Report

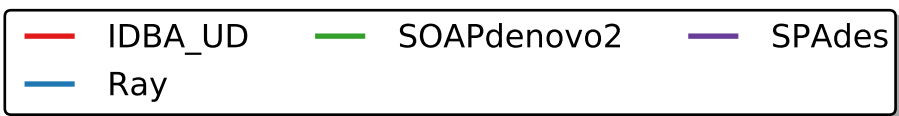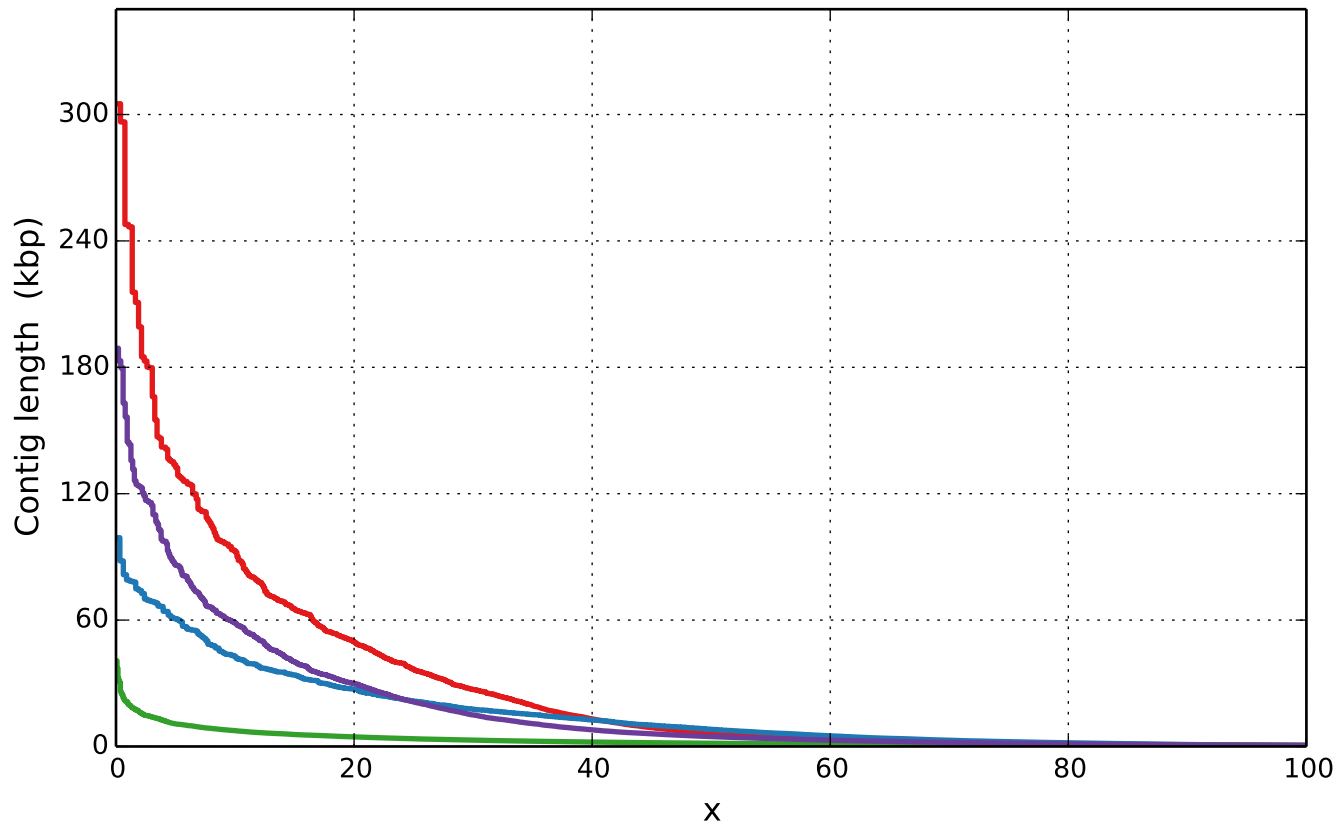|	IDBA_UD	Ray	SOAPdenovo2	SPAdes
# contigs (>= 0 bp)	46096	195402	208740	92463
# contigs (>= 1000 bp)	15638	5490	13068	19235
# contigs (>= 5000 bp)	2243	1273	1037	2950
# contigs (>= 10000 bp)	1079	630	196	1255
# contigs (>= 25000 bp)	452	161	7	426
# contigs (>= 50000 bp)	182	36	0	146
Total length (>= 0 bp)	85398219	59853665	82244277	106967180
Total length (>= 1000 bp)	69223529	27080646	30720336	77823828
Total length (>= 5000 bp)	42843090	18289015	8400340	44989853
Total length (>= 10000 bp)	34930908	13755677	2800864	33477263
Total length (>= 25000 bp)	25310756	6553349	223453	20919132
Total length (>= 50000 bp)	16008349	2346322	0	11409912
# contigs	31224	10327	36468	40546
Largest contig	305144	99107	40707	189063
Total length	80325286	30411921	46741224	92397329
Reference length	306971432	306971432	306971432	306971432
N50	6111	8131	1525	4692
N75	1696	2279	814	1525
L50	1756	790	7020	3200
L75	8674	2651	17886	12282
# misassemblies	1132	407	831	1240
# misassembled contigs	857	299	683	936
Misassembled contigs length	10448260	4115772	911826	10780557
# local misassemblies	313	1217	10977	287
# structural variations	108	50	56	99
# unaligned contigs	20053 + 3031 part	6857 + 624 part	21087 + 2213 part	28661 + 4358 part
Unaligned length	50549753	18285373	30129289	62386985
Genome fraction (%)	12.796	4.386	8.055	11.585
Duplication ratio	1.044	1.094	1.039	1.046
# N's per 100 kbp	238.48	2087.27	3730.51	1425.14
# mismatches per 100 kbp	904.95	1054.68	888.21	1401.84
# indels per 100 kbp	31.88	27.70	17.09	51.64
Largest alignment	179515	72570	21339	108559

