

Report

	IDBA_UD	Ray	SOAPdenovo2	SPAdes
# contigs (>= 1000 bp)	8	4	17	8
# contigs (>= 5000 bp)	2	2	3	4
# contigs (>= 10000 bp)	2	1	0	3
# contigs (>= 25000 bp)	1	1	0	1
# contigs (>= 50000 bp)	1	1	0	1
Total length (>= 1000 bp)	105000	72165	53677	104100
Total length (>= 5000 bp)	93042	69065	21987	92939
Total length (>= 10000 bp)	93042	60771	0	85288
Total length (>= 25000 bp)	68188	60771	0	54211
Total length (>= 50000 bp)	68188	60771	0	54211
# contigs	9	5	38	10
Largest contig	68188	60771	9696	54211
Total length	105745	72674	68759	105257
Reference length	4629061	4629061	4629061	4629061
GC (%)	43.39	45.89	43.65	43.62
Reference GC (%)	45.13	45.13	45.13	45.13
N50	68188	60771	2869	54211
N75	24854	60771	1319	14791
L50	1	1	7	1
L75	2	1	16	3
# misassemblies	0	0	0	0
# misassembled contigs	0	0	0	0
Misassembled contigs length	0	0	0	0
# local misassemblies	0	0	0	0
# structural variations	0	0	0	0
# unaligned contigs	0 + 4 part	0 + 3 part	0 + 5 part	0 + 6 part
Unaligned length	87455	63310	9613	88577
Genome fraction (%)	0.378	0.202	1.272	0.320
Duplication ratio	1.045	1.001	1.005	1.127
# N's per 100 kbp	43.50	1508.10	397.04	0.00
# mismatches per 100 kbp	1828.68	1656.16	489.14	2358.75
# indels per 100 kbp	131.44	64.11	23.78	135.17
Largest alignment	8218	6002	9696	6852
NA50	-	-	1801	-
NGA50	-	-	-	-
NA75	-	-	730	-
LA50	-	-	9	-
LA75	-	-	24	-

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

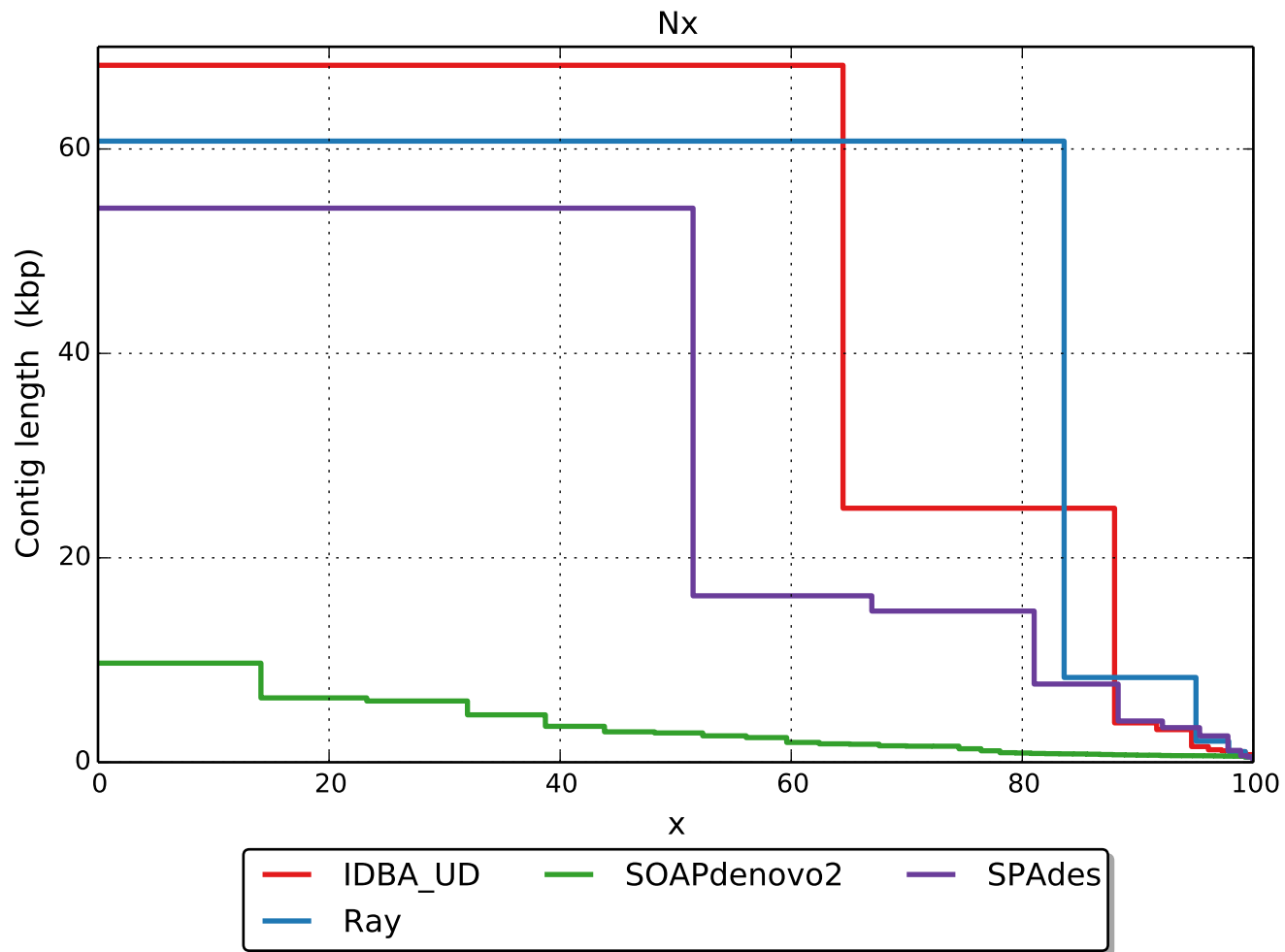
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# misassemblies	0	0	0	0
# relocations	0	0	0	0
# translocations	0	0	0	0
# inversions	0	0	0	0
# possibly misassembled contigs	2	3	0	4
# misassembled contigs	0	0	0	0
Misassembled contigs length	0	0	0	0
# local misassemblies	0	0	0	0
# structural variations	0	0	0	0
# mismatches	320	155	288	349
# indels	23	6	14	20
# short indels	22	6	14	18
# long indels	1	0	0	2
Indels length	40	9	14	41

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	4	3	5	6
# with misassembly	0	0	0	0
# both parts are significant	2	3	0	4
Partially unaligned length	87455	63310	9613	88577
# N's	46	1096	273	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).



NGx

