Report

	Gold_Assembly	IDBA_UD	Ray	SOAPdenovo2	SPAdes
# contigs (>= 1000 bp)	670	1488	48	811	1526
# contigs (>= 5000 bp)	322	76	0	1	49
# contigs (>= 10000 bp)	127	6	0	0	3
# contigs (>= 25000 bp)	10	1	0	0	0
# contigs (>= 50000 bp)	0	0	0	0	0
Total length (>= 1000 bp)	4267498	3519317	65534	1142152	3355784
Total length (>= 5000 bp)	3307973	533197	0	6470	317182
Total length (>= 10000 bp)	1937091	108372	0	0	43445
Total length (>= 25000 bp)	283334	33144	0	0	0
Total length (>= 50000 bp)	0	0	0	0	0
# contigs	754	2182	774	2740	2379
Largest contig	33667	33144	3526	6470	22474
Total length	4331011	4025473	514391	2476254	3977895
Reference length	4375813	4375813	4375813	4375813	4375813
GC (%)	44.96	44.98	45.17	45.14	45.06
Reference GC (%)	44.96	44.96	44.96	44.96	44.96
N50	8816	2360	638	943	2122
NG50	8743	2178	-	583	1917
N75	5208	1449	553	692	1289
NG75	5116	1221	-	-	1058
L50	152	530	310	910	594
LG50	154	607	-	2206	693
L75	311	1079	529	1684	1199
LG75	317	1276	-	-	1455
# misassemblies	0	30	0	4	31
# misassembled contigs	0	27	0	4	30
Misassembled contigs length	0	93543	0	14697	85856
# local misassemblies	0	3	2	0	1
# structural variations	0	0	0	0	0
# unaligned contigs	0 + 0 part	0 + 76 part	0 + 2 part	0 + 5 part	0 + 73 part
Unaligned length	0	127810	56	841	62462
Genome fraction (%)	98.858	88.466	11.737	56.528	88.741
Duplication ratio	1.001	1.007	1.001	1.001	1.008
# N's per 100 kbp	0.00	0.00	8.36	104.31	10.38
# mismatches per 100 kbp	0.00	161.76	2.14	224.98	433.18
# indels per 100 kbp	0.02	1.24	0.00	35.13	2.32
Largest alignment	33667	10962	3526	6065	10663
NA50	8816	2189	638	942	2025
NGA50	8743	2028	-	583	1846
NA75	5208	1327	553	691	1222
NGA75	5116	1095	-	-	995
LA50	152	582	310	912	626
LGA50	154	664	-	2209	728
LA75	311	1174	529	1686	1257
LGA75	317	1392	-	-	1528

