

Report

	SPAdes-3.6	SPAdes-3.6.scaffolds	SPAdes-3.7	SPAdes-3.7.scaffolds	SOAPdenovo2
# contigs (>= 0 bp)	152	151	152	149	930
# contigs (>= 1000 bp)	79	78	80	79	168
# contigs (>= 5000 bp)	56	55	56	55	127
# contigs (>= 10000 bp)	52	51	52	51	105
# contigs (>= 25000 bp)	45	44	45	44	62
# contigs (>= 50000 bp)	31	30	31	30	26
Total length (>= 0 bp)	4571503	4571747	4570605	4569724	4614535
Total length (>= 1000 bp)	4548386	4548629	4549301	4549419	4526969
Total length (>= 5000 bp)	4496902	4497145	4496699	4496943	4429815
Total length (>= 10000 bp)	4467209	4467452	4467005	4467249	4256422
Total length (>= 25000 bp)	4364333	4364576	4364167	4364411	3571206
Total length (>= 50000 bp)	3878732	3878975	3878287	3878531	2277663
# contigs	95	94	93	91	181
Largest contig	285114	285114	285114	285114	165487
Total length	4559192	4559435	4558330	4557803	4535469
Reference length	4639675	4639675	4639675	4639675	4639675
GC (%)	50.74	50.74	50.74	50.74	50.74
Reference GC (%)	50.79	50.79	50.79	50.79	50.79
N50	132831	133309	132831	133309	52524
NG50	132831	133309	132831	133309	49626
N75	67335	67335	67340	67340	29555
NG75	64399	64399	64399	64399	28099
L50	13	12	13	12	26
LG50	13	12	13	12	27
L75	24	23	24	23	56
LG75	25	24	25	24	59
# misassemblies	0	0	0	0	0
# misassembled contigs	0	0	0	0	0
Misassembled contigs length	0	0	0	0	0
# local misassemblies	12	13	12	13	0
# unaligned contigs	4 + 0 part	4 + 0 part	4 + 0 part	4 + 0 part	0 + 1 part
Unaligned length	2947	2947	2947	2947	54
Genome fraction (%)	98.175	98.181	98.139	98.143	97.696
Duplication ratio	1.000	1.000	1.000	1.000	1.001
# N's per 100 kbp	0.00	0.00	0.00	0.00	0.00
# mismatches per 100 kbp	2.44	2.59	2.72	2.64	0.15
# indels per 100 kbp	0.29	0.33	0.26	0.33	0.09
# genes	4203 + 29 part	4205 + 29 part	4203 + 29 part	4204 + 30 part	4132 + 53 part
Largest alignment	285114	285114	285114	285114	165487
Total aligned length	4555870	4556113	4554957	4554430	4535148
NA50	132831	133309	132831	133309	52524
NGA50	132831	133309	132831	133309	49626
NA75	67335	67335	67340	67340	29555
NGA75	64399	64399	64399	64399	28099
LA50	13	12	13	12	26
LGA50	13	12	13	12	27
LA75	24	23	24	23	56
LGA75	25	24	25	24	59

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

	SPAdes-3.6	SPAdes-3.6.scaffolds	SPAdes-3.7	SPAdes-3.7.scaffolds	SOAPdenovo2
# misassemblies	0	0	0	0	0
# relocations	0	0	0	0	0
# translocations	0	0	0	0	0
# inversions	0	0	0	0	0
# misassembled contigs	0	0	0	0	0
Misassembled contigs length	0	0	0	0	0
# local misassemblies	12	13	12	13	0
# mismatches	111	118	124	120	7
# indels	13	15	12	15	4
# short indels	13	15	12	15	4
# long indels	0	0	0	0	0
Indels length	20	23	19	23	6

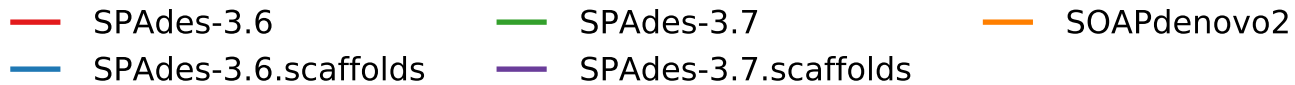
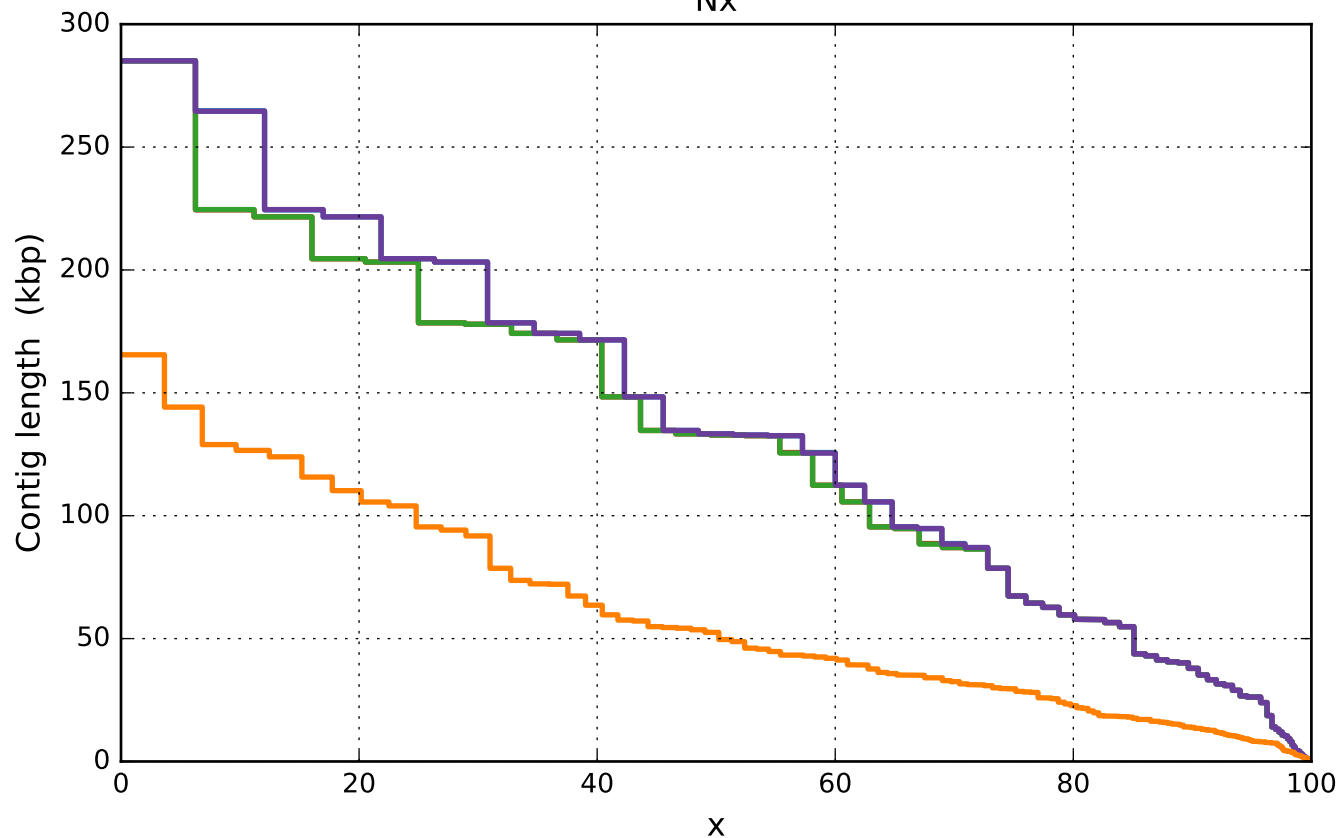
All statistics are based on contigs of size ≥ 500 bp, unless otherwise noted (e.g., "# contigs (≥ 0 bp)" and "Total length (≥ 0 bp)" include all contigs).

