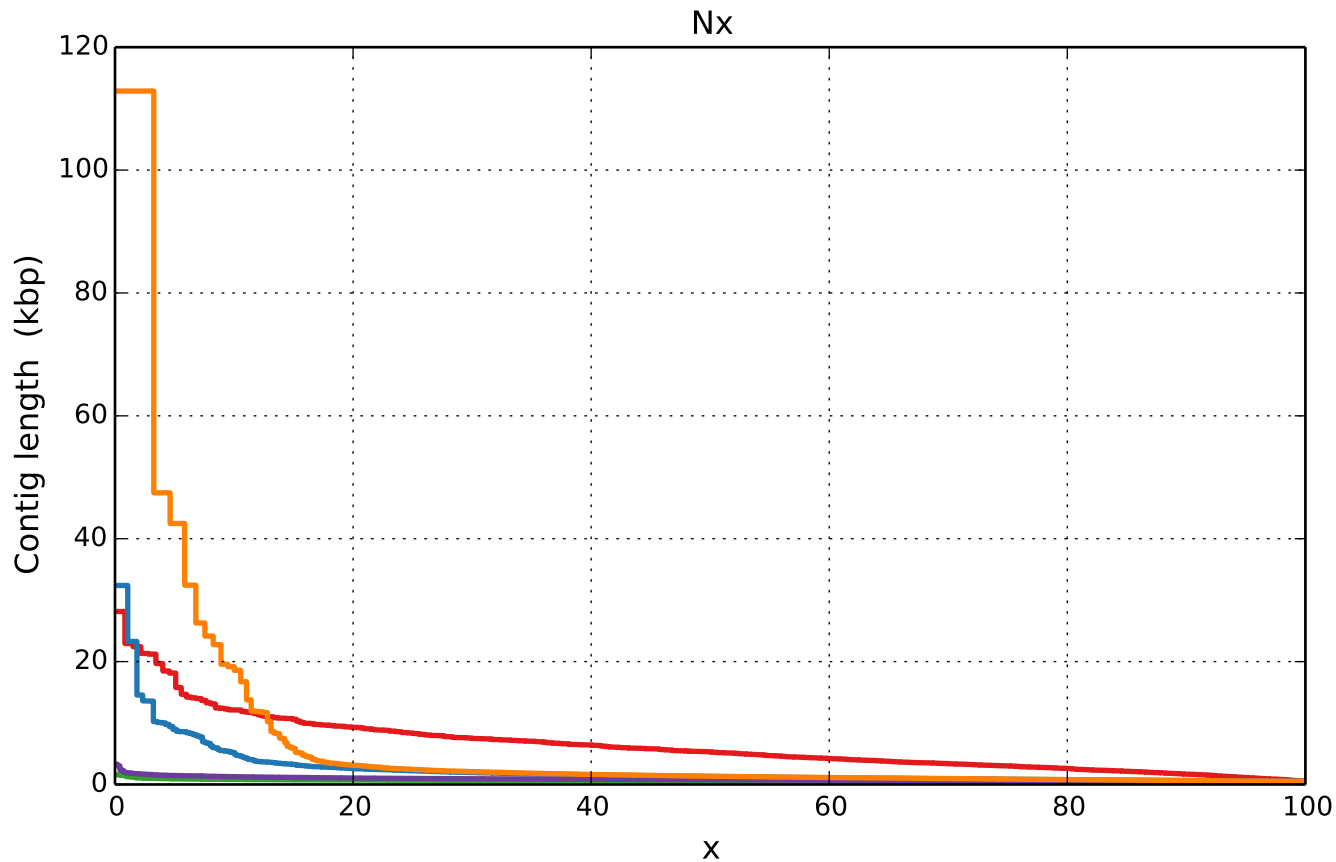
	Gold_Assembly	IDBA_UD	Ray	SOAPdenovo2	SPAdes
# misassemblies	55	38	0	0	13
# relocations	1	1	0	0	1
# translocations	54	37	0	0	12
# inversions	0	0	0	0	0
# possibly misassembled contigs	5	63	0	0	45
# misassembled contigs	28	35	0	0	12
Misassembled contigs length	202757	48560	0	0	18893
# local misassemblies	12	4	0	2	4
# structural variations	0	0	0	0	0
# mismatches	12091	13601	978	9388	26640
# indels	1178	548	37	909	761
# short indels	754	424	35	502	625
# long indels	424	124	2	407	136
Indels length	7516	2185	84	5756	2453

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).