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	1132	407	831	1240
# relocations	306	92	70	251
# translocations	84	32	22	90
# inversions	35	2	6	15
# interspecies translocations	707	281	733	884
# possibly misassembled contigs	1031	416	352	1623
# misassembled contigs	857	299	683	936
Misassembled contigs length	10448260	4115772	911826	10780557
# local misassemblies	313	1217	10977	287
# structural variations	108	50	56	99
# mismatches	355477	141995	219630	498523
# indels	12524	3729	4227	18364
# short indels	11033	3383	3899	15225
# long indels	1491	346	328	3139
Indels length	35483	9447	9641	63455

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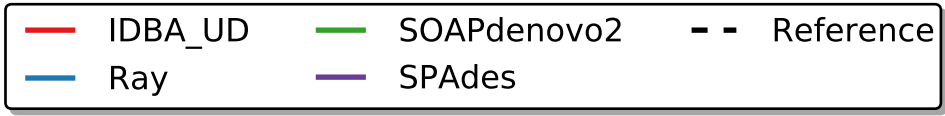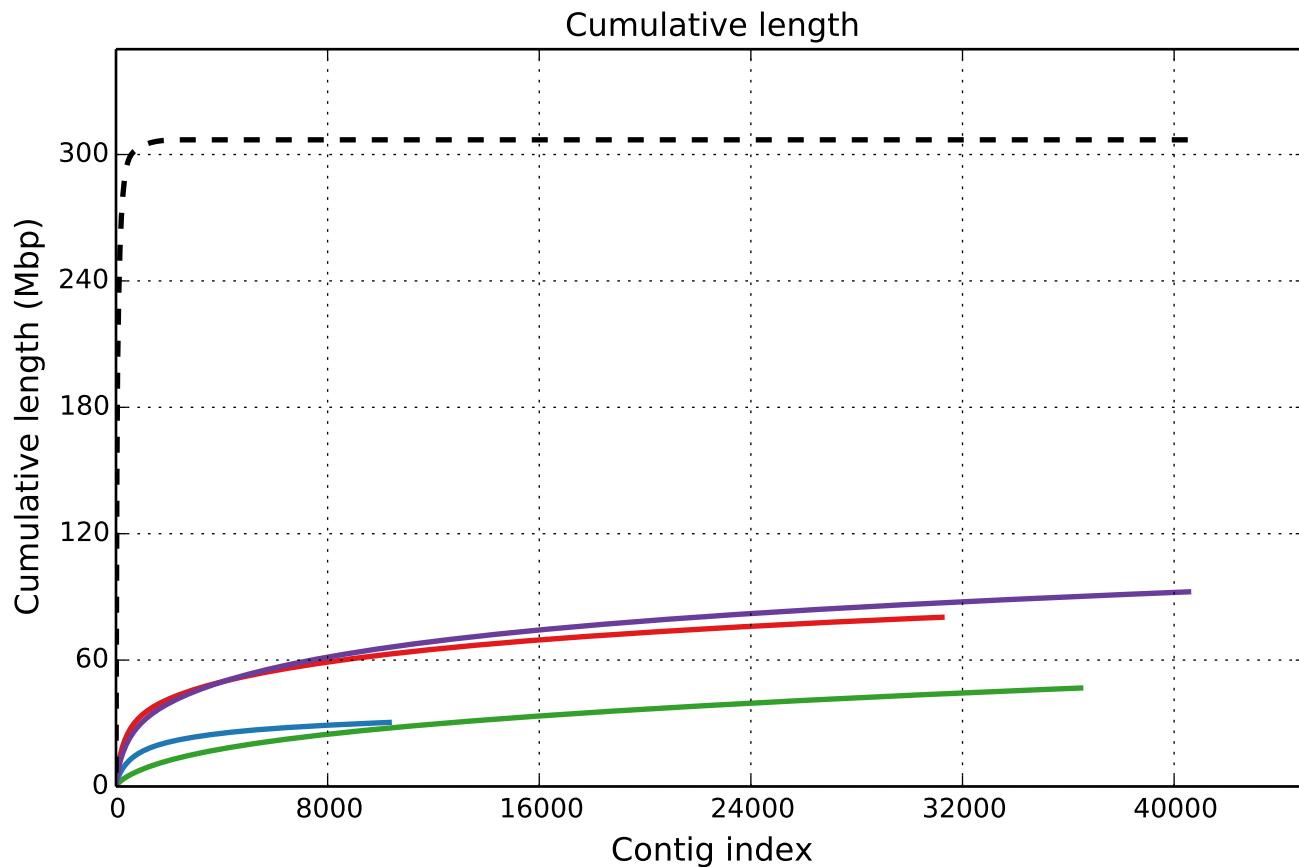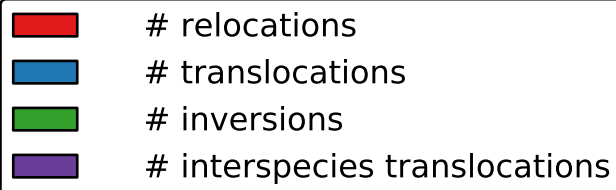(e.g., "# contigs (>= 0 bp)" and "Total length (>= 0 bp)" include all contigs).