Unaligned report

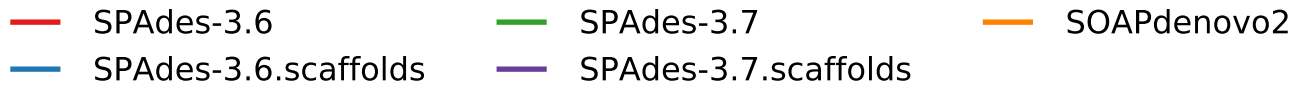
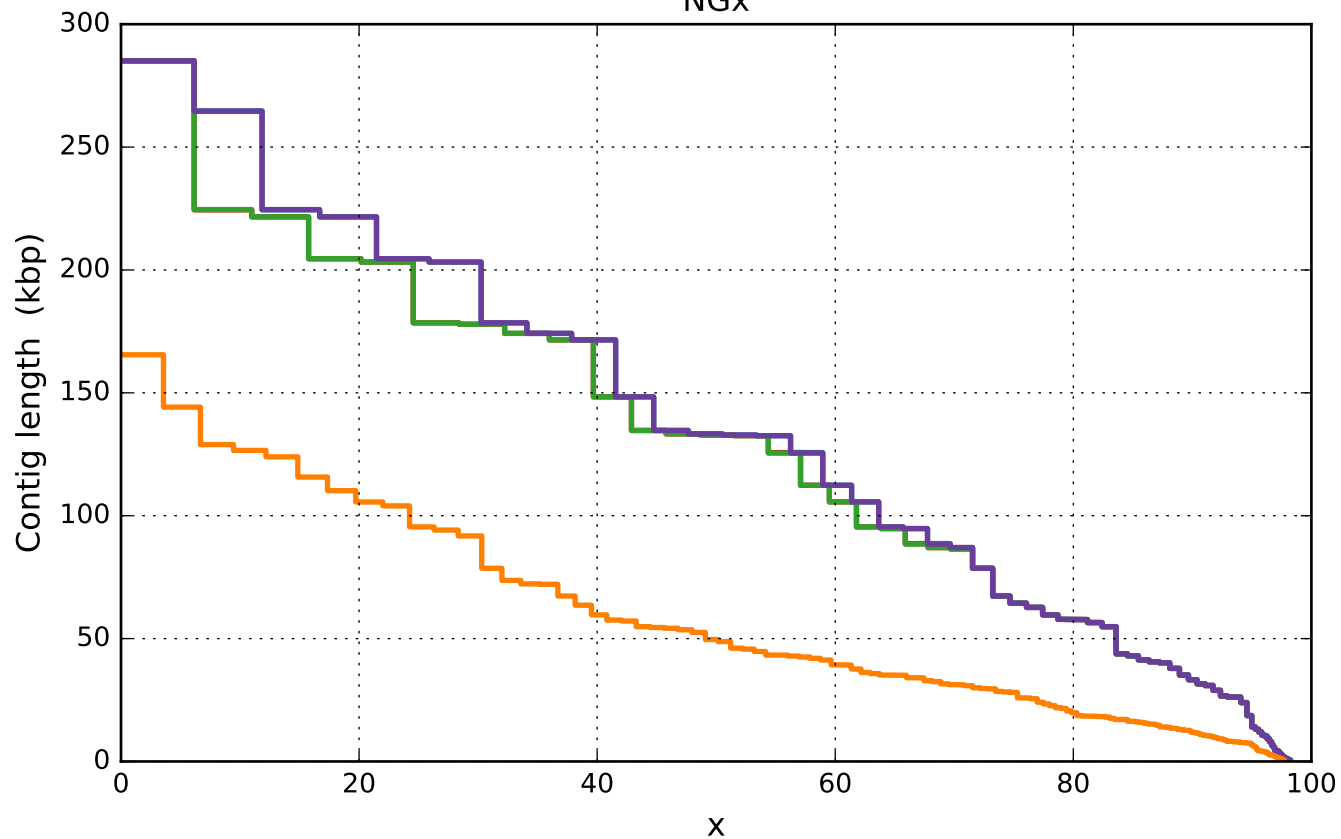
	SPAdes-3.6	SPAdes-3.6.scaffolds	SPAdes-3.7	SPAdes-3.7.scaffolds	SOAPdenovo2
# fully unaligned contigs	4	4	4	4	0
Fully unaligned length	2947	2947	2947	2947	0
# partially unaligned contigs	0	0	0	0	1
# with misassembly	0	0	0	0	0
# both parts are significant	0	0	0	0	0
Partially unaligned length	0	0	0	0	54
# N's	0	0	0	0	0