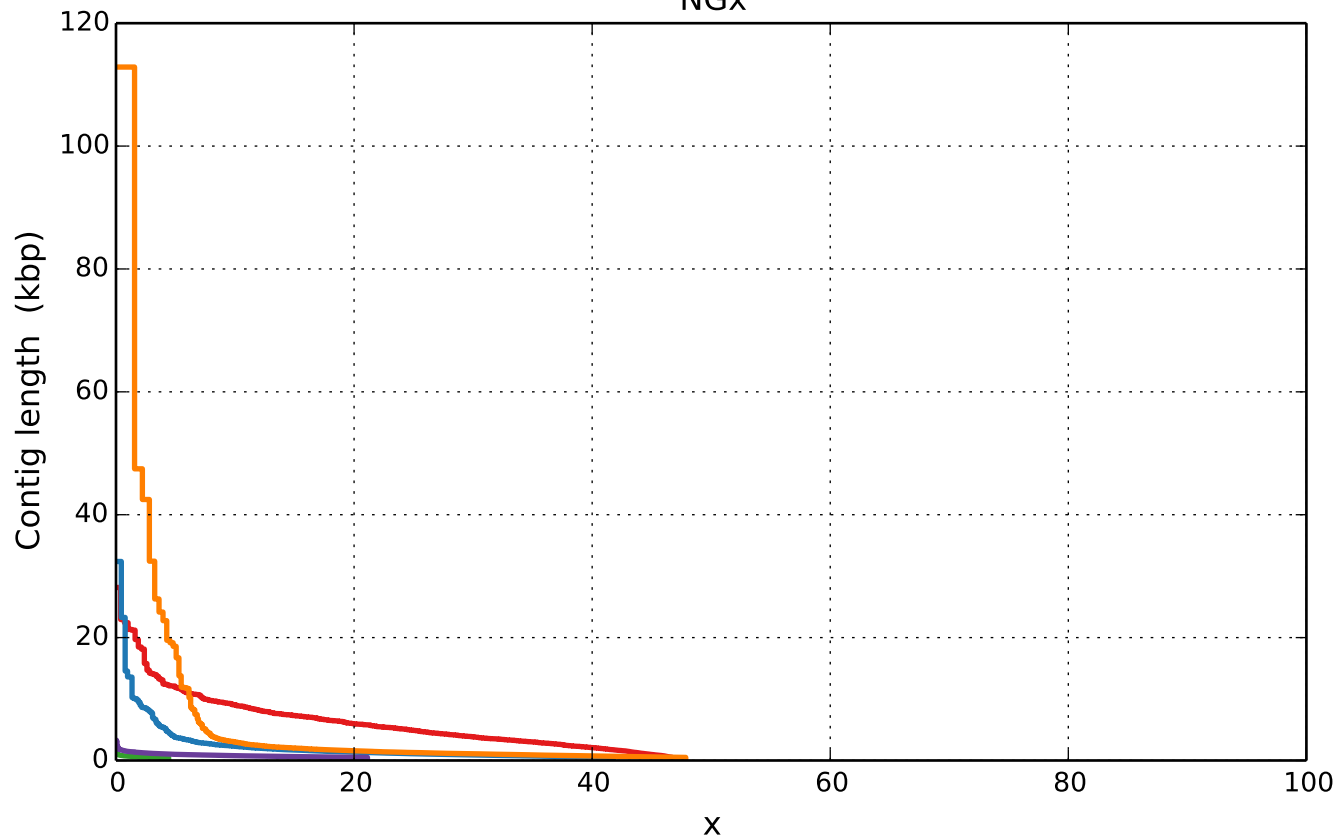
## Unaligned report

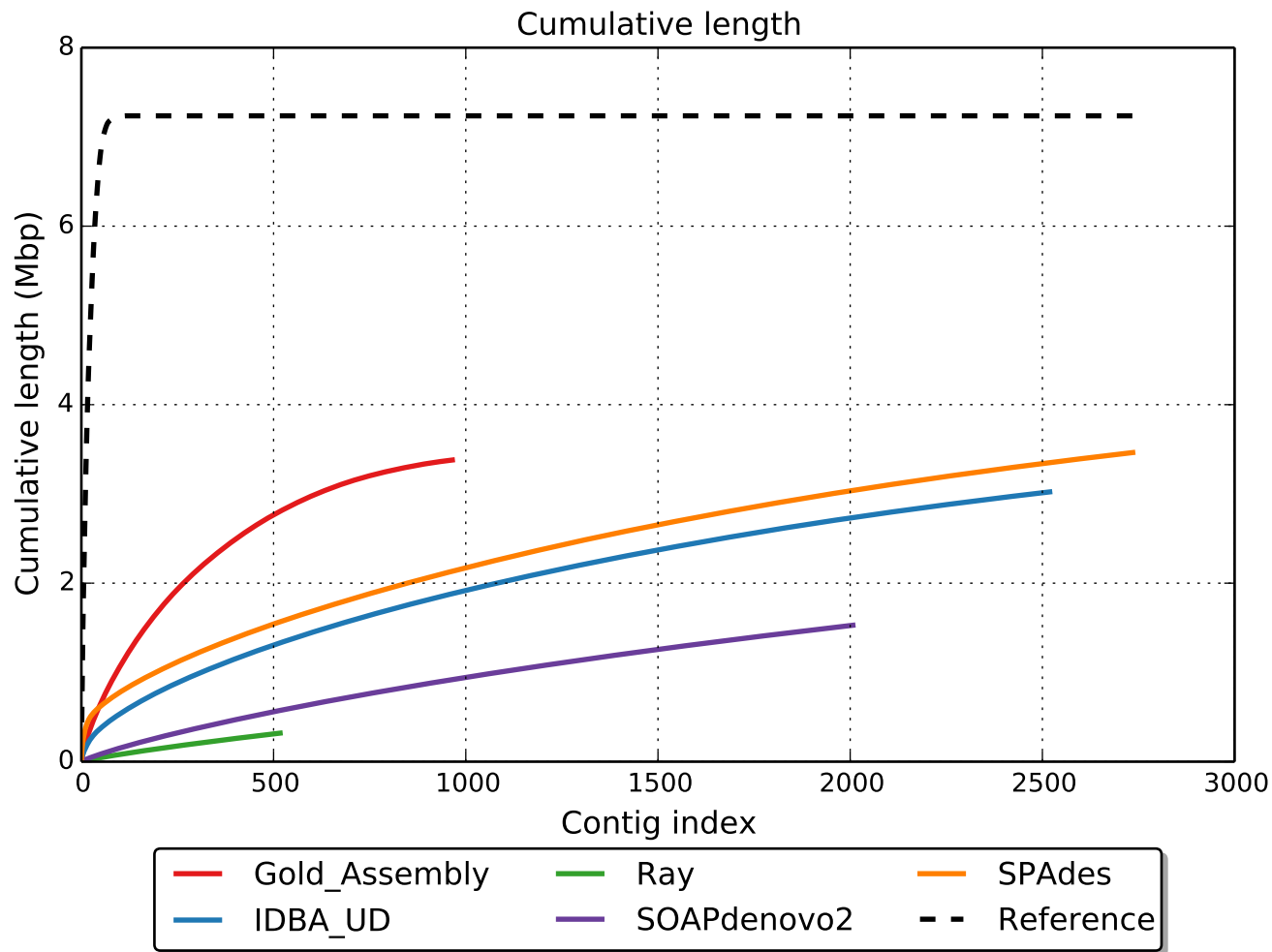
	Gold_Assembly	IDBA_UD	Ray	SOAPdenovo2	SPAdes
# fully unaligned contigs	0	0	0	0	0
Fully unaligned length	0	0	0	0	0
# partially unaligned contigs	1	243	1	8	221
# with misassembly	0	8	0	0	1
# both parts are significant	1	62	0	0	44
Partially unaligned length	682	437128	42	513	616430
# N's	51	0	0	1574	420

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).