Unaligned report

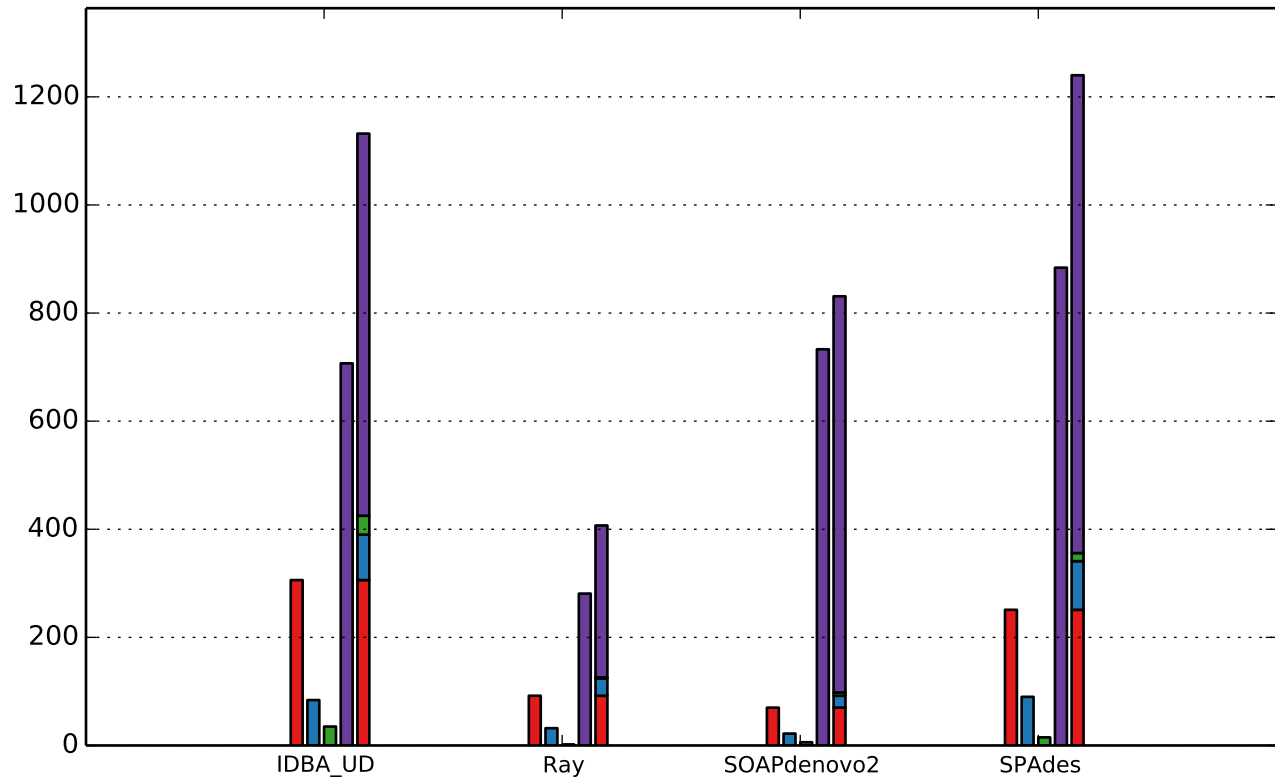|	IDBA_UD	Ray	SOAPdenovo2	SPAdes
# fully unaligned contigs	20053	6857	21087	28661
Fully unaligned length	38837027	15942170	28626572	52077982
# partially unaligned contigs	3031	624	2213	4358
# with misassembly	284	87	395	294
# both parts are significant	742	203	250	1215
Partially unaligned length	11712726	2343203	1502717	10309003
# N's	191558	634779	1743687	1316794

