Report

	Gold_Assembly	IDBA_UD	Ray	SOAPdenovo2	SPAdes
# contigs (>= 1000 bp)	1108	1541	12	340	1635
# contigs (>= 5000 bp)	358	7	0	0	9
# contigs (>= 10000 bp)	76	3	0	0	1
# contigs (>= 25000 bp)	2	0	0	0	0
# contigs (>= 50000 bp)	0	0	0	0	0
Total length (>= 1000 bp)	5004123	2585066	14086	426279	2650617
Total length (>= 5000 bp)	3047584	76315	0	0	66121
Total length (>= 10000 bp)	1076386	50986	0	0	12405
Total length (>= 25000 bp)	59875	0	0	0	0
Total length (>= 50000 bp)	0	0	0	0	0
# contigs	1329	3427	607	2383	3783
Largest contig	31717	21623	1574	3036	12405
Total length	5172507	3938496	377054	1815150	4182738
Reference length	5938083	5938083	5938083	5938083	5938083
GC (%)	68.41	68.31	68.81	68.21	68.30
Reference GC (%)	68.46	68.46	68.46	68.46	68.46
N50	5945	1278	604	761	1203
NG50	5171	853	-	-	888
N75	3357	858	545	613	835
NG75	2251	-	-	-	-
L50	274	994	262	892	1126
LG50	343	1957	-	-	1973
L75	559	1940	427	1559	2168
LG75	765	-	-	-	-
# misassemblies	97	356	0	6	174
# misassembled contigs	71	330	0	6	167
Misassembled contigs length	537661	492292	0	5794	252696
# local misassemblies	20	8	3	3	5
# structural variations	2	1	0	0	0
# unaligned contigs	0 + 15 part	0 + 397 part	0 + 5 part	0 + 35 part	0 + 628 part
Unaligned length	13401	228269	88	3947	156547
Genome fraction (%)	85.190	61.661	6.344	30.515	66.936
Duplication ratio	1.020	1.013	1.001	1.000	1.013
# N's per 100 kbp	2.38	0.00	52.51	112.06	0.00
# mismatches per 100 kbp	20.36	223.13	18.05	311.92	622.66
# indels per 100 kbp	11.33	11.42	6.64	51.21	16.61
Largest alignment	24864	5193	1574	3036	6073
NA50	5516	1062	604	757	1113
NGA50	4865	708	-	-	812
NA75	3176	715	545	610	754
NGA75	2100	-	-	-	-
LA50	294	1194	262	896	1246
LGA50	368	2346	-	-	2169
LA75	599	2325	427	1565	2383
LGA75	821	-	-	-	-

