

Report

	Gold_Assembly	IDBA_UD	Ray	SOAPdenovo2	SPAdes
# contigs (>= 1000 bp)	372	1171	61	783	1277
# contigs (>= 5000 bp)	228	62	0	0	53
# contigs (>= 10000 bp)	126	6	0	0	3
# contigs (>= 25000 bp)	33	0	0	0	0
# contigs (>= 50000 bp)	1	0	0	0	0
Total length (>= 1000 bp)	3623092	2801429	71344	1105843	2891889
Total length (>= 5000 bp)	3246574	433679	0	0	363078
Total length (>= 10000 bp)	2512192	82478	0	0	39010
Total length (>= 25000 bp)	1106480	0	0	0	0
Total length (>= 50000 bp)	74984	0	0	0	0
# contigs	403	1737	1103	2453	1929
Largest contig	74984	21741	1591	4028	16031
Total length	3644954	3219139	742467	2283096	3369808
Reference length	3664641	3664641	3664641	3664641	3664641
GC (%)	68.14	67.92	68.29	68.02	67.99
Reference GC (%)	68.12	68.12	68.12	68.12	68.12
N50	15743	2395	658	984	2207
NG50	15645	2121	-	669	2032
N75	8559	1421	571	719	1338
NG75	8271	1068	-	-	1130
L50	71	418	452	820	473
LG50	72	518	-	1672	542
L75	150	851	755	1499	963
LG75	152	1120	-	-	1143
# misassemblies	0	72	0	0	26
# misassembled contigs	0	70	0	0	24
Misassembled contigs length	0	218852	0	0	89126
# local misassemblies	0	9	1	2	2
# structural variations	0	0	0	0	0
# unaligned contigs	0 + 0 part	0 + 97 part	0 + 1 part	0 + 8 part	0 + 181 part
Unaligned length	0	63023	38	279	40374
Genome fraction (%)	99.463	85.261	20.236	62.247	89.783
Duplication ratio	1.000	1.010	1.001	1.001	1.012
# N's per 100 kbp	0.00	0.00	3.23	124.70	0.00
# mismatches per 100 kbp	0.00	117.14	0.67	232.52	409.15
# indels per 100 kbp	0.00	1.41	0.00	42.65	4.19
Largest alignment	74984	11230	1591	4028	16031
NA50	15743	2217	658	983	2146
NGA50	15645	1996	-	668	1933
NA75	8559	1313	570	719	1278
NGA75	8271	964	-	-	1071
LA50	71	458	453	820	489
