

Report

	Gold_Assembly	IDBA_UD	Ray	SOAPdenovo2	SPAdes
# contigs (>= 1000 bp)	997	184	524	631	203
# contigs (>= 5000 bp)	297	130	0	91	138
# contigs (>= 10000 bp)	62	85	0	9	79
# contigs (>= 25000 bp)	0	19	0	0	15
# contigs (>= 50000 bp)	0	2	0	0	0
Total length (>= 1000 bp)	4221032	2173042	743048	1955578	2163655
Total length (>= 5000 bp)	2451790	2032097	0	675653	1977904
Total length (>= 10000 bp)	811562	1706210	0	115123	1531559
Total length (>= 25000 bp)	0	685506	0	0	494606
Total length (>= 50000 bp)	0	141231	0	0	0
# contigs	1152	204	1591	823	220
Largest contig	19941	89947	3356	17581	48098
Total length	4334734	2187288	1495852	2095828	2176645
Reference length	2219029	2219029	2219029	2219029	2219029
GC (%)	38.76	38.78	38.77	38.76	38.77
Reference GC (%)	38.77	38.77	38.77	38.77	38.77
N50	5646	16681	994	3641	16681
NG50	8961	16491	720	3471	15987
N75	3170	10512	714	2083	8969
NG75	7119	10224	-	1865	8624
L50	244	40	529	179	44
LG50	94	41	959	197	46
L75	499	79	976	373	90
LG75	164	81	-	420	94
# misassemblies	3	6	1	0	2
# misassembled contigs	3	5	1	0	2
Misassembled contigs length	6737	52613	2434	0	3771
# local misassemblies	0	1	14	1	4
# structural variations	0	0	0	0	0
# unaligned contigs	0 + 1 part	0 + 7 part	0 + 0 part	0 + 2 part	0 + 6 part
Unaligned length	346	7836	0	473	7649
Genome fraction (%)	99.900	97.755	66.223	94.165	97.439
Duplication ratio	1.955	1.005	1.018	1.003	1.003
# N's per 100 kbp	0.00	0.00	43.05	53.63	0.05
# mismatches per 100 kbp	0.09	32.50	2.04	85.19	101.89
# indels per 100 kbp	1.26	1.61	0.27	18.14	0.37
Largest alignment	19941	89947	3356	17581	48098
NA50	5646	16491	990	3641	16681
NGA50	8961	16398	719	3471	15987
NA75	3142	10109	713	2083	8852
NGA75	7119	10001	-	1865	8588
LA50	244	40	531	179	44
LGA50	94	41	961	197	46
LA75	499	81	978	373	90
LGA75	164	83	-	420	94