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).
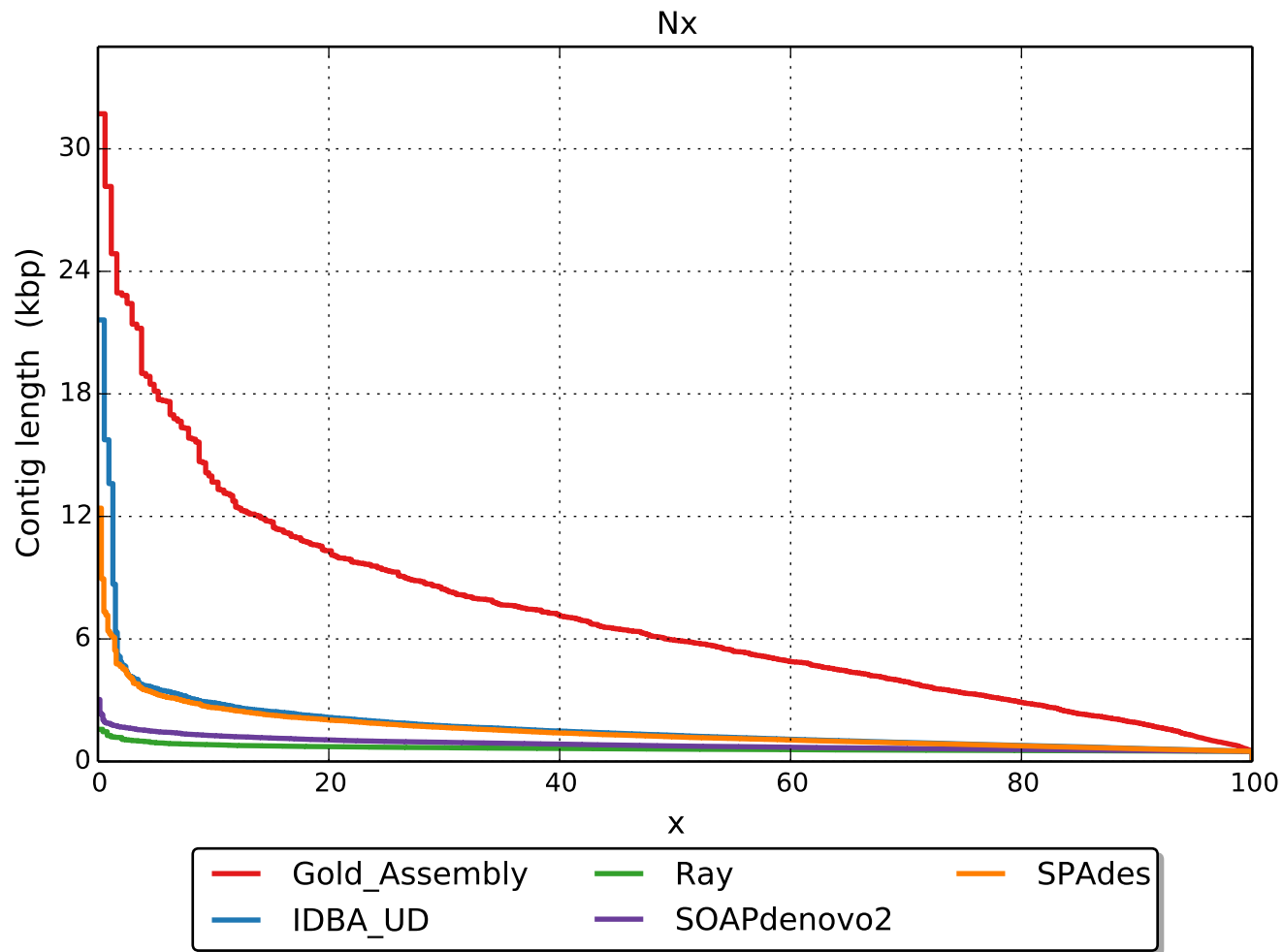