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).
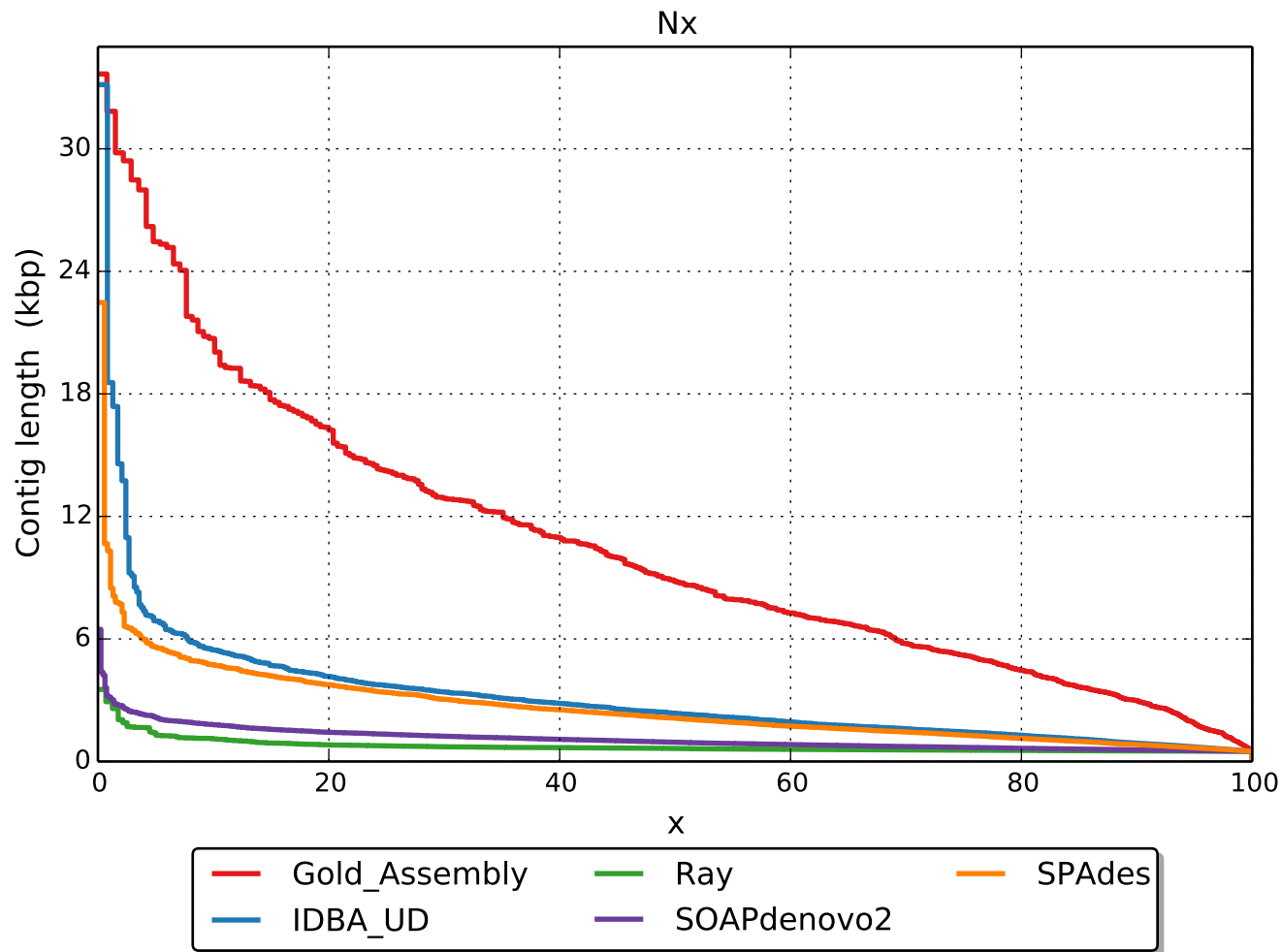
Misassemblies report
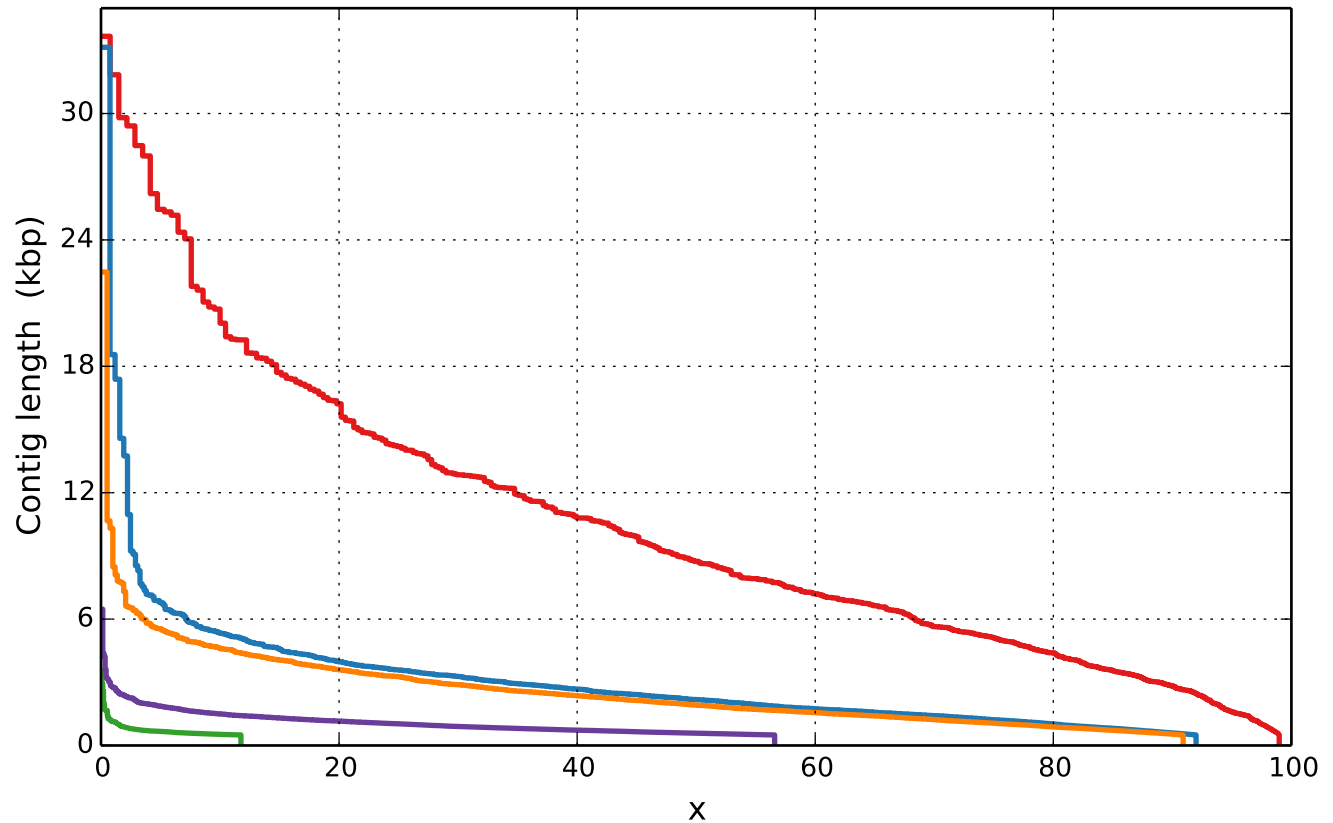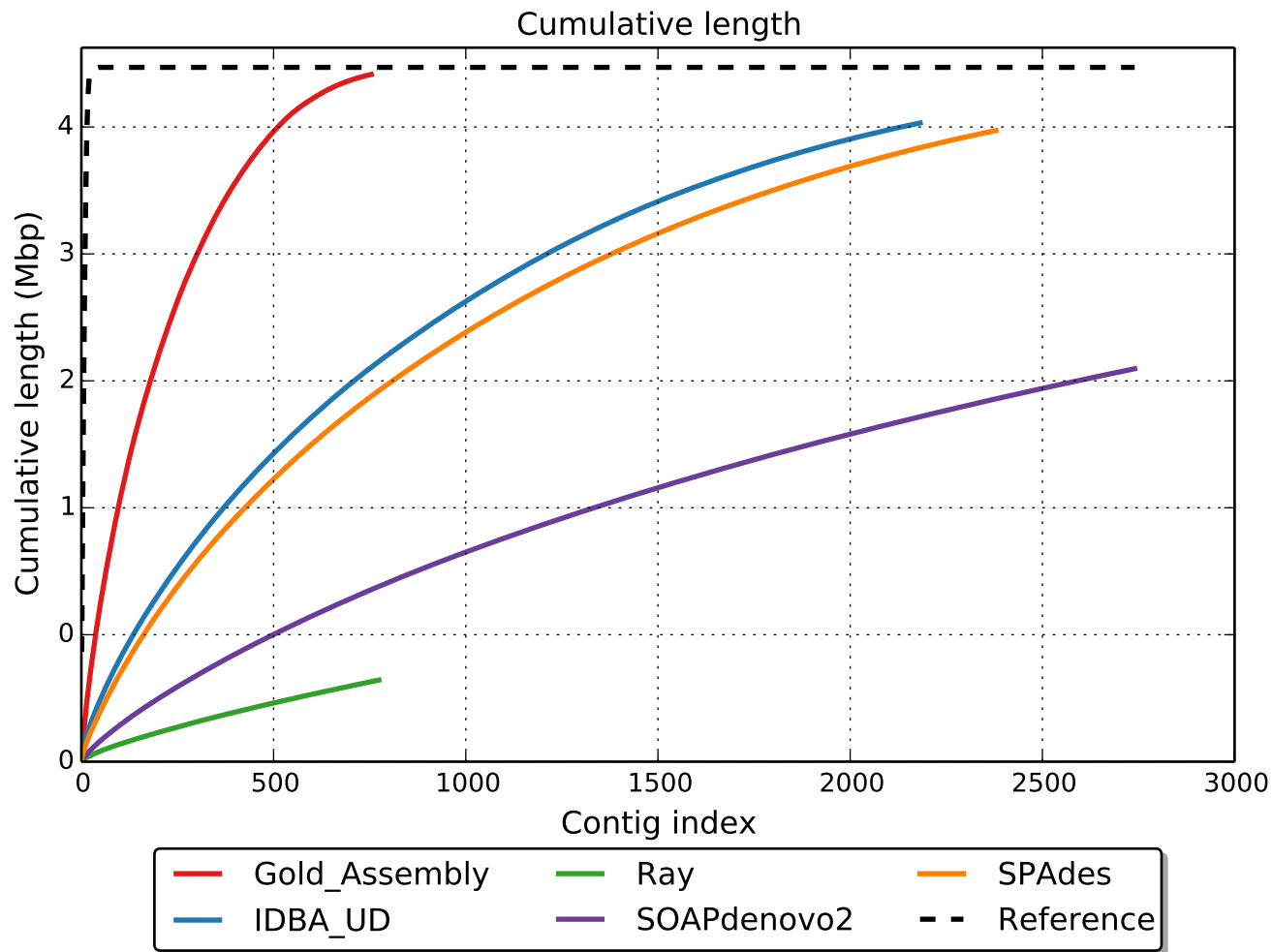
	Gold_Assembly	IDBA_UD	Ray	SOAPdenovo2	SPAdes
# misassemblies	0	30	0	4	31
# relocations	0	7	0	0	6
# translocations	0	23	0	4	25
# inversions	0	0	0	0	0
# possibly misassembled contigs	0	21	0	1	14
# misassembled contigs	0	27	0	4	30
Misassembled contigs length	0	93543	0	14697	85856
# local misassemblies	0	3	2	0	1
# structural variations	0	0	0	0	0
# mismatches	0	6262	11	5565	16821
# indels	1	48	0	869	90
# short indels	0	44	0	378	76
# long indels	1	4	0	491	14
Indels length	6	177	0	7016	612