LGA50	72	565	-	1673	561
LA75	150	926	756	1500	998
LGA75	152	1221	-	-	1187

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

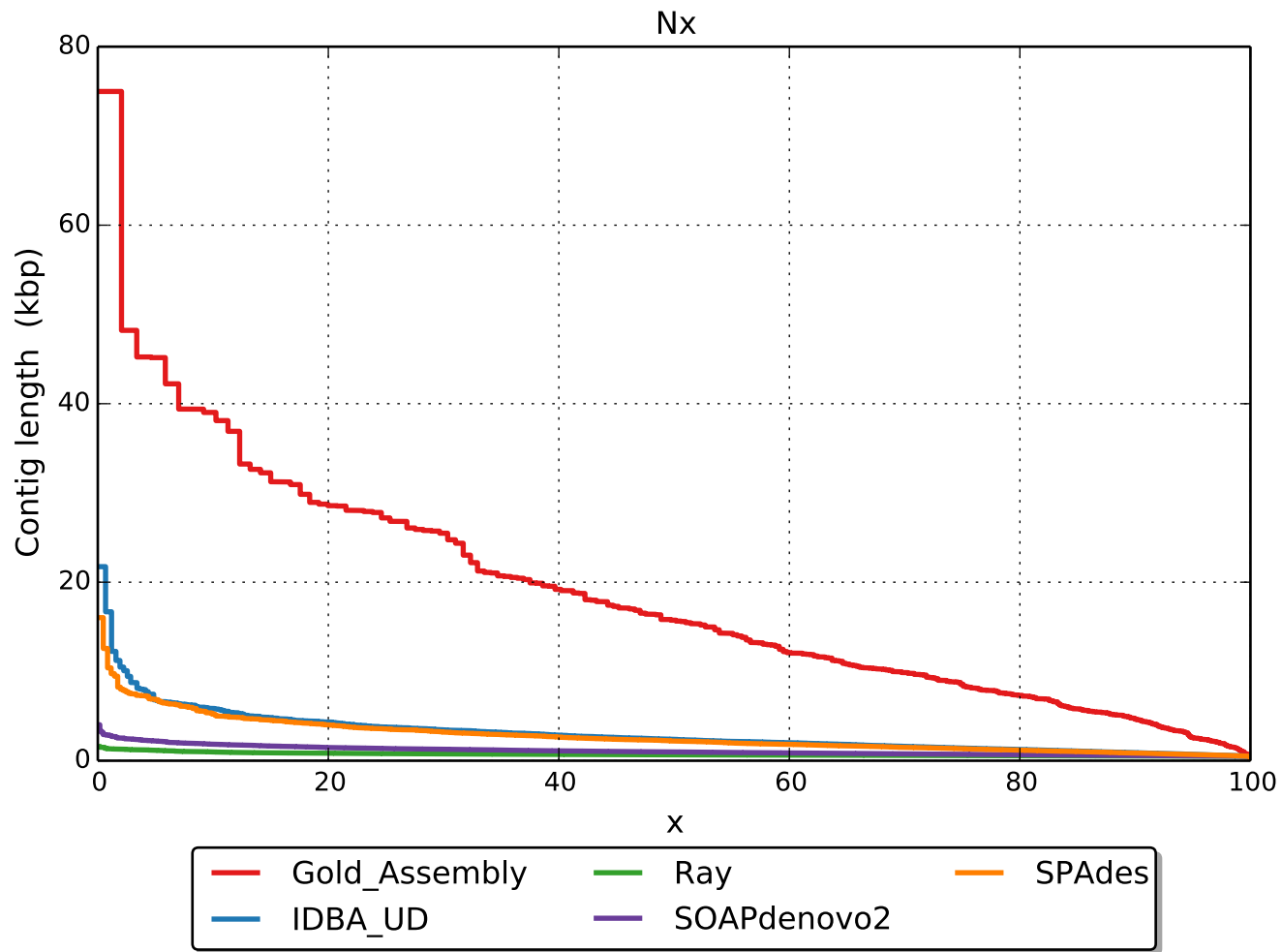
	Gold_Assembly	IDBA_UD	Ray	SOAPdenovo2	SPAdes
# misassemblies	0	72	0	0	26
# relocations	0	9	0	0	6
# translocations	0	63	0	0	20
# inversions	0	0	0	0	0
# possibly misassembled contigs	0	8	0	0	7
# misassembled contigs	0	70	0	0	24
Misassembled contigs length	0	218852	0	0	89126
# local misassemblies	0	9	1	2	2
# structural variations	0	0	0	0	0
# mismatches	0	3660	5	5304	13462
# indels	0	44	0	973	138
# short indels	0	38	0	420	116
# long indels	0	6	0	553	22
Indels length	0	258	0	7850	897

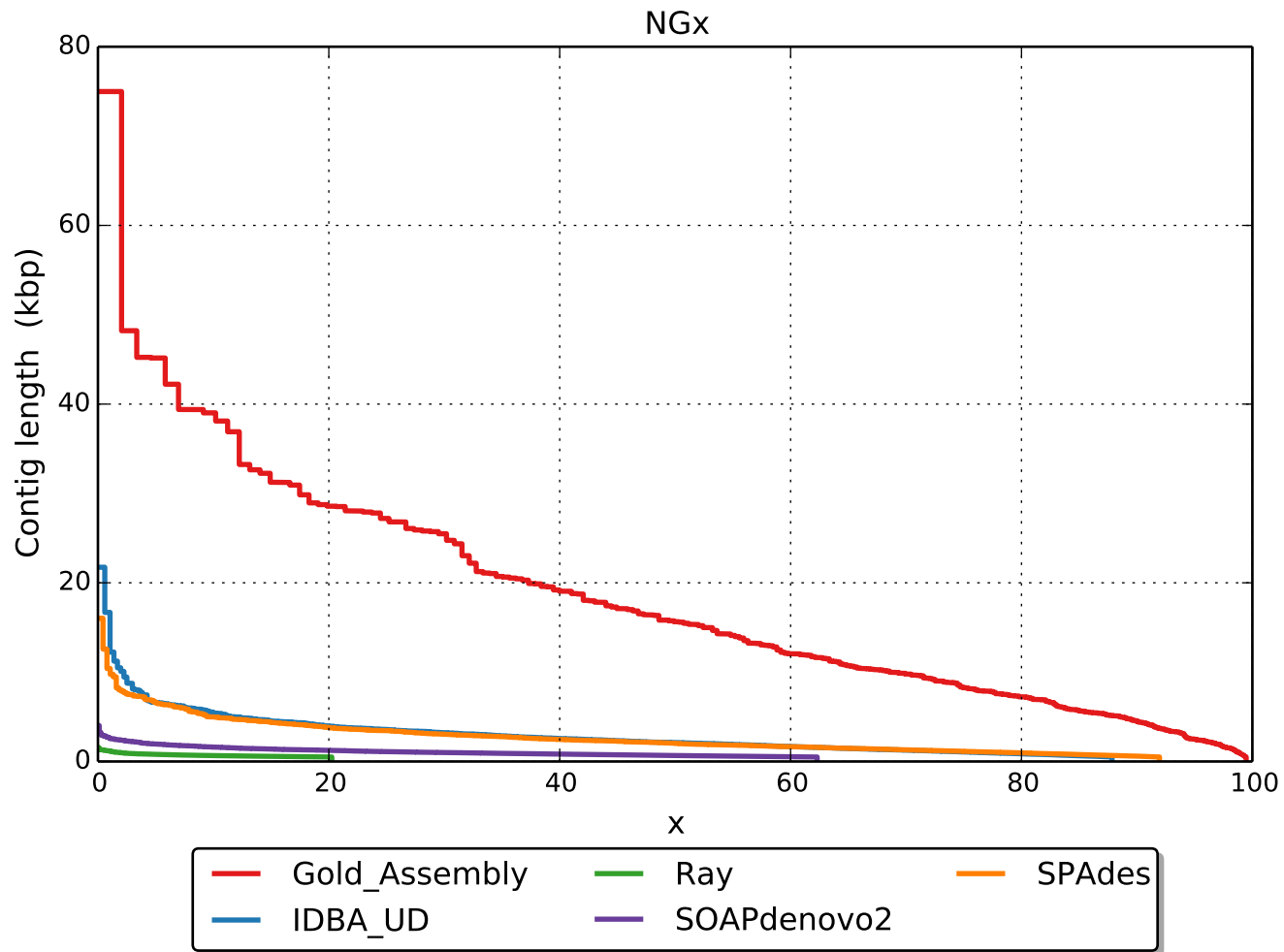
All statistics are based on contigs of size ≥ 500 bp, unless otherwise noted (e.g., "# contigs (≥ 0 bp)" and "Total length (≥ 0 bp)" include all contigs).