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).
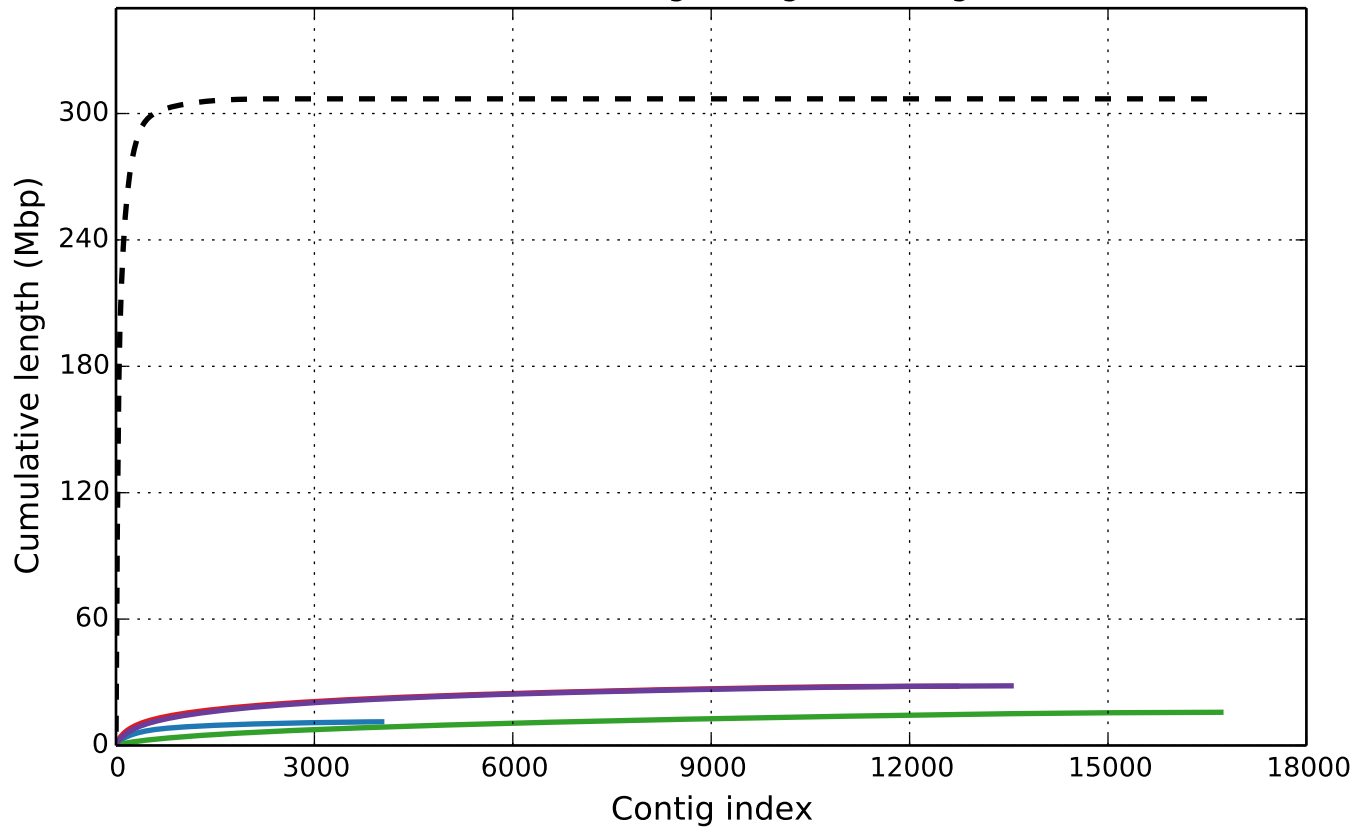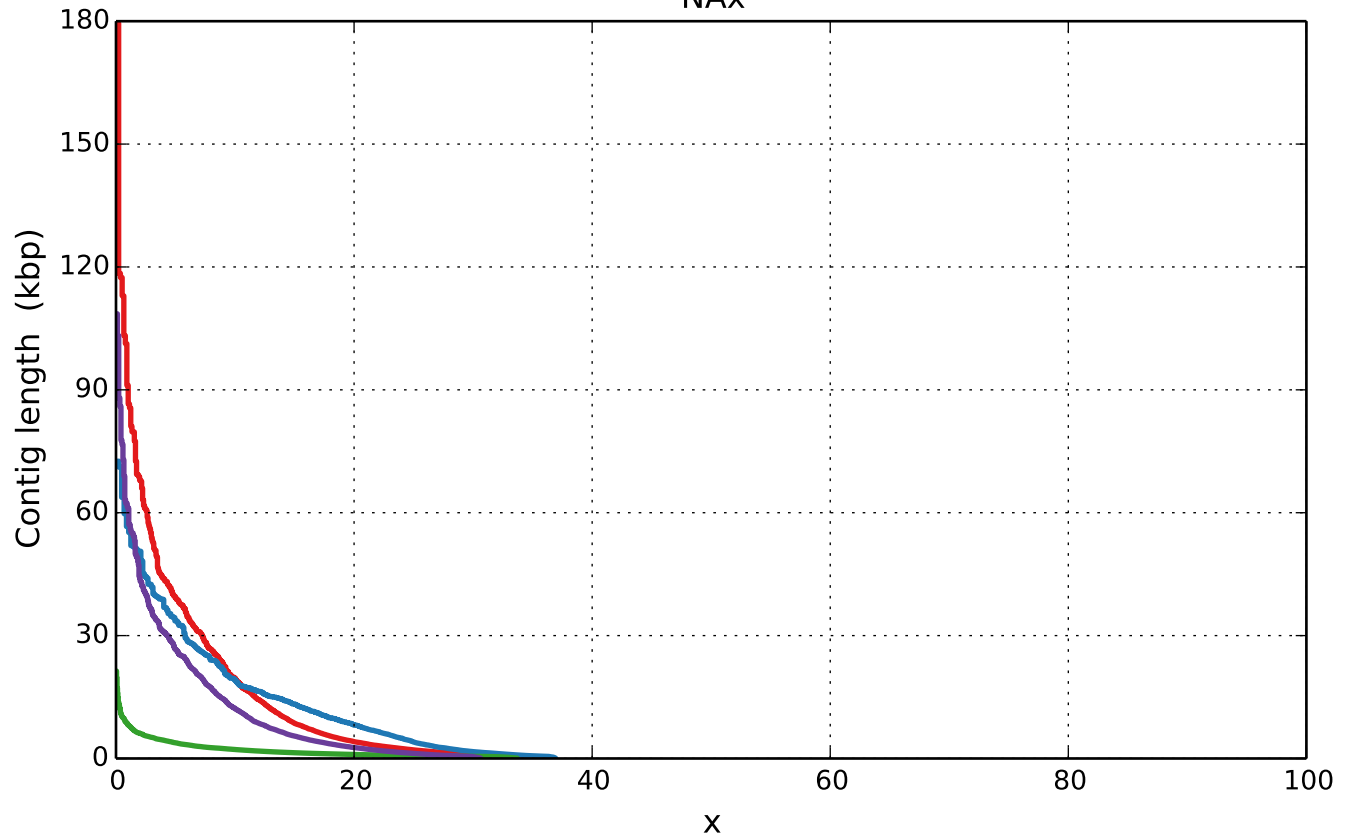
Cumulative length

Misassemblies

Legend:
- # relocations
- # translocations
- # inversions
- # interspecies translocations

Cumulative length (aligned contigs)

Genome fraction, %

IDBA_UD
Ray
SOAPdenovo2
SPAdes