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
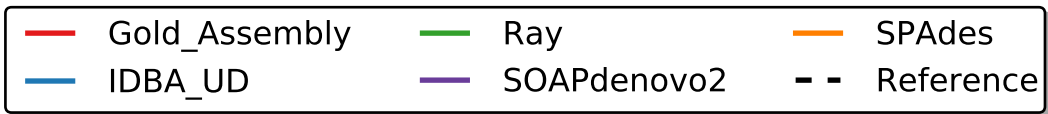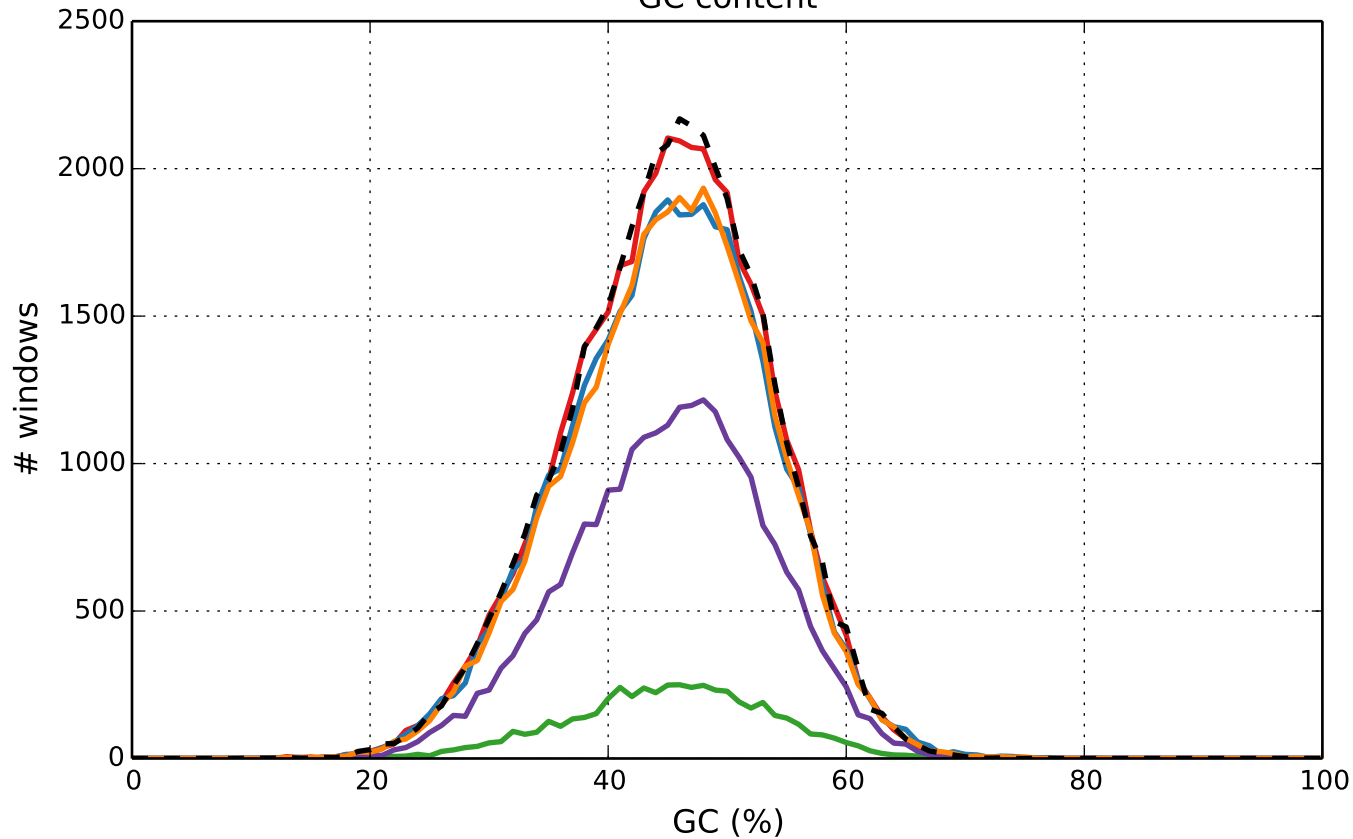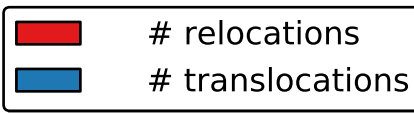
	Gold_Assembly	IDBA_UD	Ray	SOAPdenovo2	SPAdes
# fully unaligned contigs	0	0	0	0	0
Fully unaligned length	0	0	0	0	0
# partially unaligned contigs	0	76	2	5	73
# with misassembly	0	0	0	0	0
# both parts are significant	0	21	0	1	14
Partially unaligned length	0	127810	56	841	62462
# N's	0	0	43	2583	413