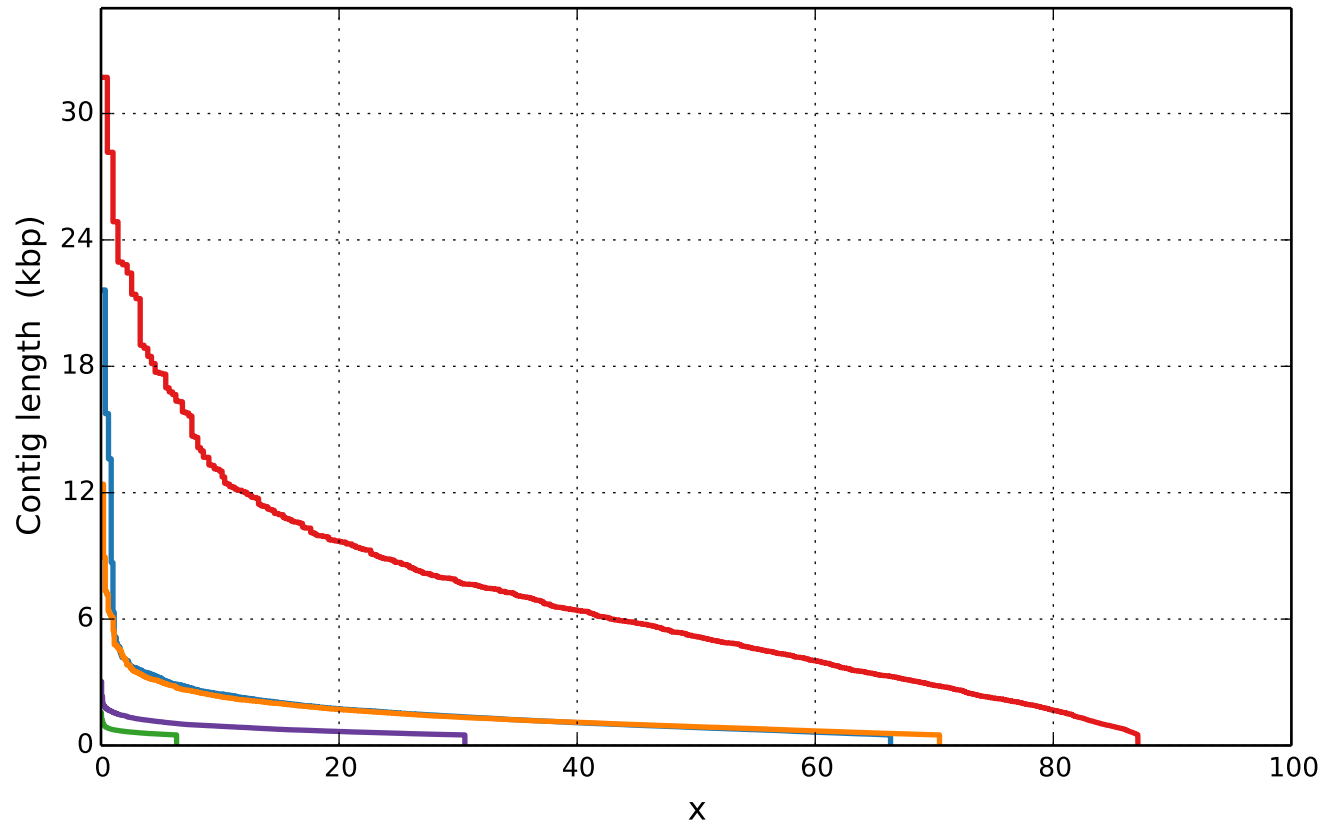
Misassemblies report