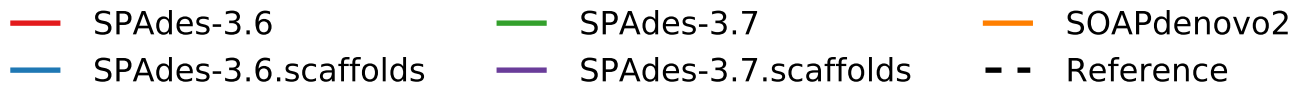
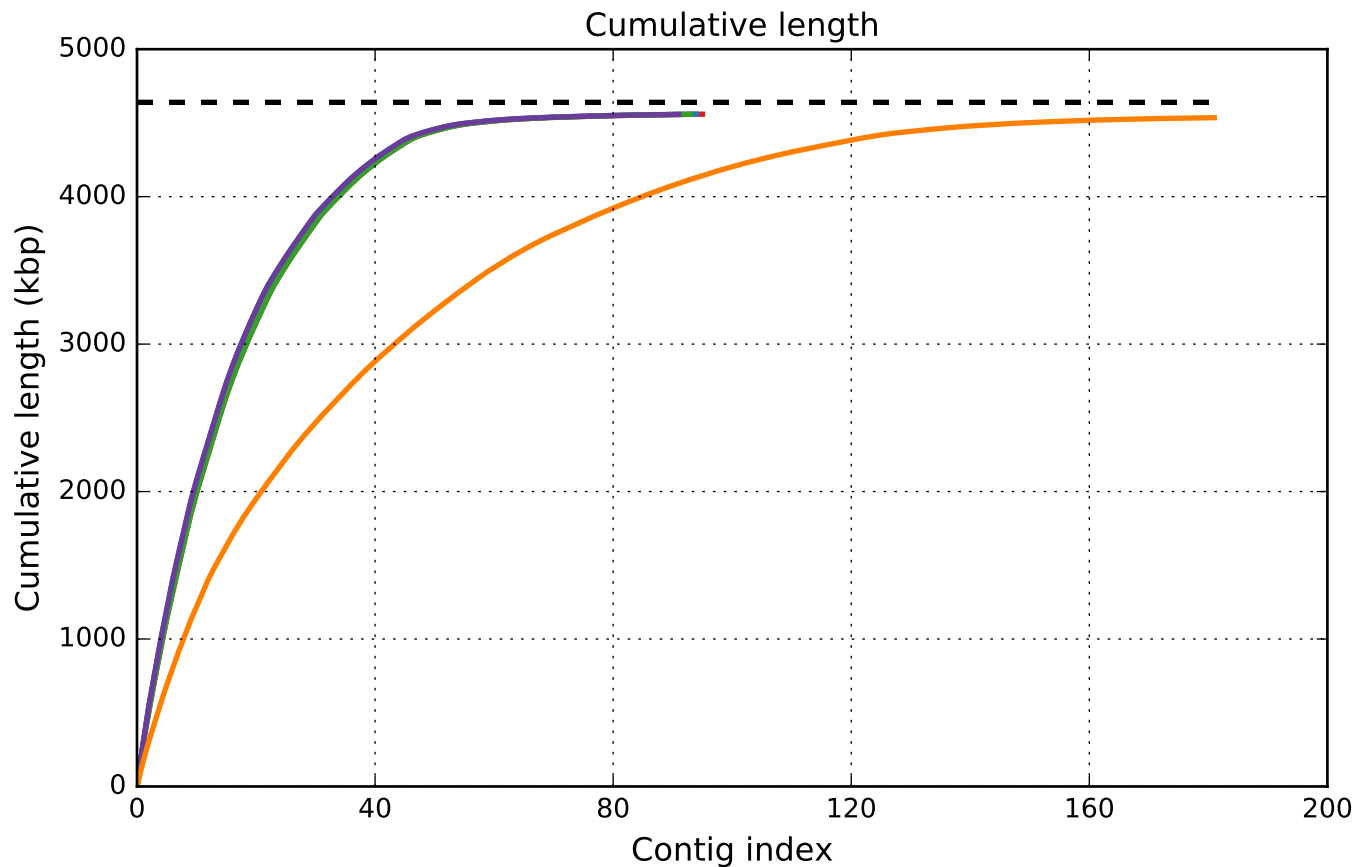
All statistics are based on contigs of size ≥ 500 bp, unless otherwise noted (e.g., "# contigs (≥ 0 bp)" and "Total length (≥ 0 bp)" include all contigs).

Nx

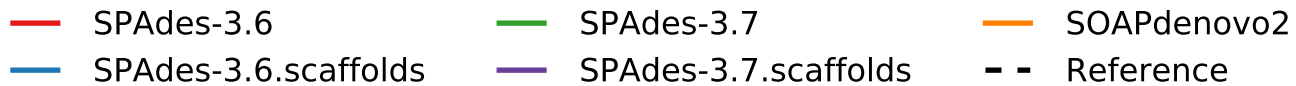
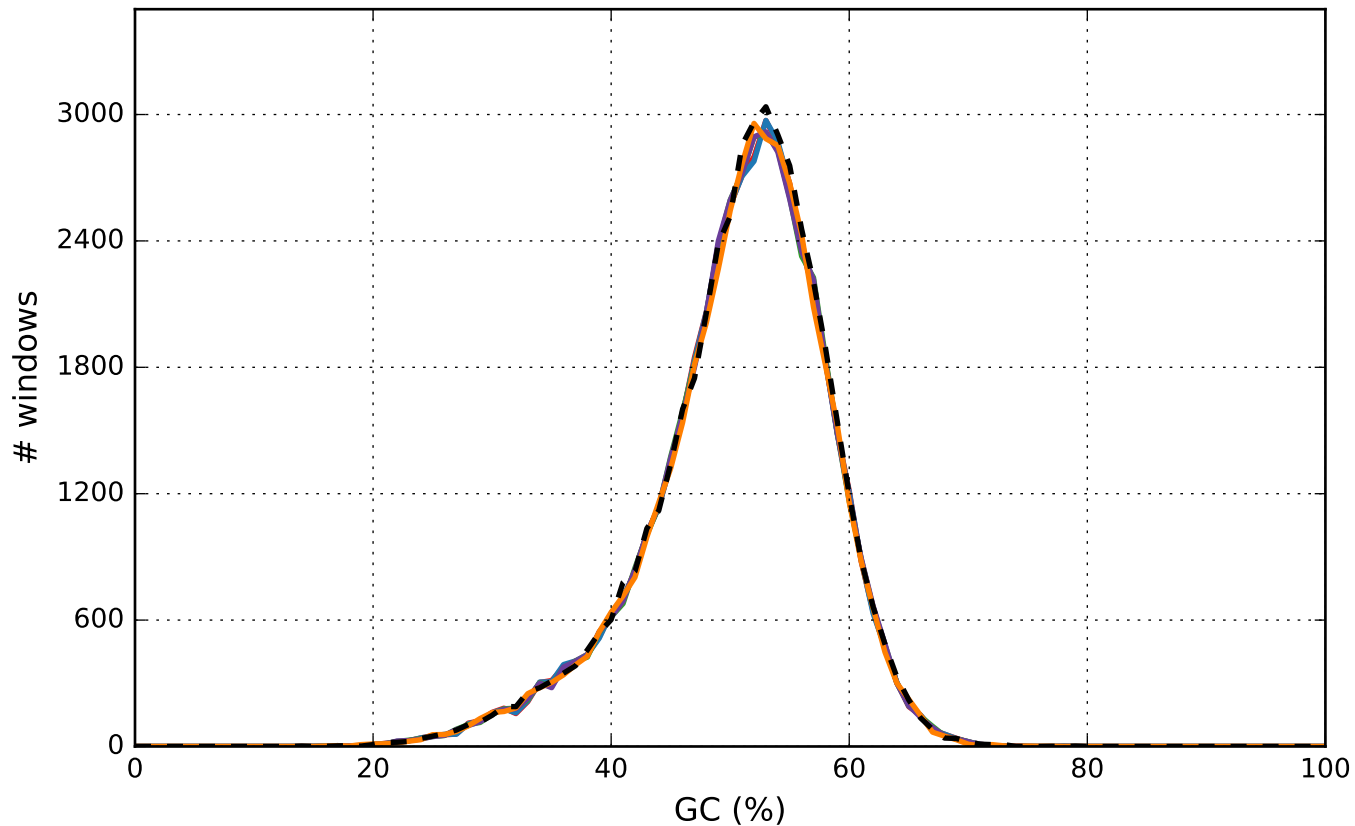