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

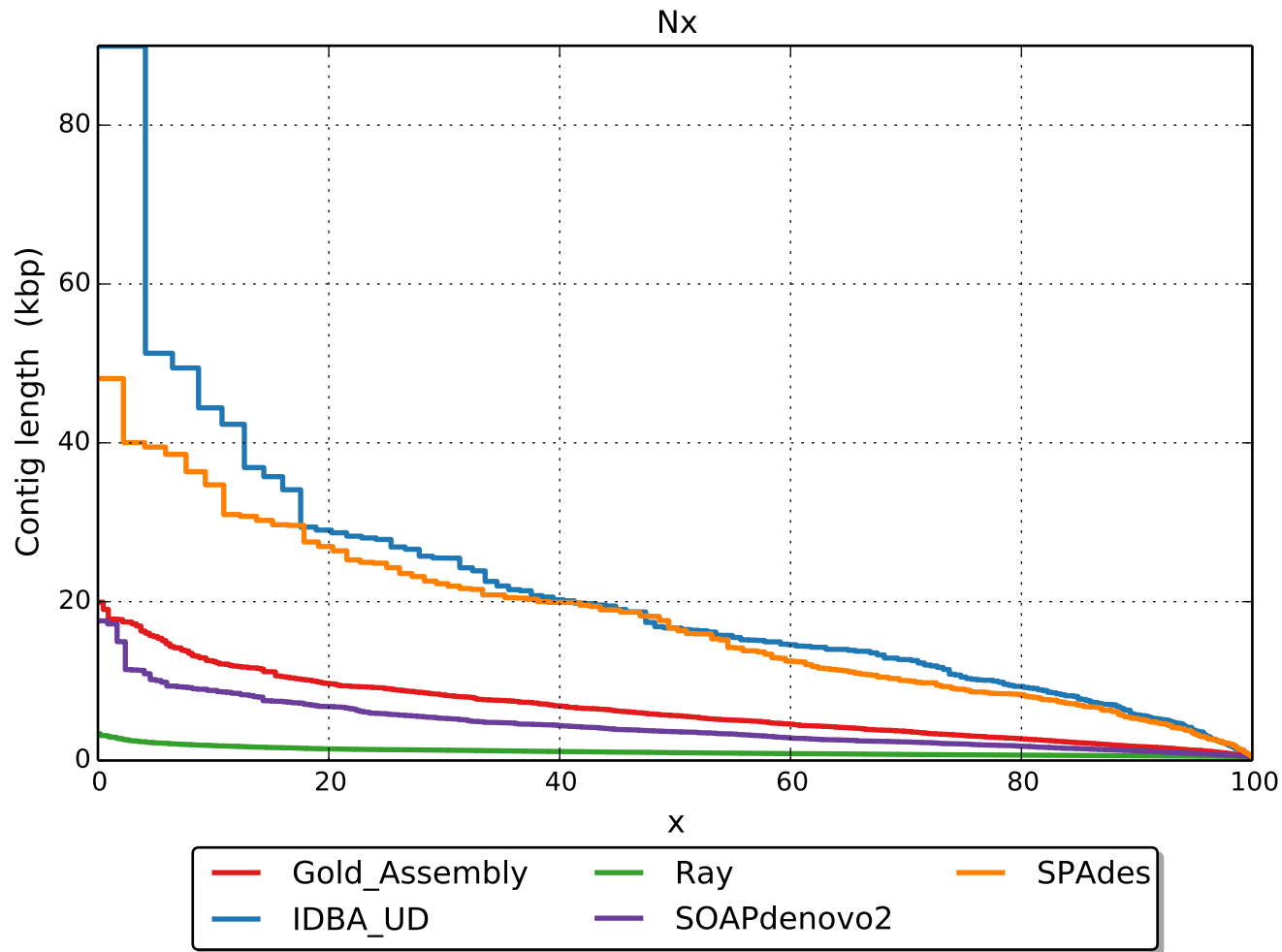
	Gold_Assembly	IDBA_UD	Ray	SOAPdenovo2	SPAdes
# misassemblies	3	6	1	0	2
# relocations	3	6	1	0	2
# translocations	0	0	0	0	0
# inversions	0	0	0	0	0
# possibly misassembled contigs	0	7	0	0	2
# misassembled contigs	3	5	1	0	2
Misassembled contigs length	6737	52613	2434	0	3771
# local misassemblies	0	1	14	1	4
# structural variations	0	0	0	0	0
# mismatches	2	705	30	1780	2203
# indels	28	35	4	379	8
# short indels	28	33	4	172	8
# long indels	0	2	0	207	0
Indels length	40	119	7	2966	10

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).