	Gold_Assembly	IDBA_UD	Ray	SOAPdenovo2	SPAdes
# misassemblies	97	356	0	6	174
# relocations	50	56	0	0	38
# translocations	36	299	0	6	136
# inversions	11	1	0	0	0
# possibly misassembled contigs	9	56	0	0	29
# misassembled contigs	71	330	0	6	167
Misassembled contigs length	537661	492292	0	5794	252696
# local misassemblies	20	8	3	3	5
# structural variations	2	1	0	0	0
# mismatches	1030	8170	68	5652	24749
# indels	573	418	25	928	660
# short indels	241	262	14	414	480
# long indels	332	156	11	514	180
Indels length	6476	2415	153	6928	3269

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).
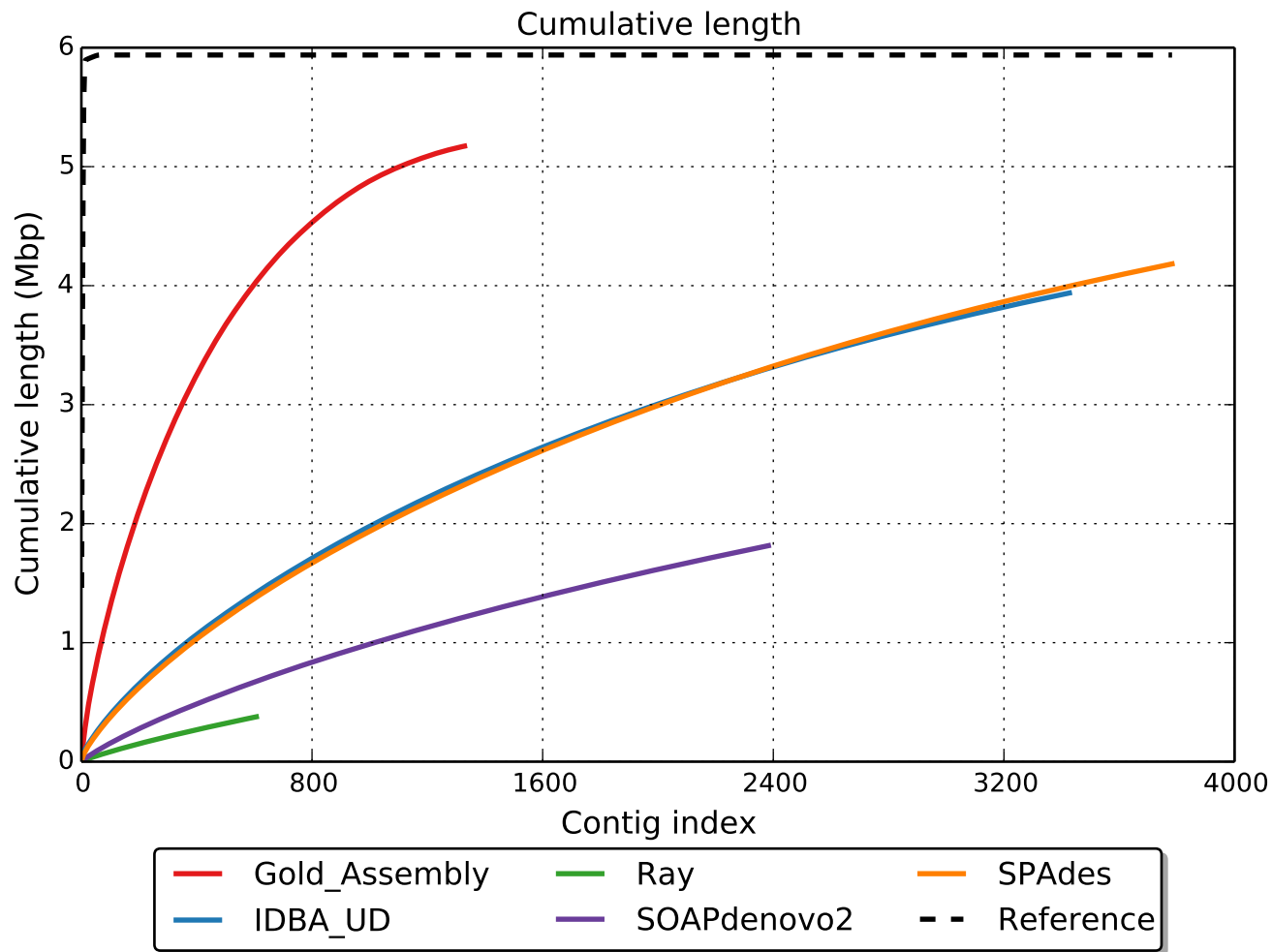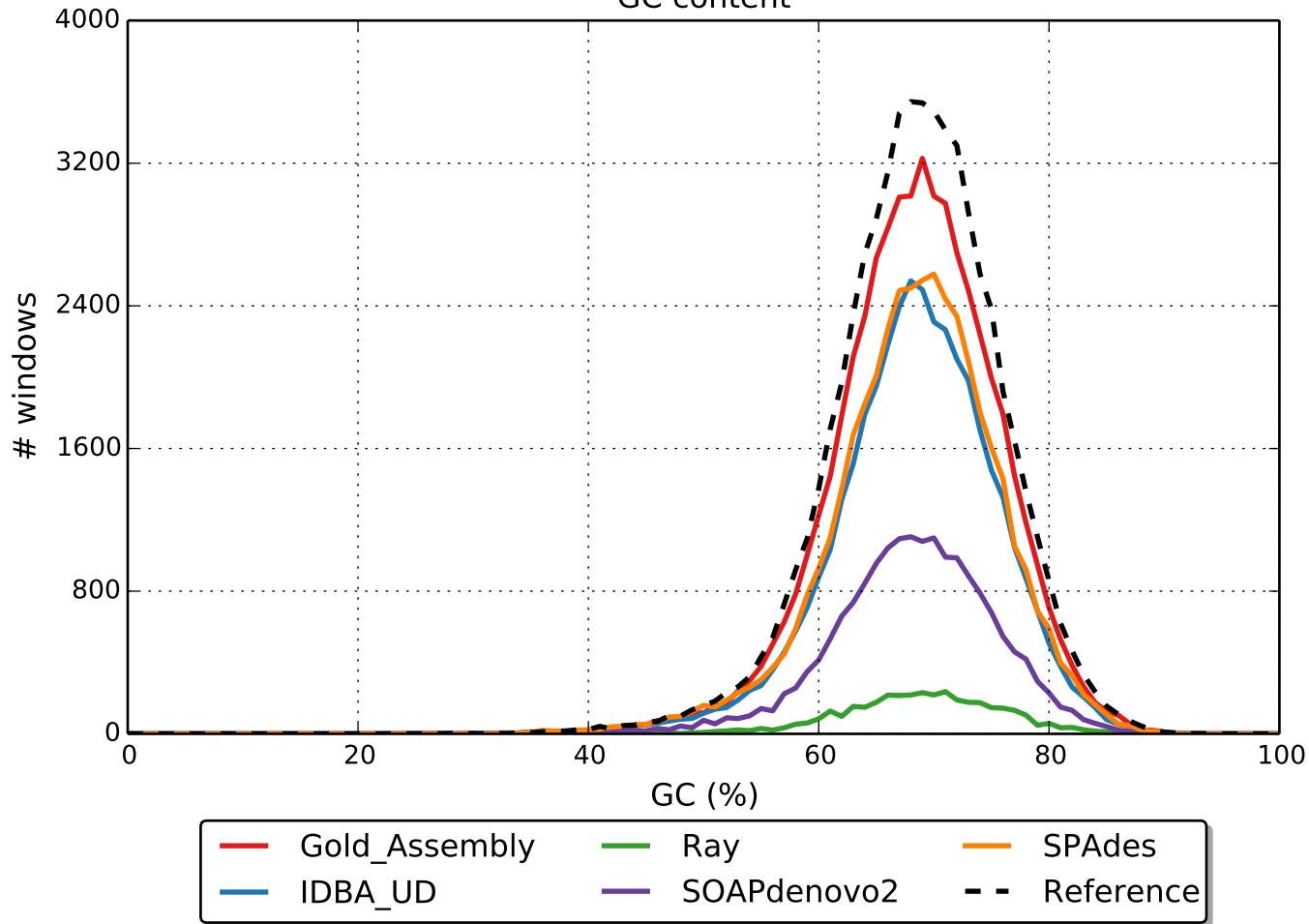
Unaligned report