NGx

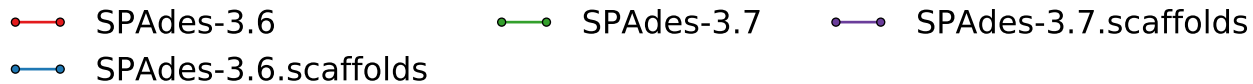
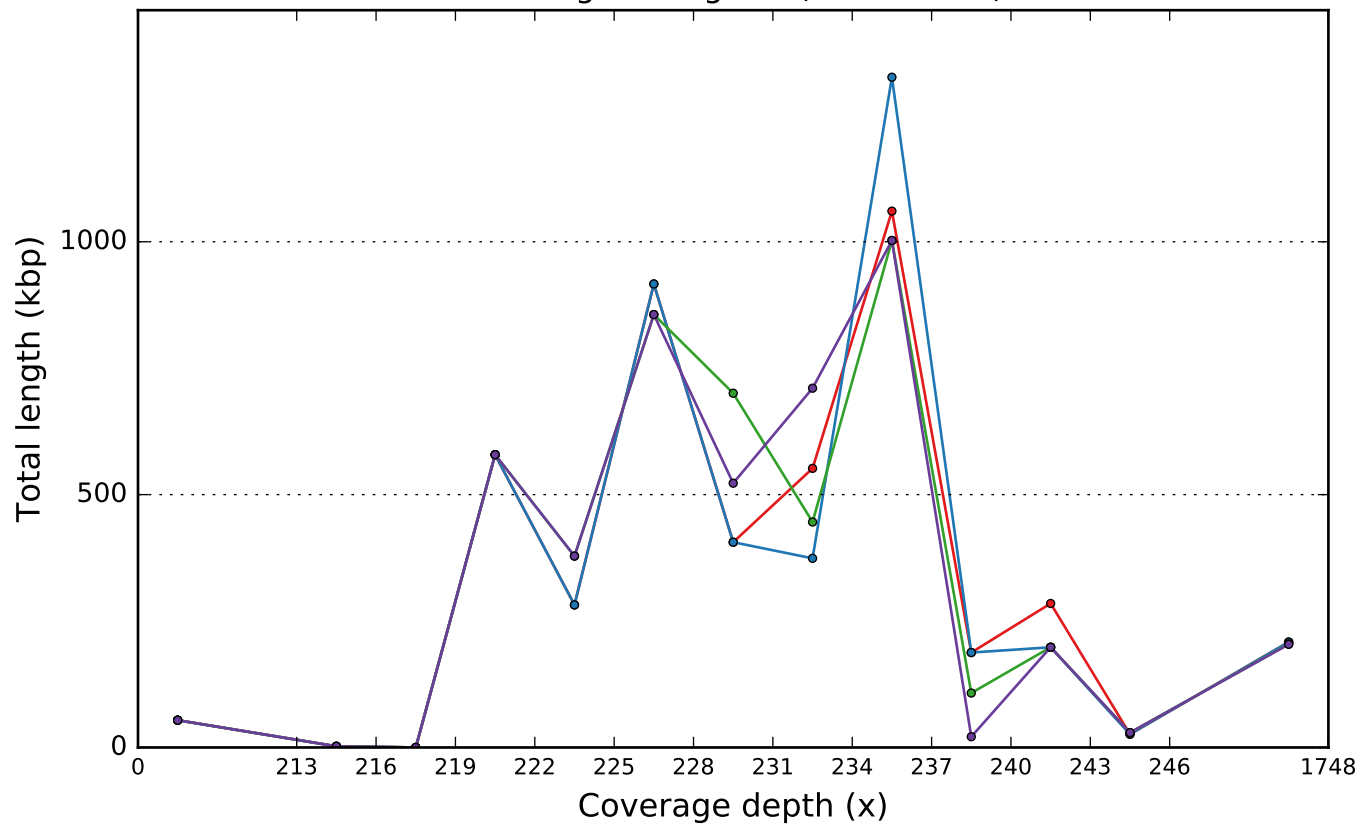