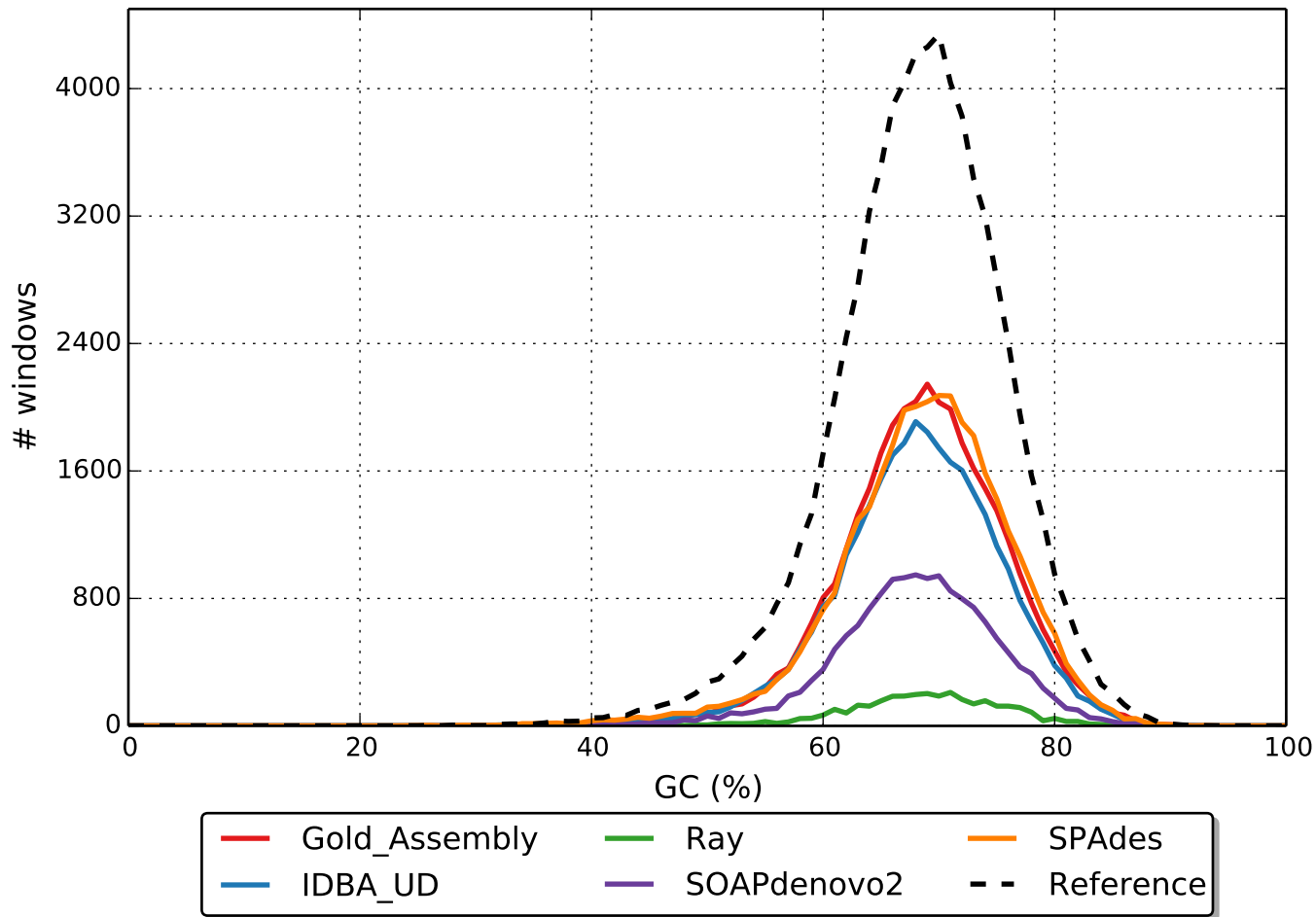


NGx





GC content



# Misassemblies