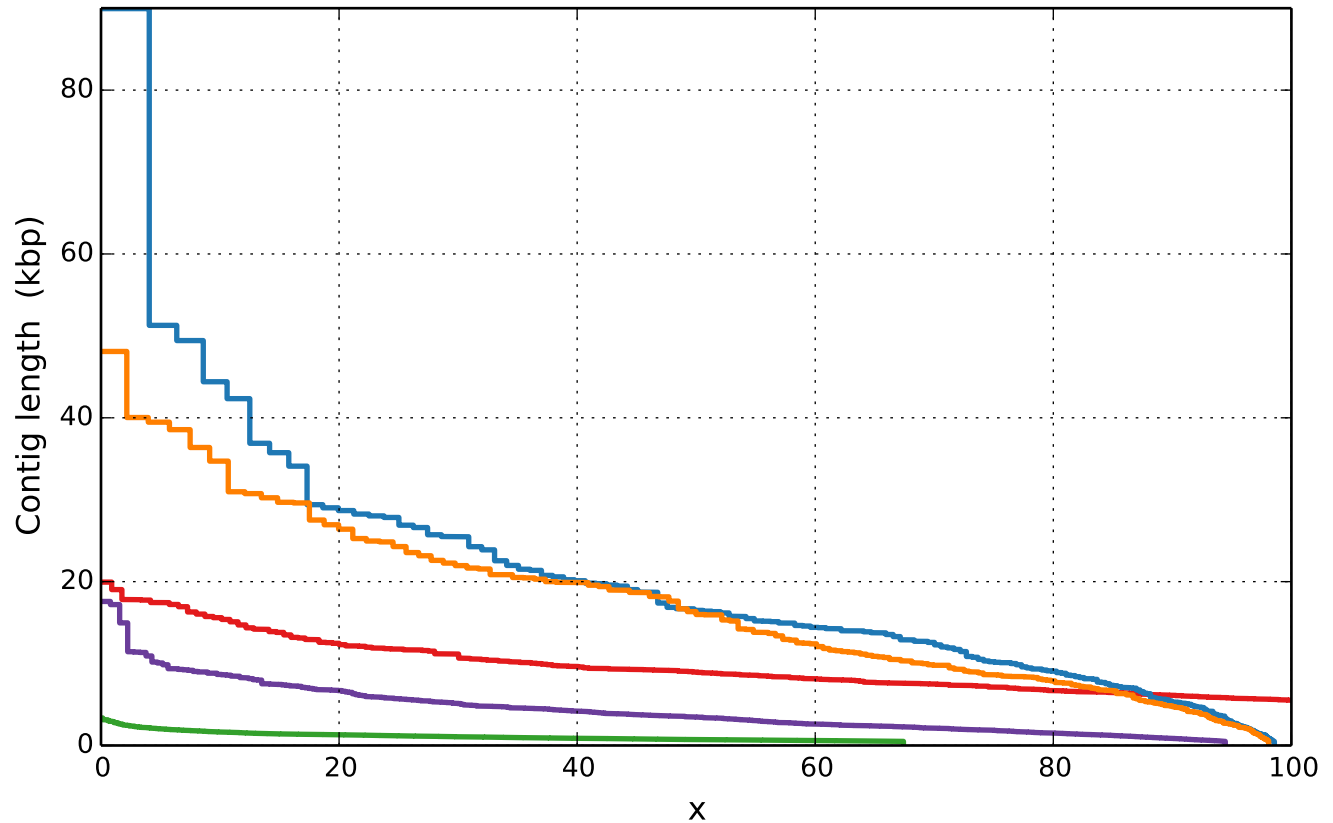
Unaligned report

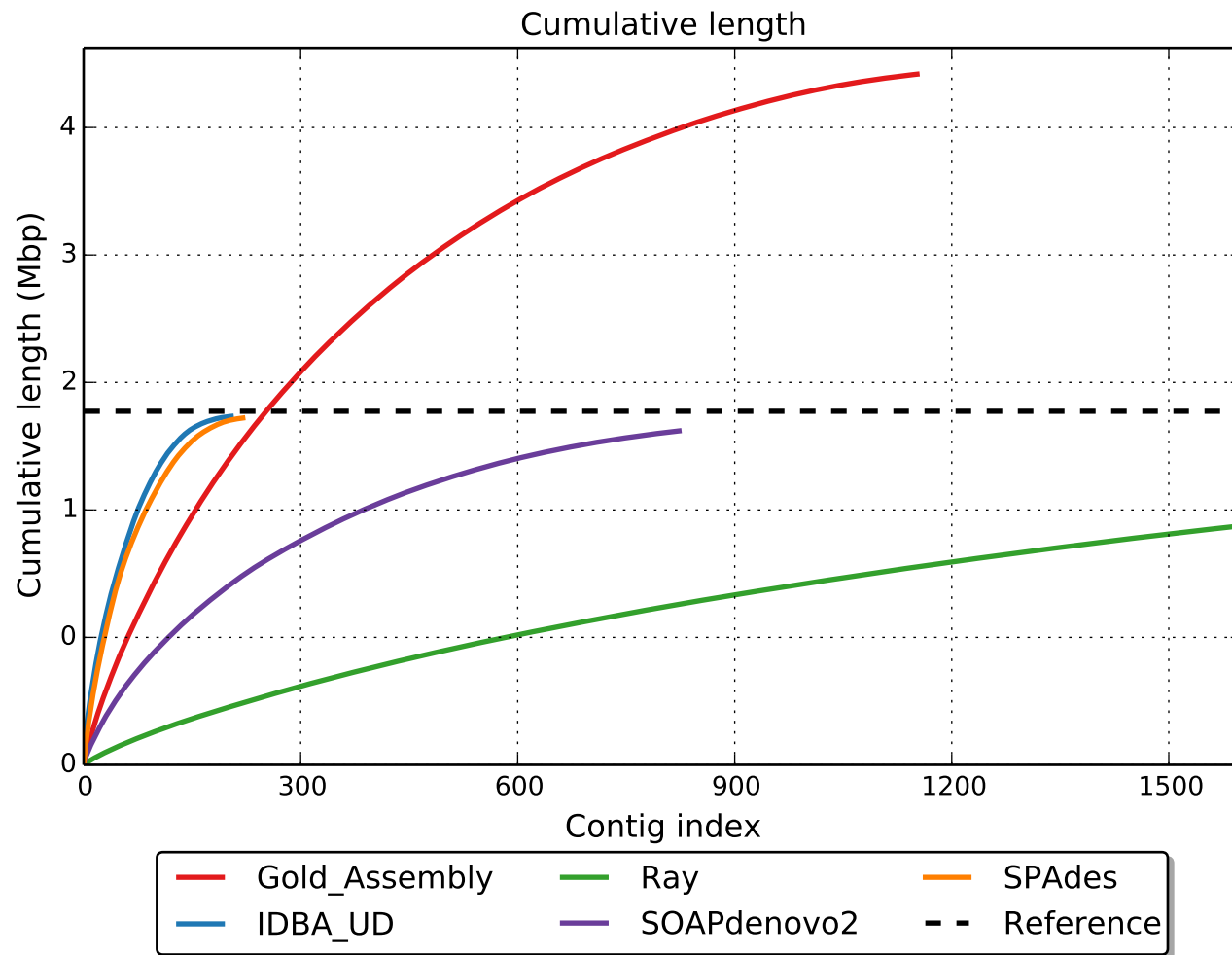
	Gold_Assembly	IDBA_UD	Ray	SOAPdenovo2	SPAdes
# fully unaligned contigs	0	0	0	0	0
Fully unaligned length	0	0	0	0	0
# partially unaligned contigs	1	7	0	2	6
# with misassembly	0	0	0	0	0
# both parts are significant	0	4	0	0	2
Partially unaligned length	346	7836	0	473	7649
# N's	0	0	644	1124	1