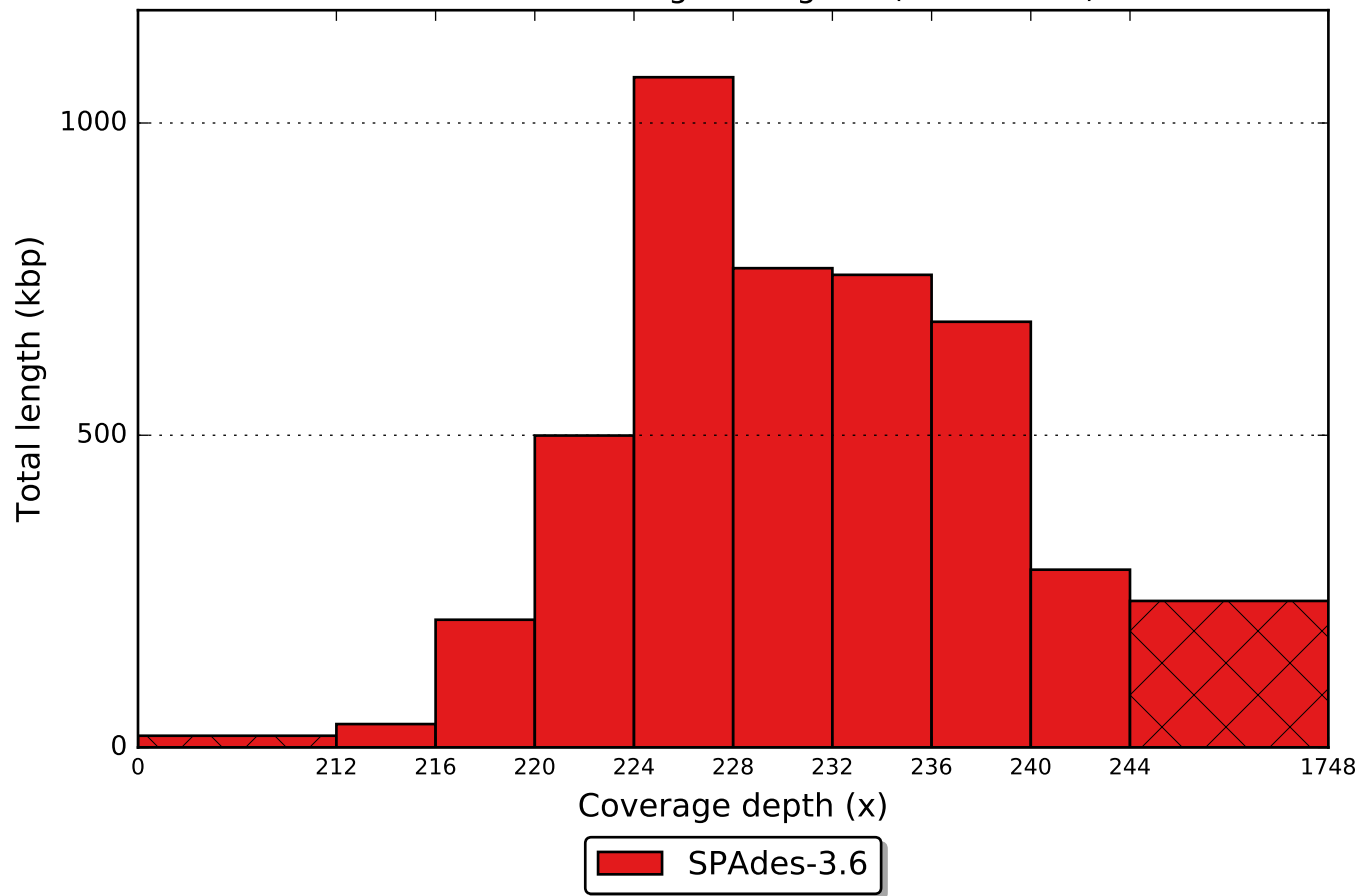
GC content



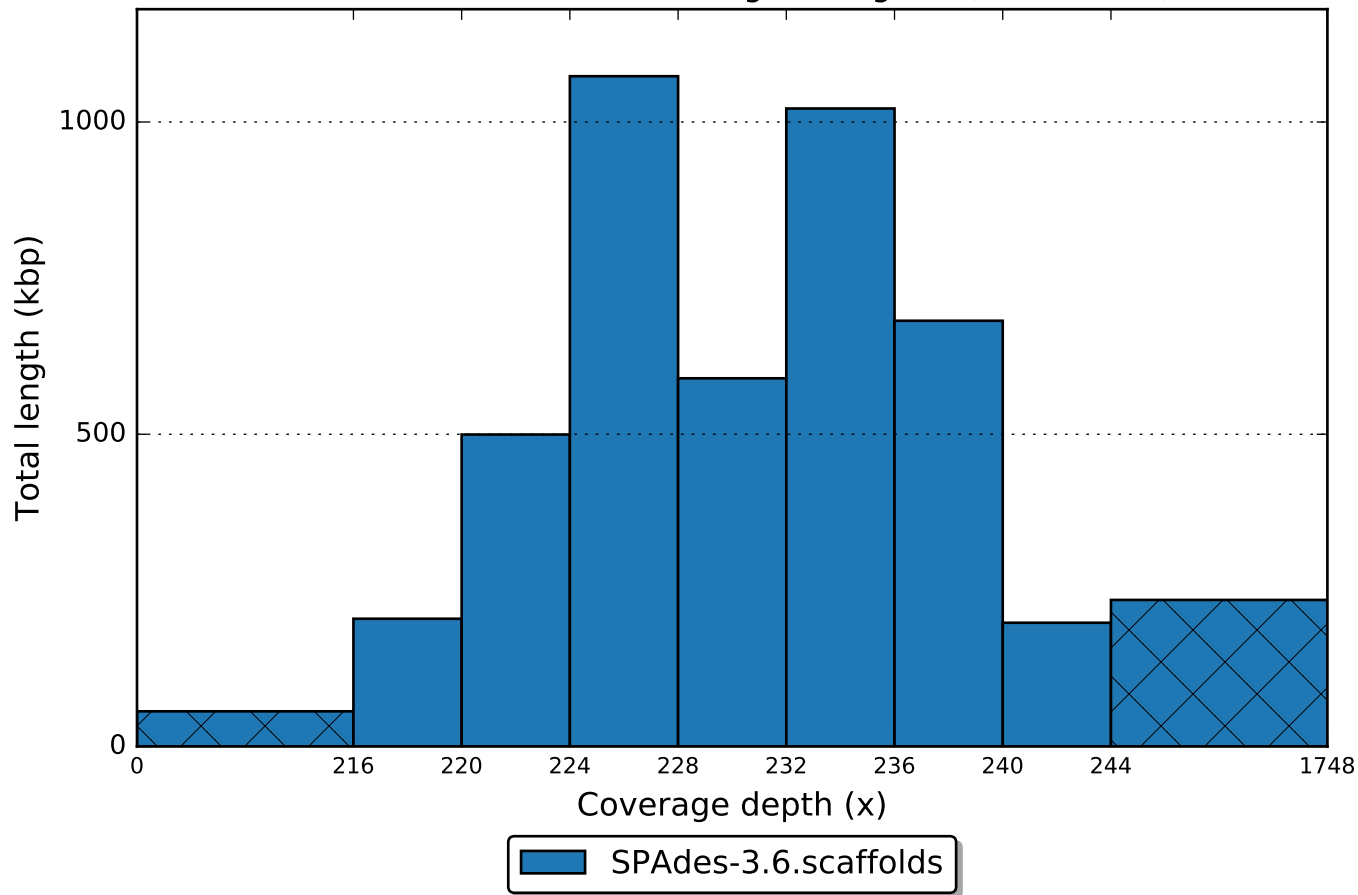
Coverage histogram (bin size: 3x)



