Report

	IDBA_UD	Ray	SOAPdenovo2	SPAdes
# contigs (>= 1000 bp)	732	19	208	637
# contigs (>= 5000 bp)	158	7	2	134
# contigs (>= 10000 bp)	51	5	1	38
# contigs (>= 25000 bp)	5	0	0	6
# contigs (>= 50000 bp)	2	0	0	3
Total length (>= 1000 bp)	2994025	109798	307612	2556144
Total length (>= 5000 bp)	1608891	87424	21685	1422541
Total length (>= 10000 bp)	872397	71876	16218	758862
Total length (>= 25000 bp)	239689	0	0	304413
Total length (>= 50000 bp)	135583	0	0	198492
# contigs	1013	106	936	911
Largest contig	84389	17196	16218	79105
Total length	3202386	163663	808776	2753572
Reference length	6260361	6260361	6260361	6260361
GC (%)	43.29	41.67	42.46	42.99
Reference GC (%)	42.84	42.84	42.84	42.84
N50	5043	6040	868	5183
NG50	697	-	-	-
N75	2675	709	657	2394
L50	157	7	312	125
LG50	894	-	-	-
L75	378	36	582	324
# misassemblies	22	0	12	13
# misassembled contigs	18	0	11	13
Misassembled contigs length	100972	0	12662	114082
# local misassemblies	10	0	537	9
# structural variations	9	0	6	11
# unaligned contigs	0 + 74 part	0 + 11 part	0 + 53 part	0 + 109 part
Unaligned length	343741	70993	39702	512230
Genome fraction (%)	45.003	1.475	11.501	34.928
Duplication ratio	1.015	1.004	1.068	1.025
# N's per 100 kbp	166.09	922.63	4167.28	403.51
# mismatches per 100 kbp	1208.19	481.95	1076.55	1459.91
# indels per 100 kbp	42.52	6.50	15.00	49.35
Largest alignment	20493	14202	5467	19393
NA50	3703	530	738	2736
NGA50	-	-	-	-
NA75	1549	-	550	834
LA50	230	84	369	258
LA75	553	-	687	705

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).
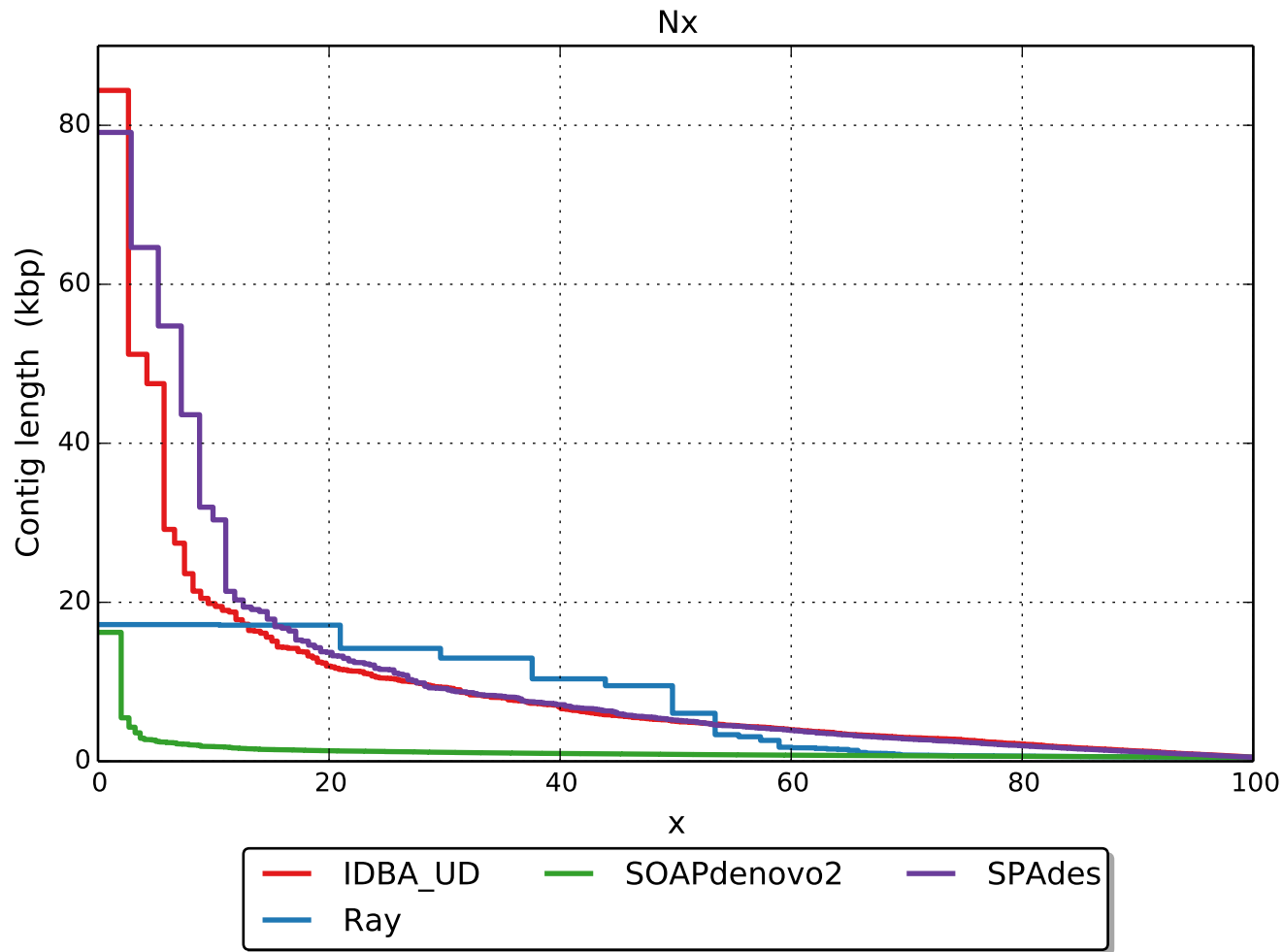
Misassemblies report

	IDBA_UD	Ray	SOAPdenovo2	SPAdes
# misassemblies	22	0	12	13
# relocations	21	0	12	13
# translocations	0	0	0	0
# inversions	1	0	0	0
# possibly misassembled contigs	38	5	11	72
# misassembled contigs	18	0	11	13
Misassembled contigs length	100972	0	12662	114082
# local misassemblies	10	0	537	9
# structural variations	9	0	6	11
# mismatches	34039	445	7751	31923
# indels	1198	6	108	1079
# short indels	1051	5	100	918
# long indels	147	1	8	161
Indels length	3604	26	203	3615

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

	IDBA_UD	Ray	SOAPdenovo2	SPAdes
# fully unaligned contigs	0	0	0	0
Fully unaligned length	0	0	0	0
# partially unaligned contigs	74	11	53	109
# with misassembly	4	1	19	10
# both parts are significant	31	5	3	56
Partially unaligned length	343741	70993	39702	512230
# N's	5319	1510	33704	11111

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).

Cumulative length

| | IDBA_UD | | SOAPdenovo2 | - - | Reference |
| | Ray | | SPAdes | | |

GC content

Misassemblies

Cumulative length (aligned contigs)

Genome fraction, %

IDBA_UD
Ray
SOAPdenovo2
SPAdes