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).

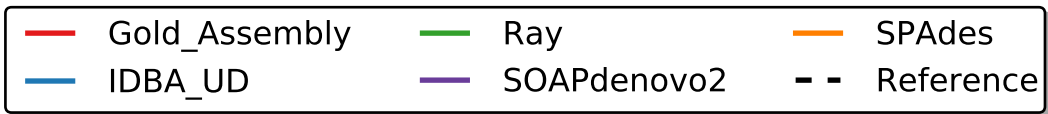
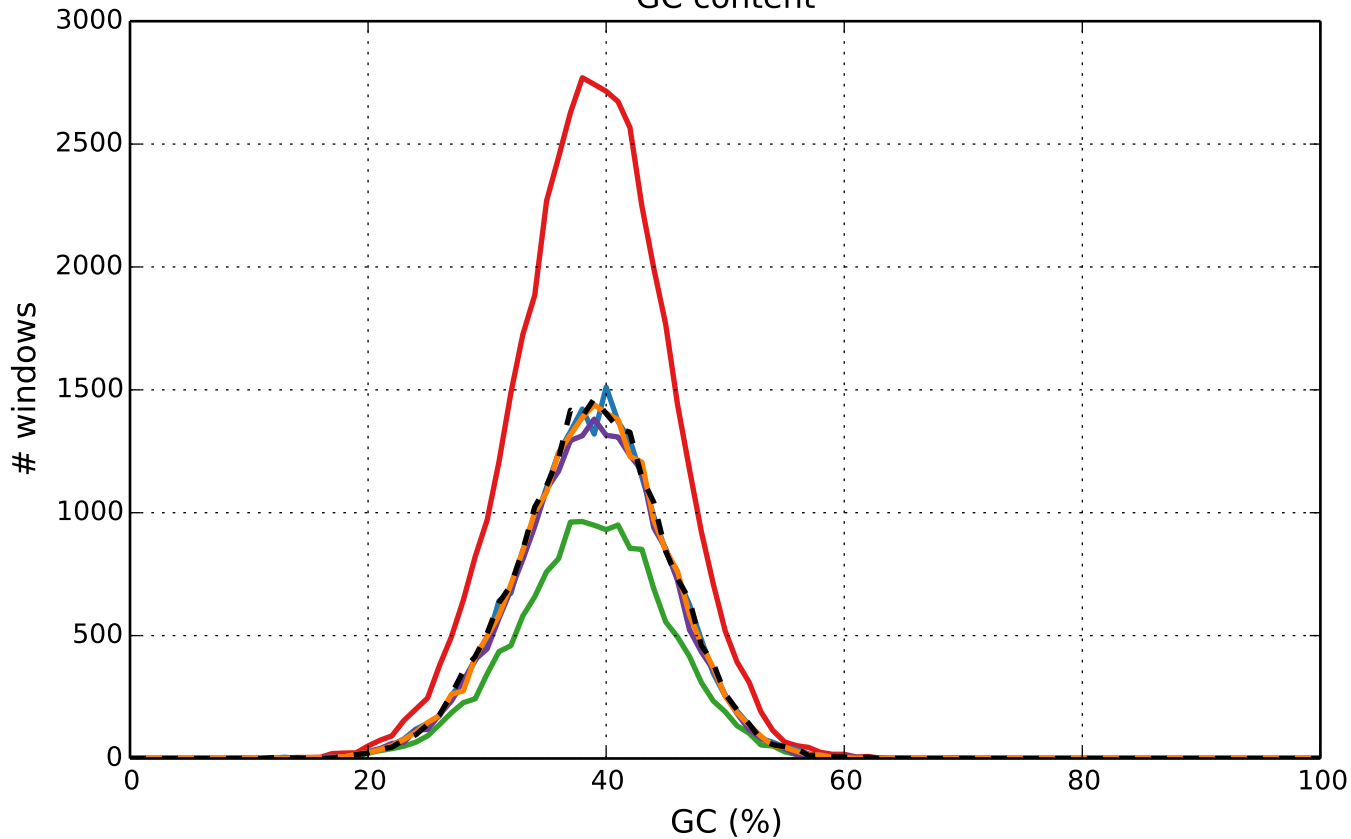