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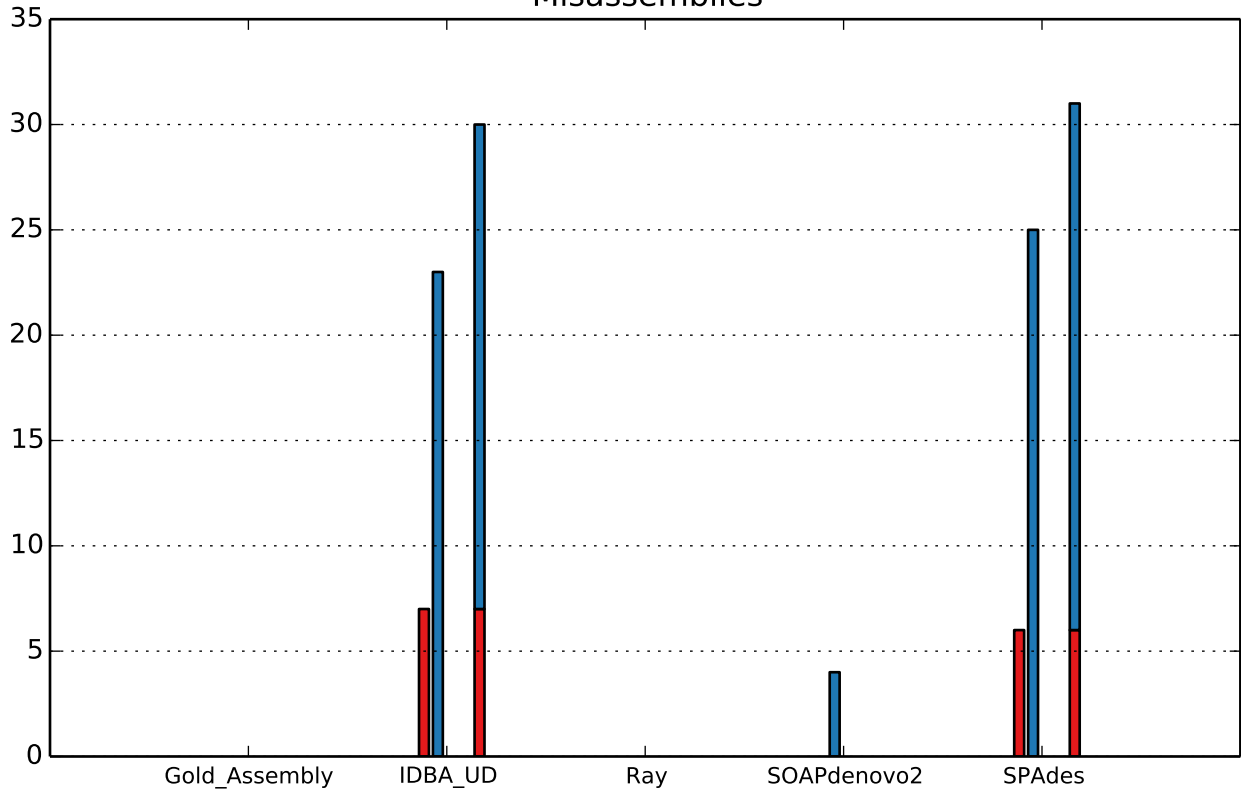(e.g., "# contigs (>= 0 bp)" and "Total length (>= 0 bp)" include all contigs).

NGx

Cumulative length

GC content

Misassemblies

Cumulative length (aligned contigs)

NAx

Contig length (kbp)

x

Gold_Assembly
IDBA_UD
Ray
SOAPdenovo2
SPAdes

Genome fraction, %