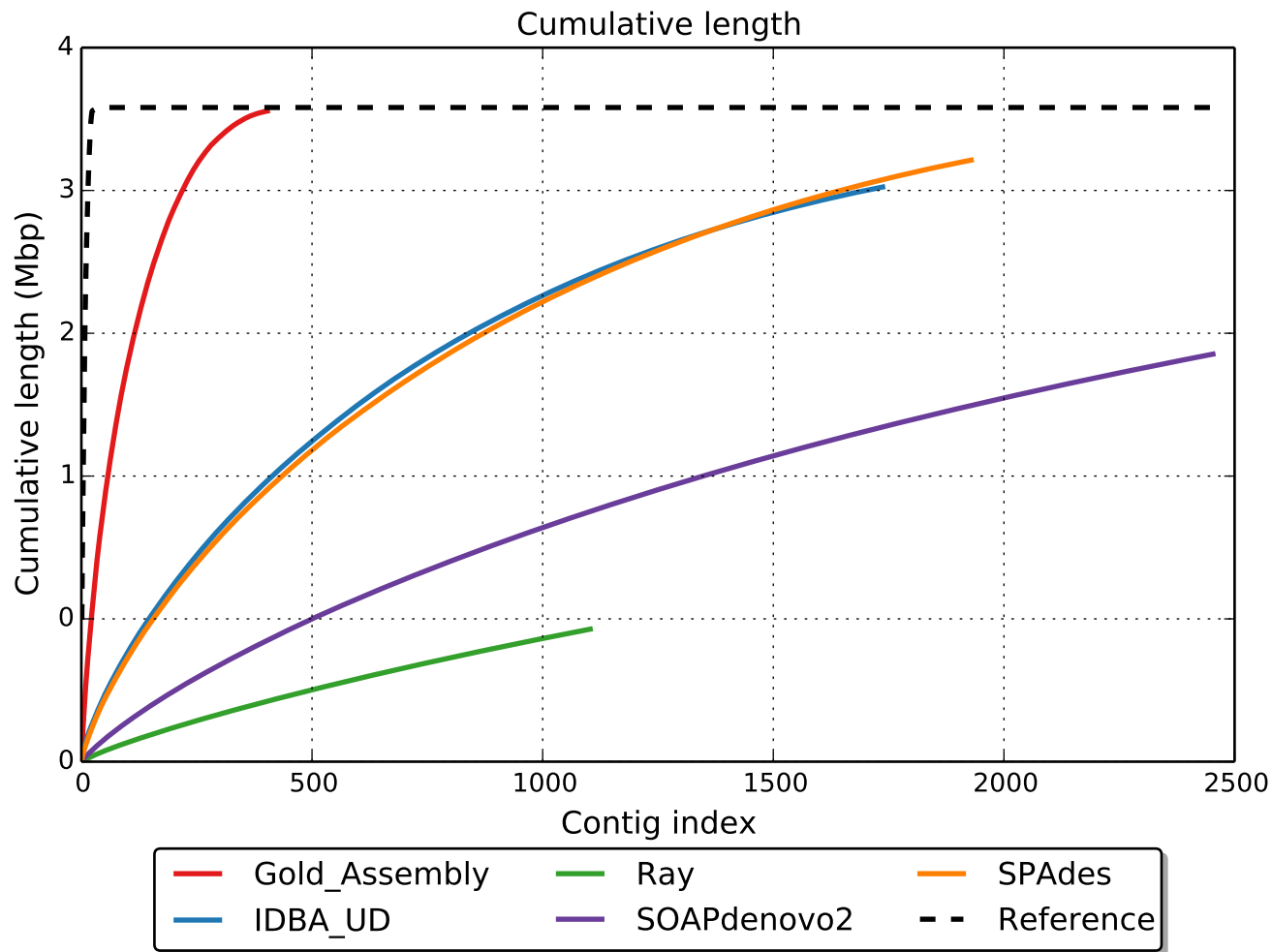
Unaligned report

	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	0	97	1	8	181
# with misassembly	0	0	0	0	1
# both parts are significant	0	8	0	0	7
Partially unaligned length	0	63023	38	279	40374