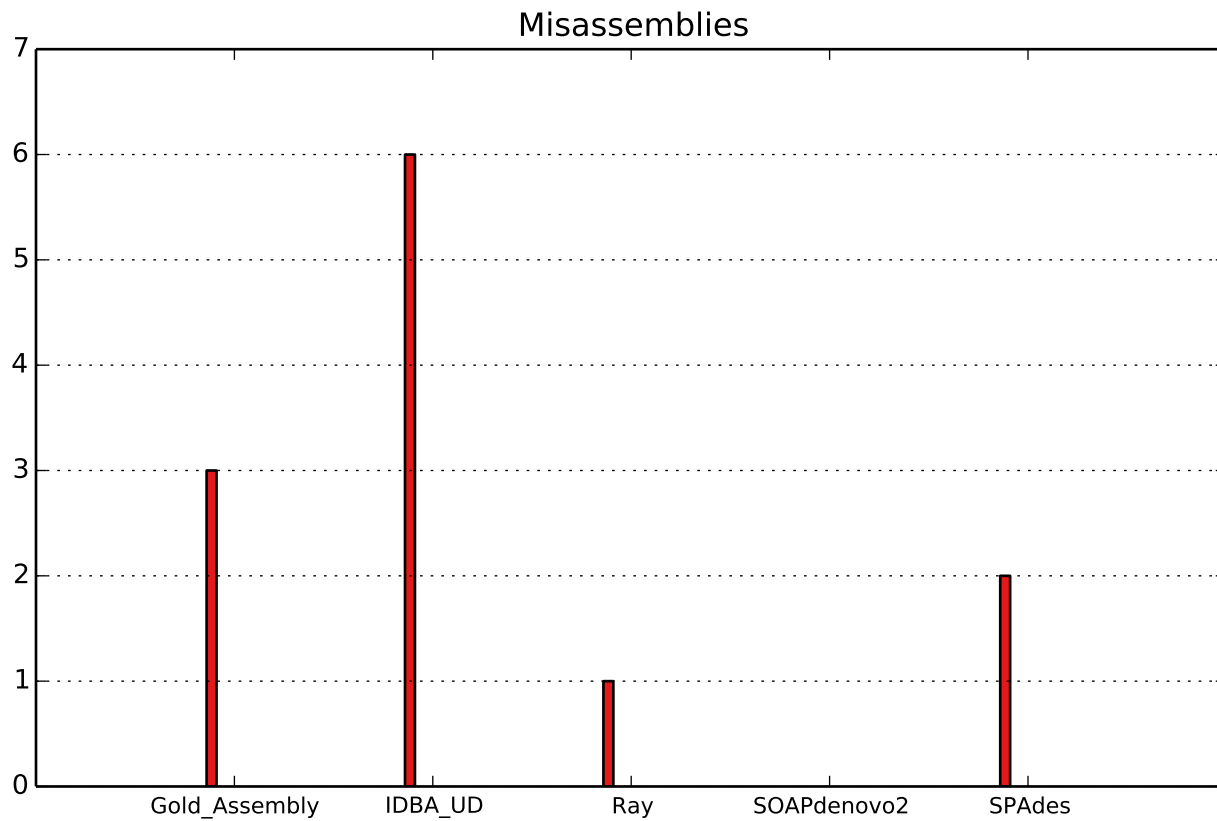
NGx



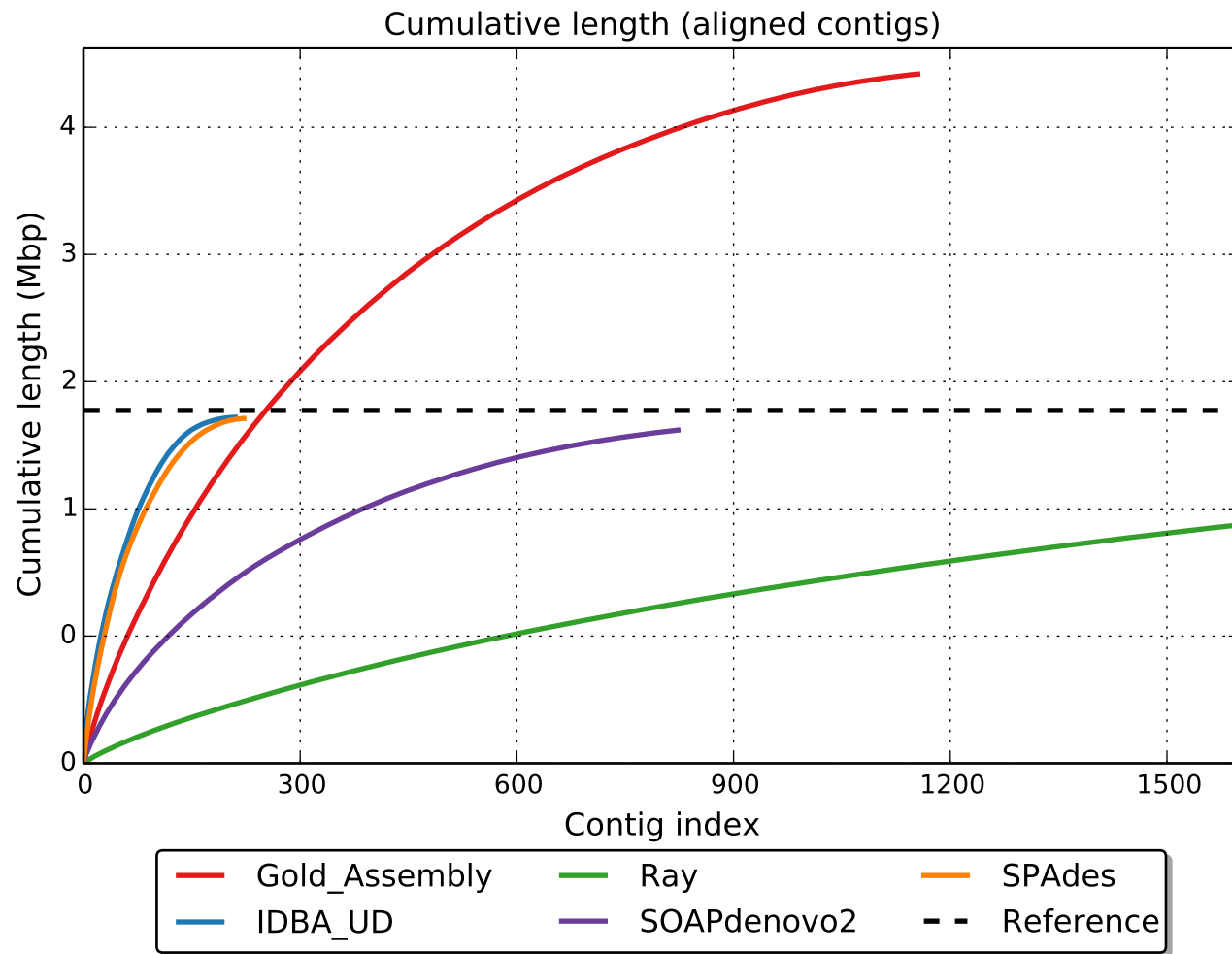