	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	15	397	5	35	628
# with misassembly	1	7	0	0	0
# both parts are significant	5	54	0	0	29
Partially unaligned length	13401	228269	88	3947	156547
# N's	123	0	198	2034	0

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).
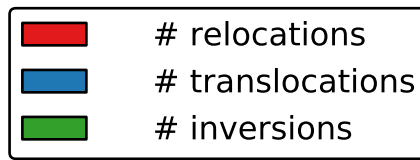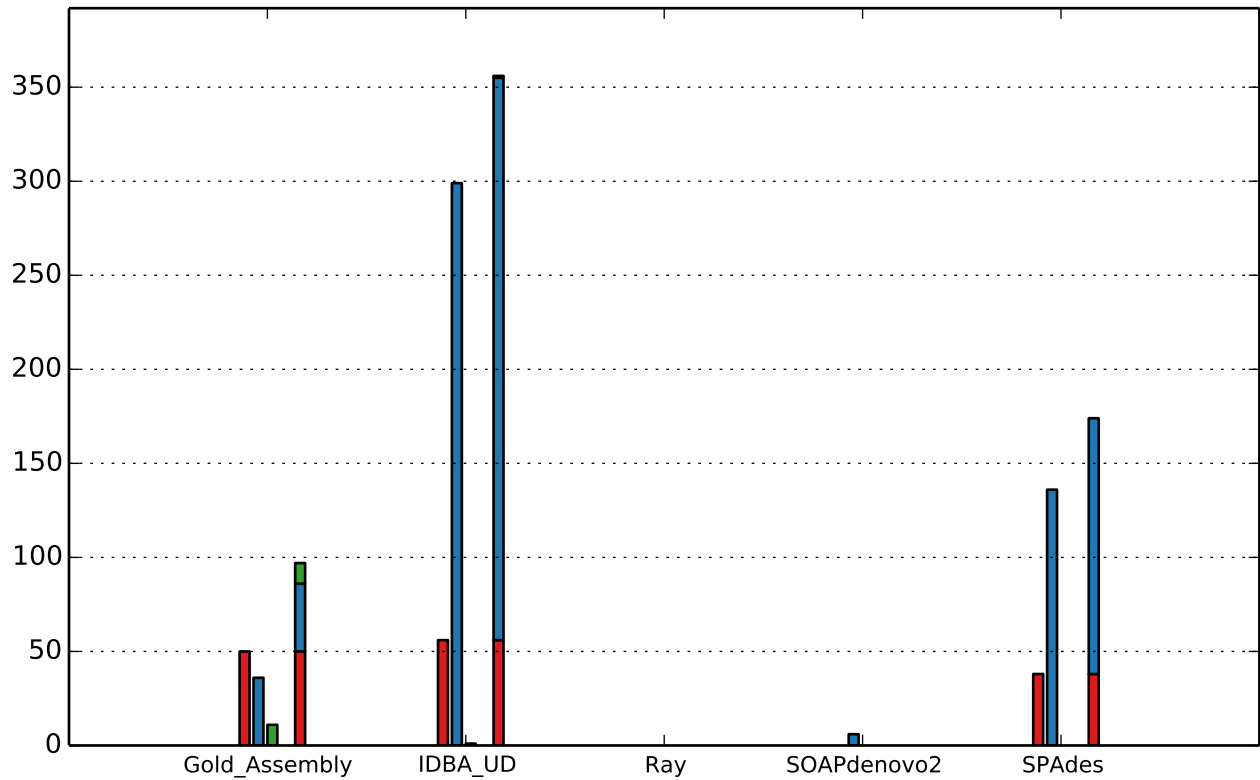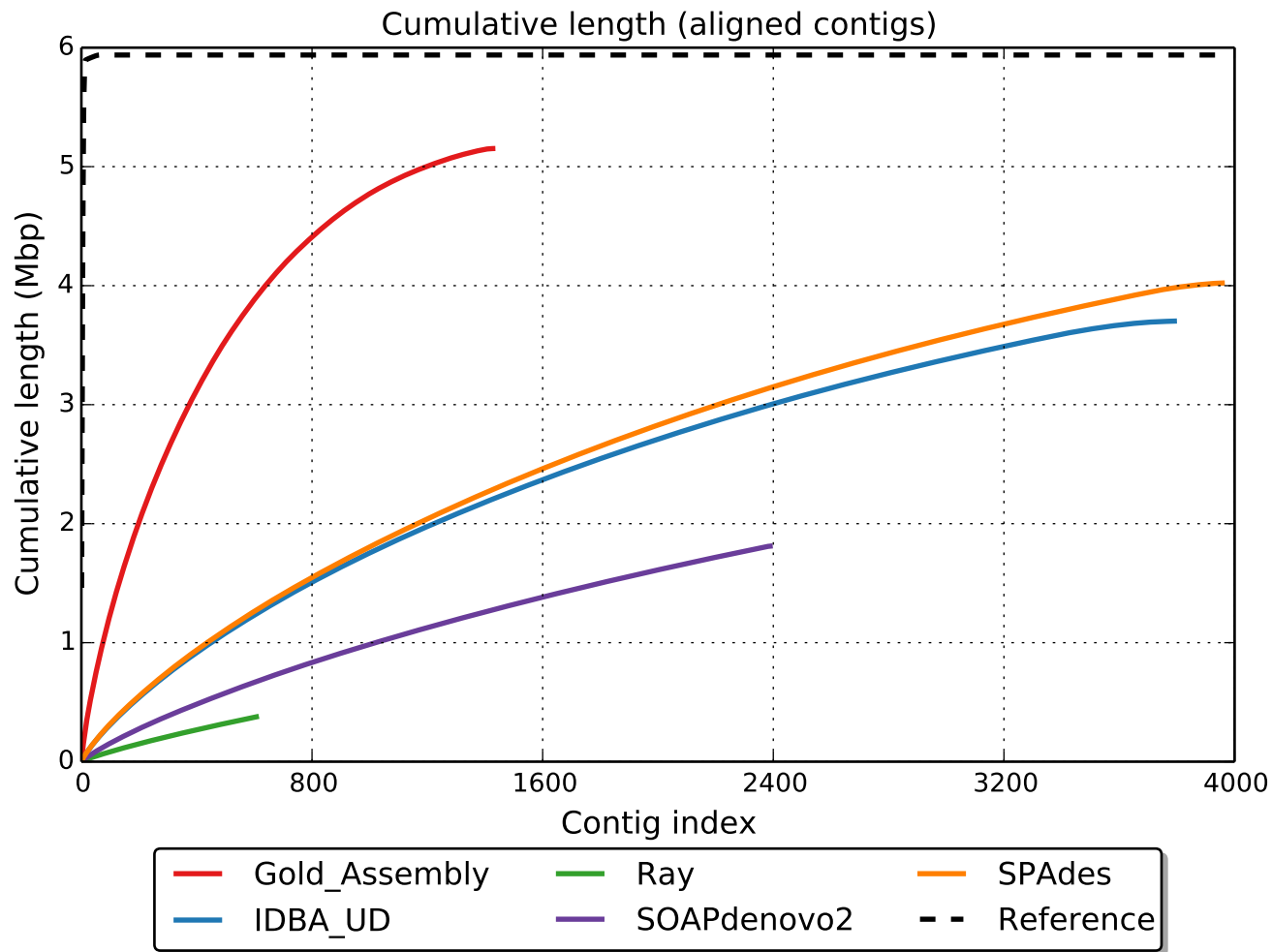
Nx