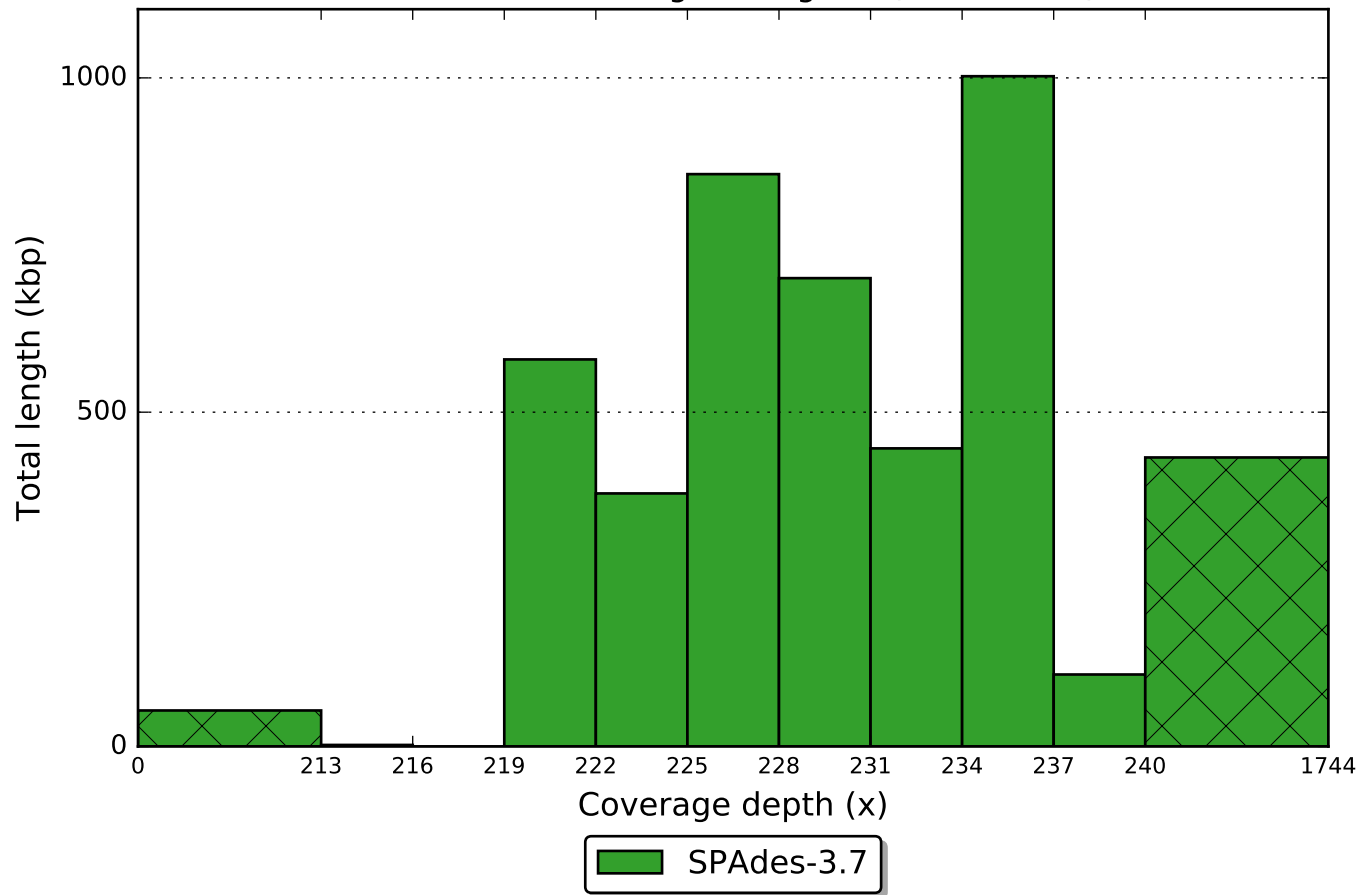
SPAdes-3.6 coverage histogram (bin size: 4x)



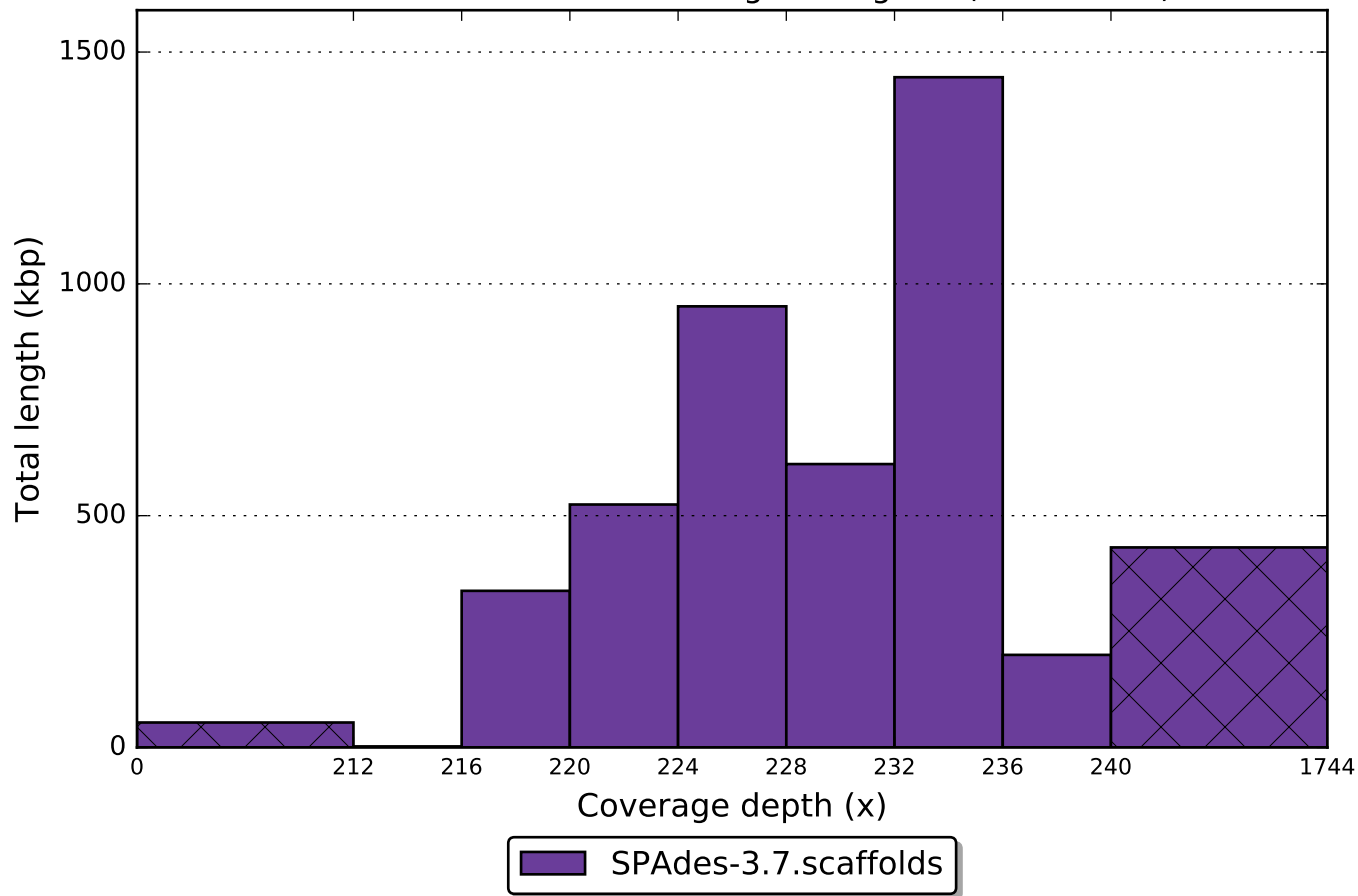
SPAdes-3.6.scaffolds coverage histogram (bin size: 4x)