# N's	0	0	24	2847	0

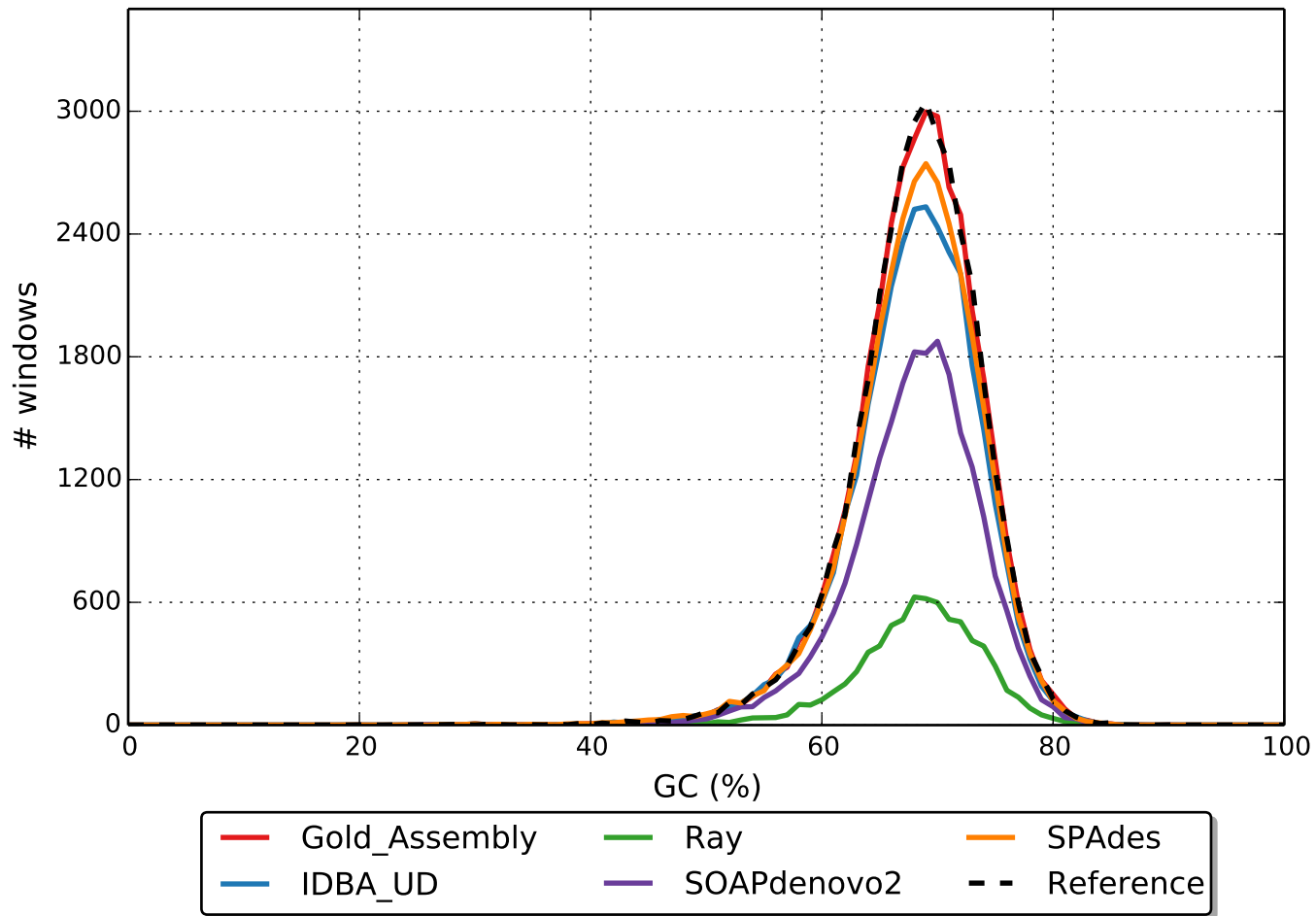
All statistics are based on contigs of size ≥ 500 bp, unless otherwise noted (e.g., "# contigs (≥ 0 bp)" and "Total length (≥ 0 bp)" include all contigs).