Contig length (kbp)

x

Gold_Assembly
IDBA_UD
Ray
SOAPdenovo2
SPAdes

NGx
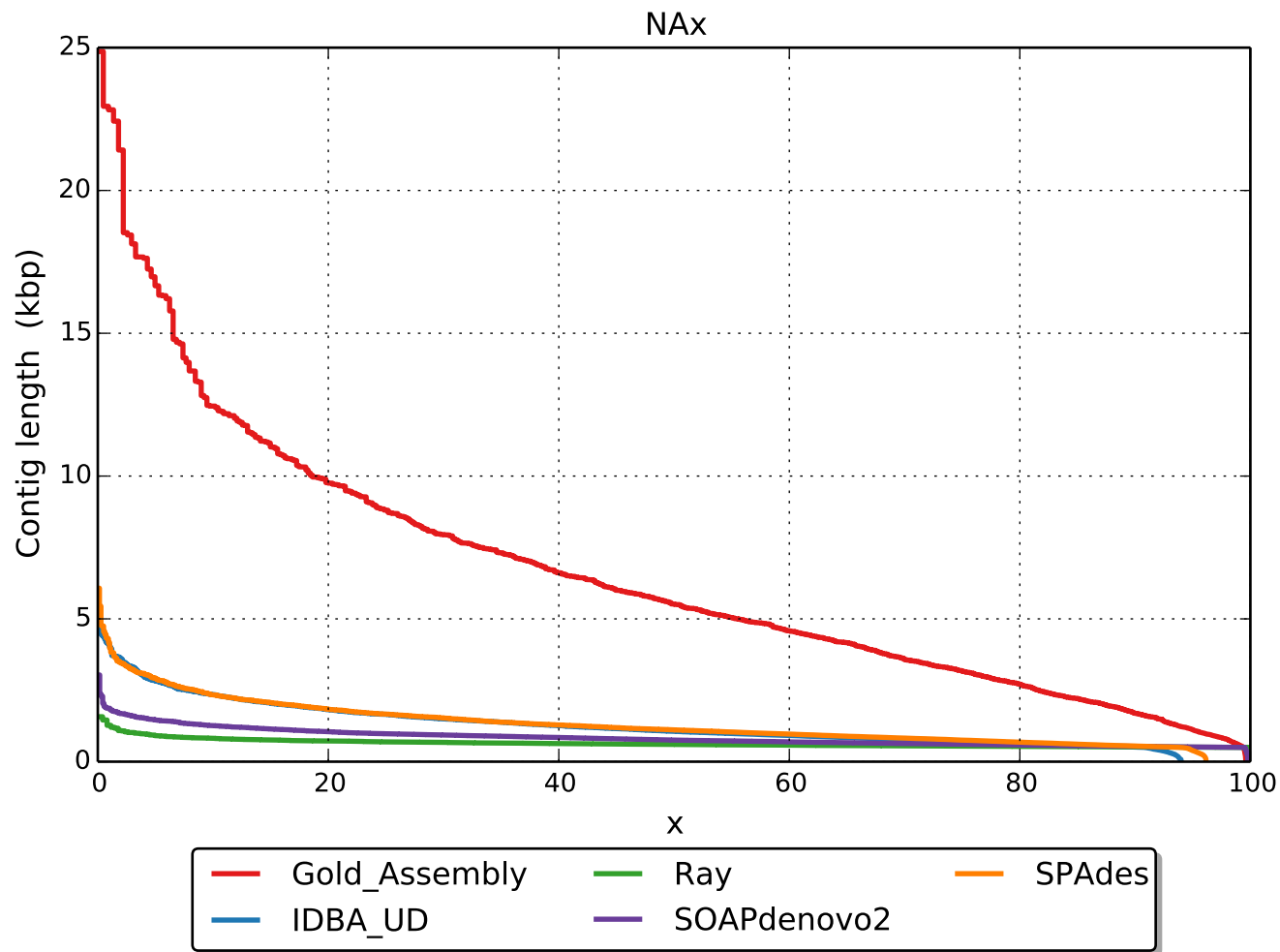
GC content

Misassemblies

Cumulative length (aligned contigs)

Genome fraction, %

Legend: Gold_Assembly, IDBA_UD, Ray, SOAPdenovo2, SPAdes