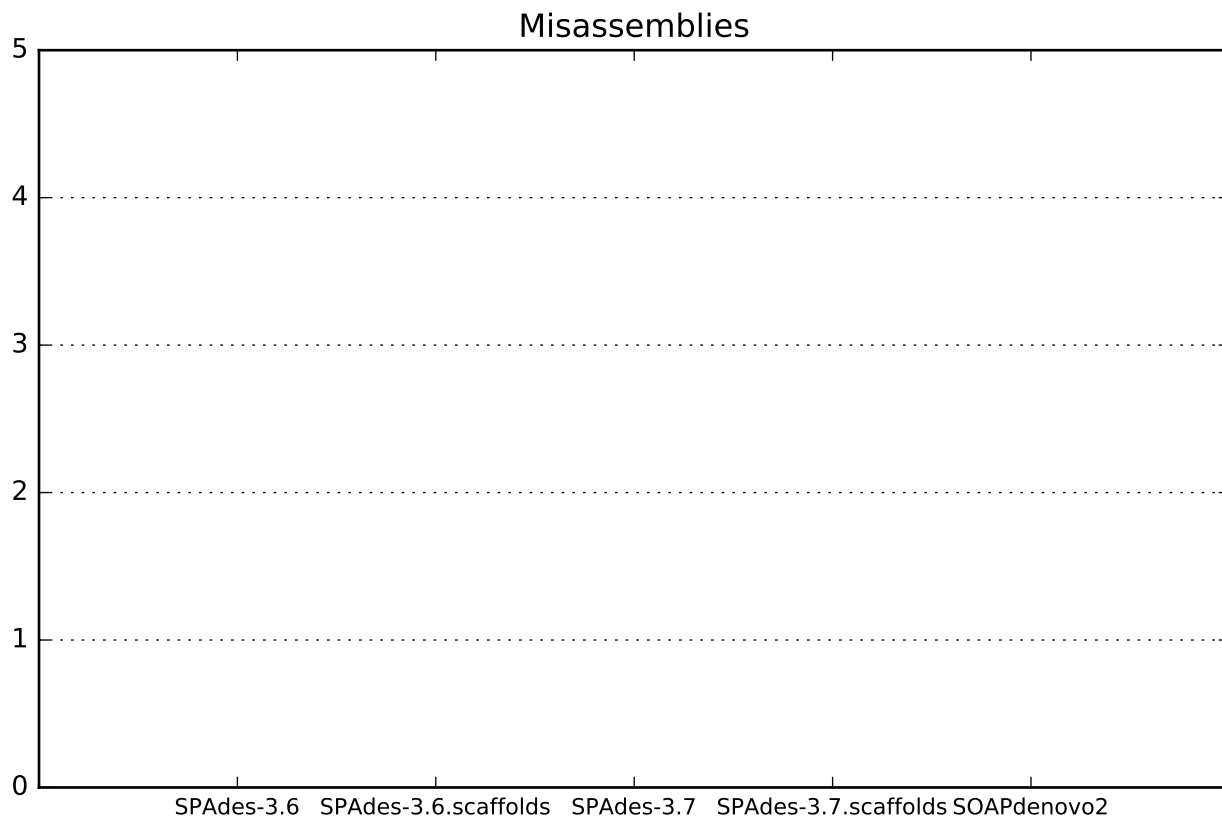


SPAdes-3.7 coverage histogram (bin size: 3x)

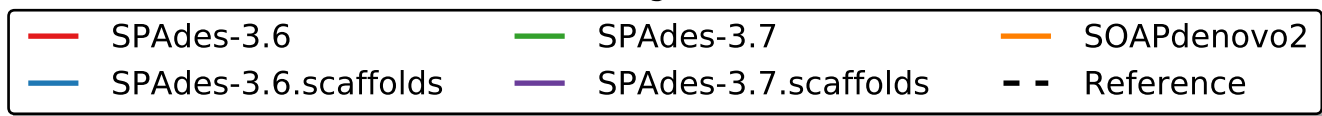
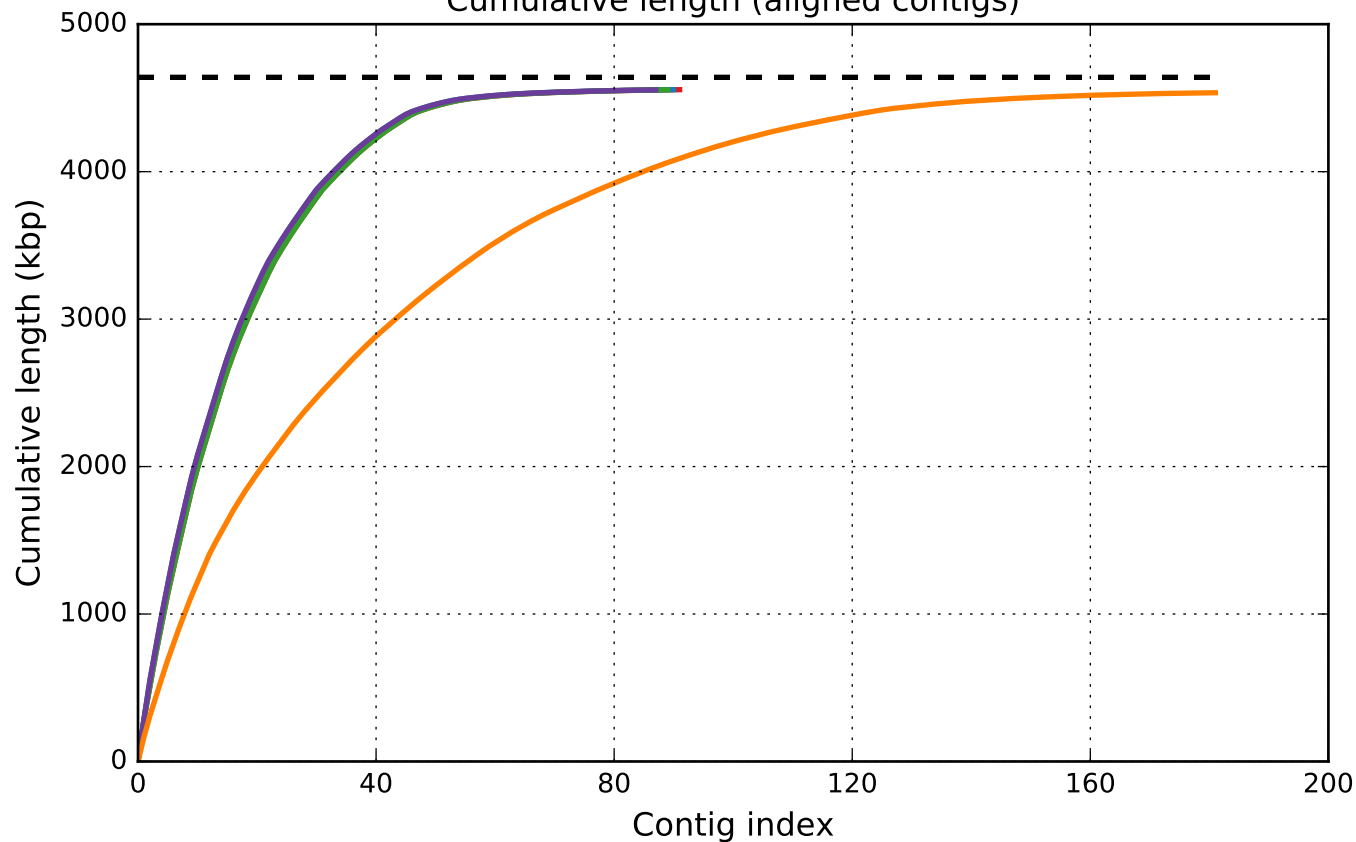