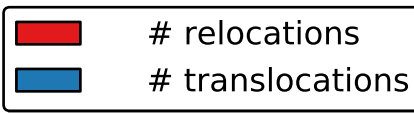
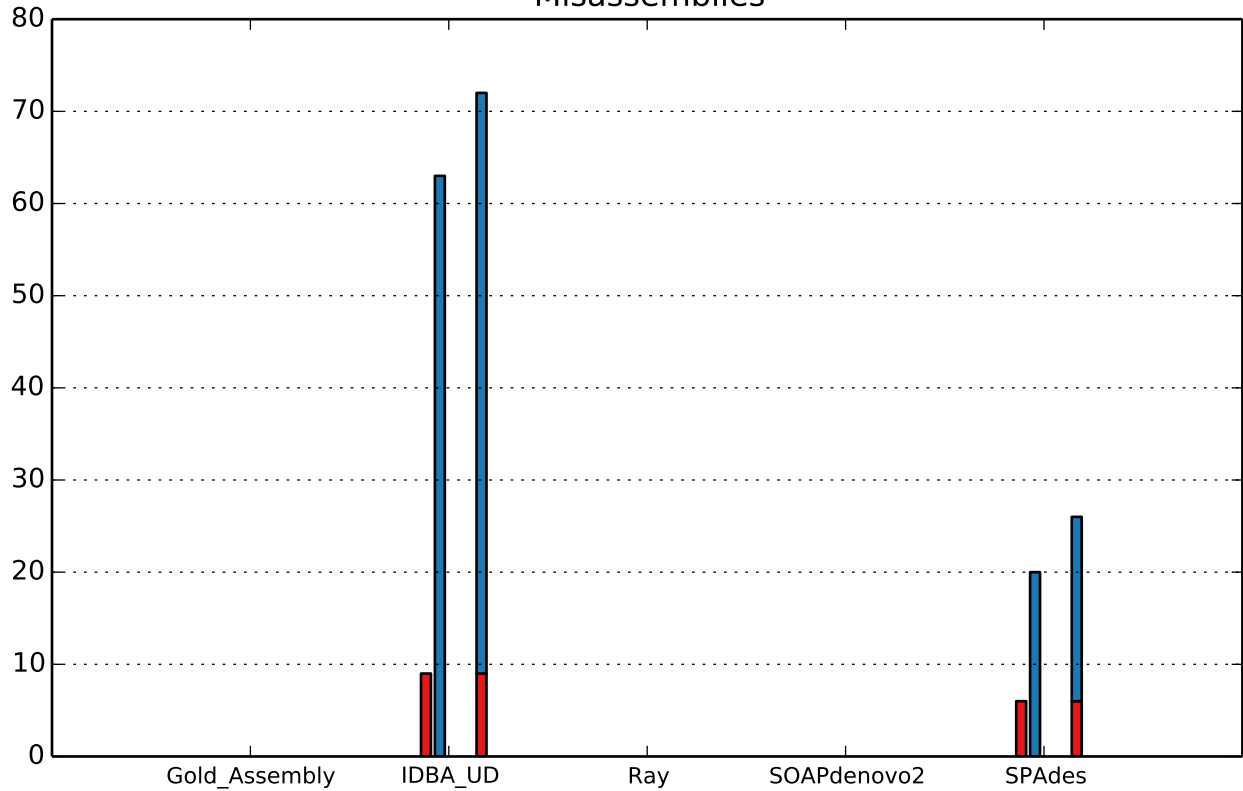