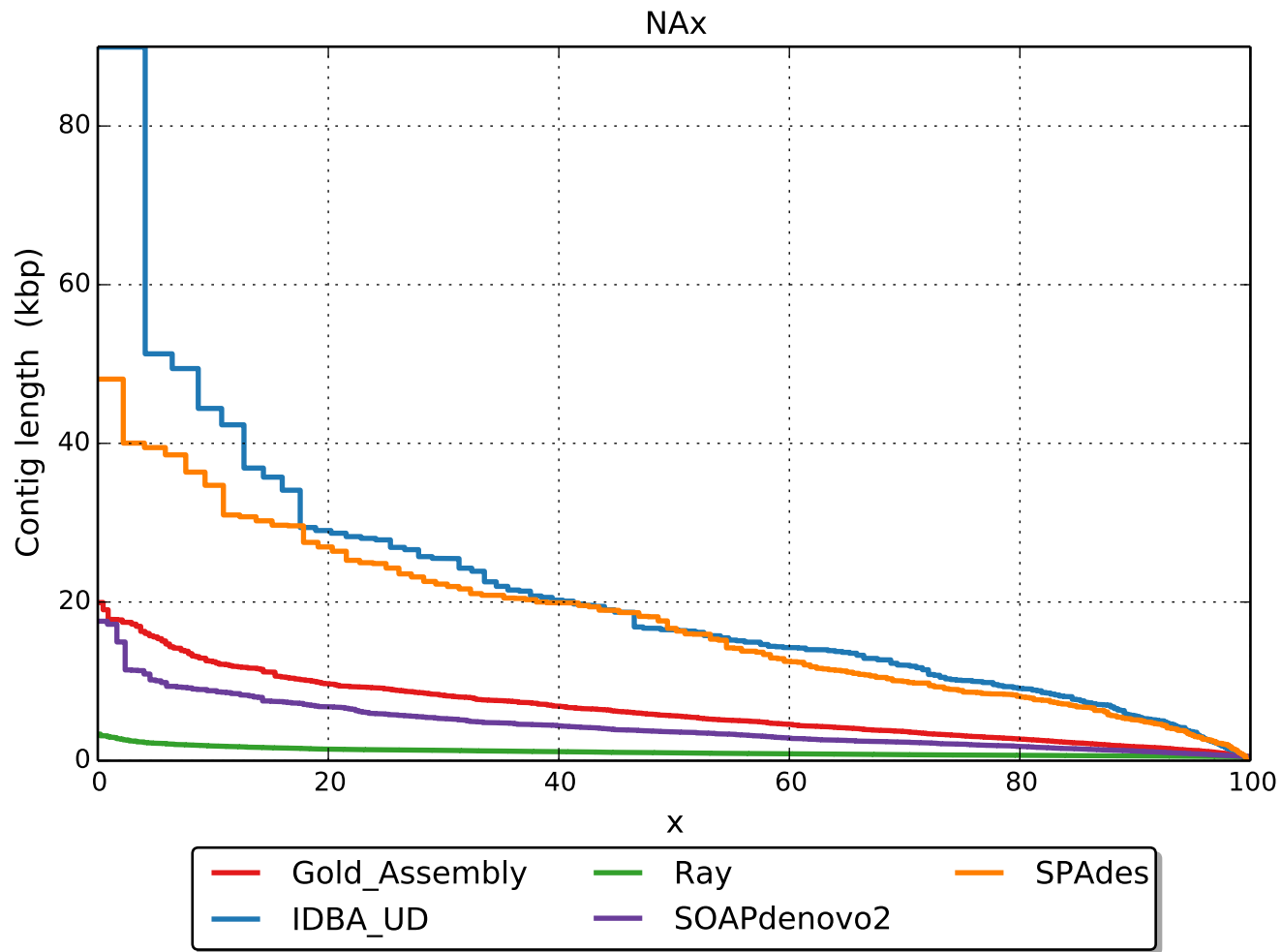
GC content





 # relocations





NGAx