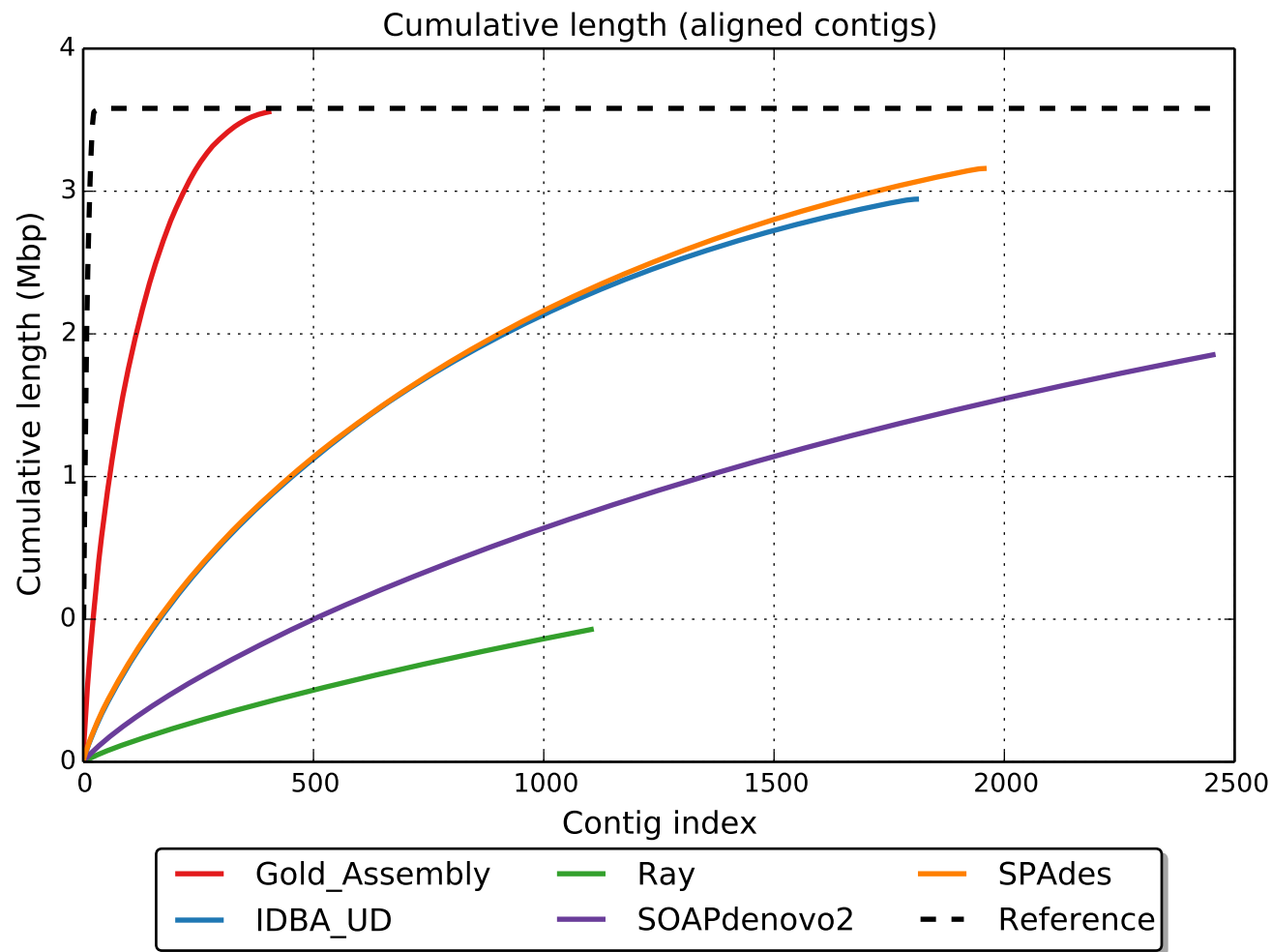


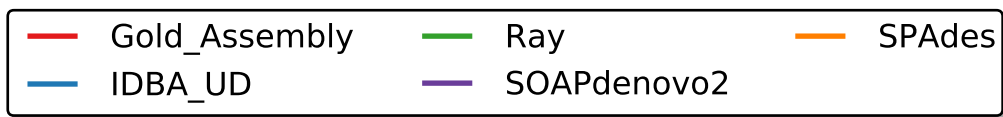
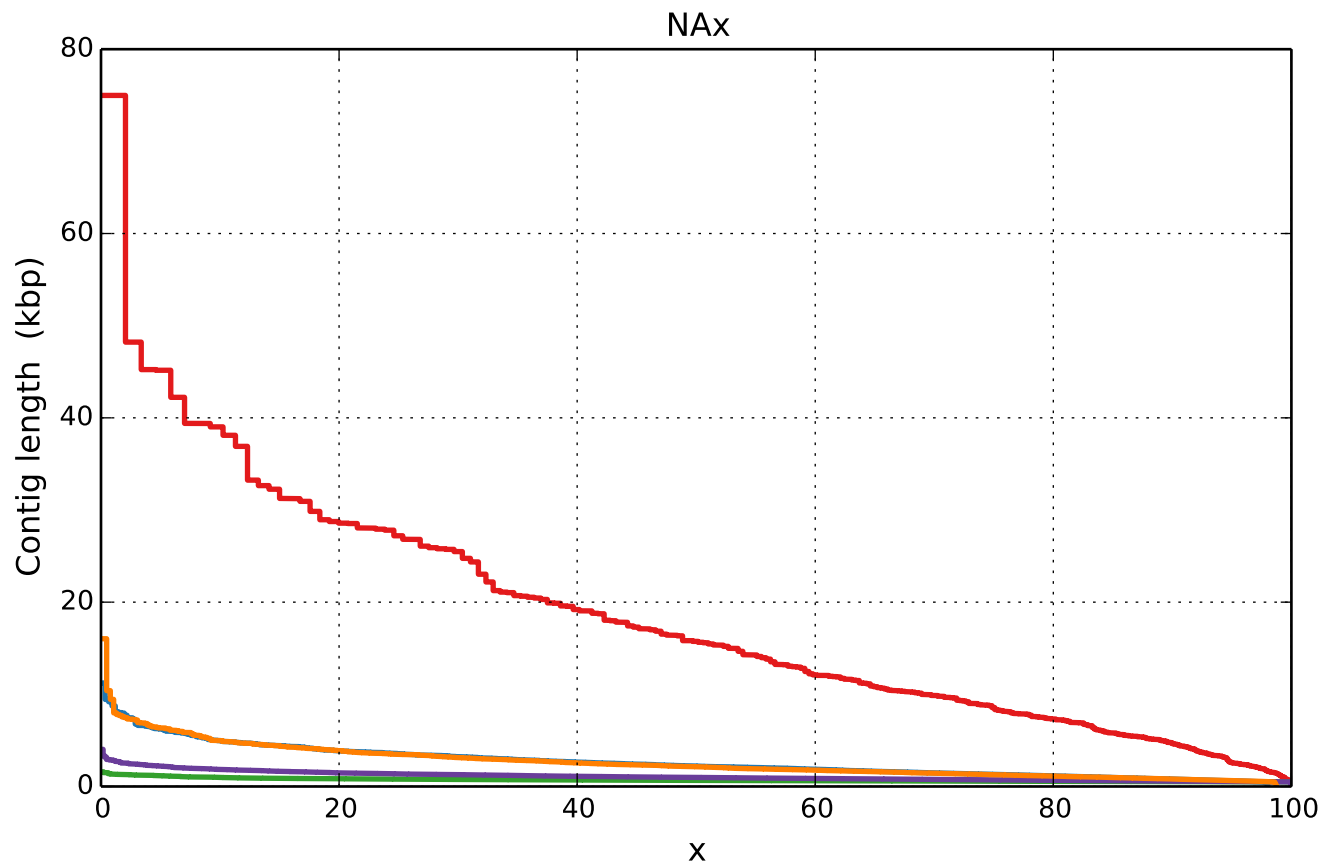
GC content



Misassemblies







NGAx