SPAdes-3.7.scaffolds coverage histogram (bin size: 4x)

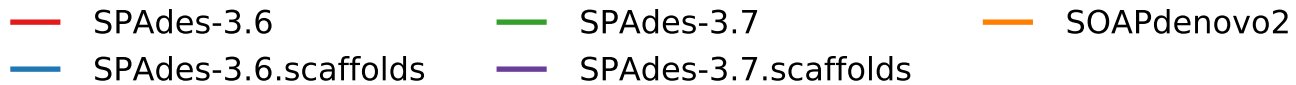
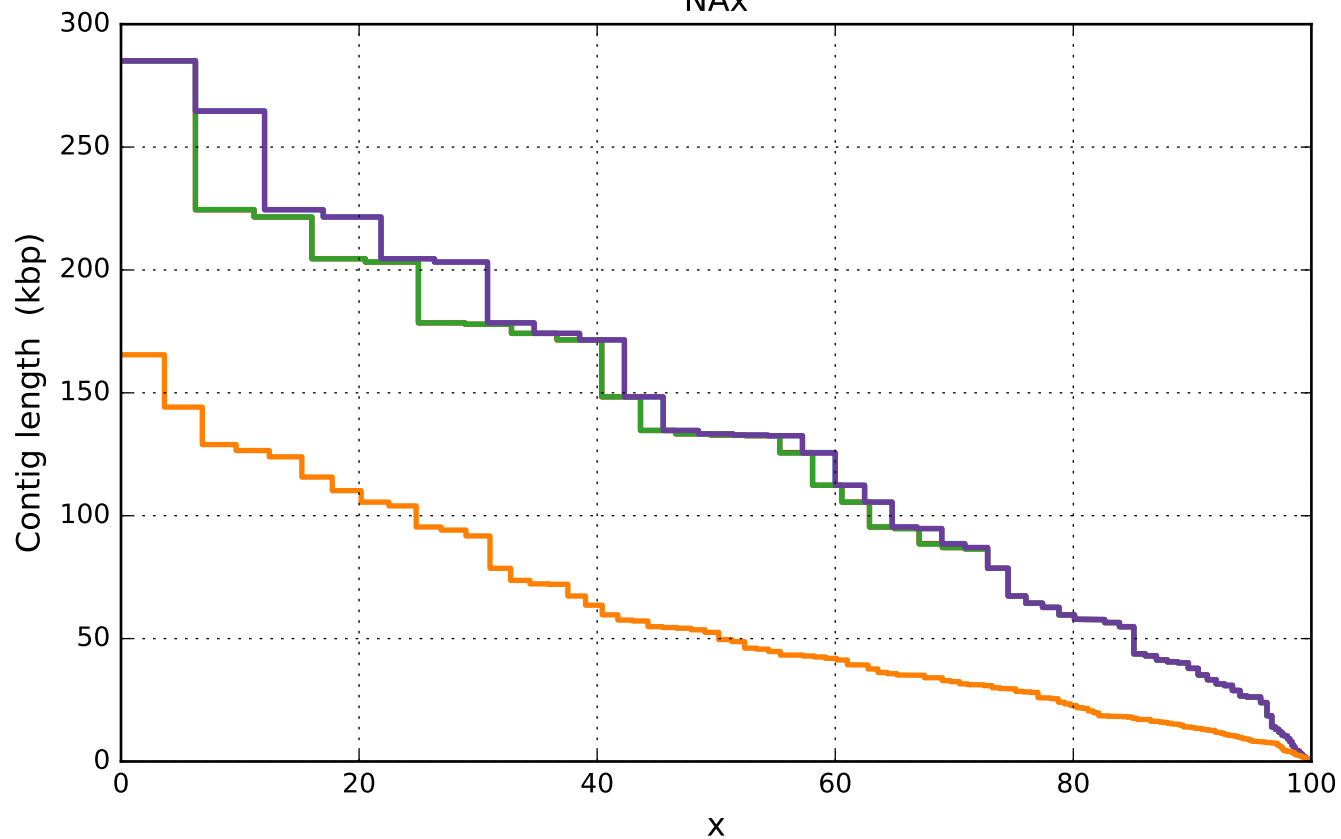




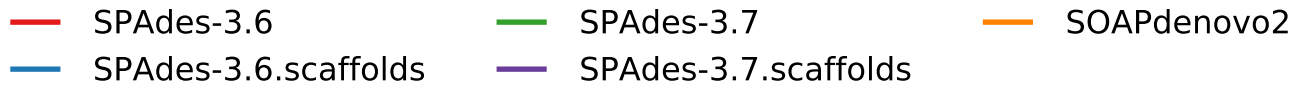
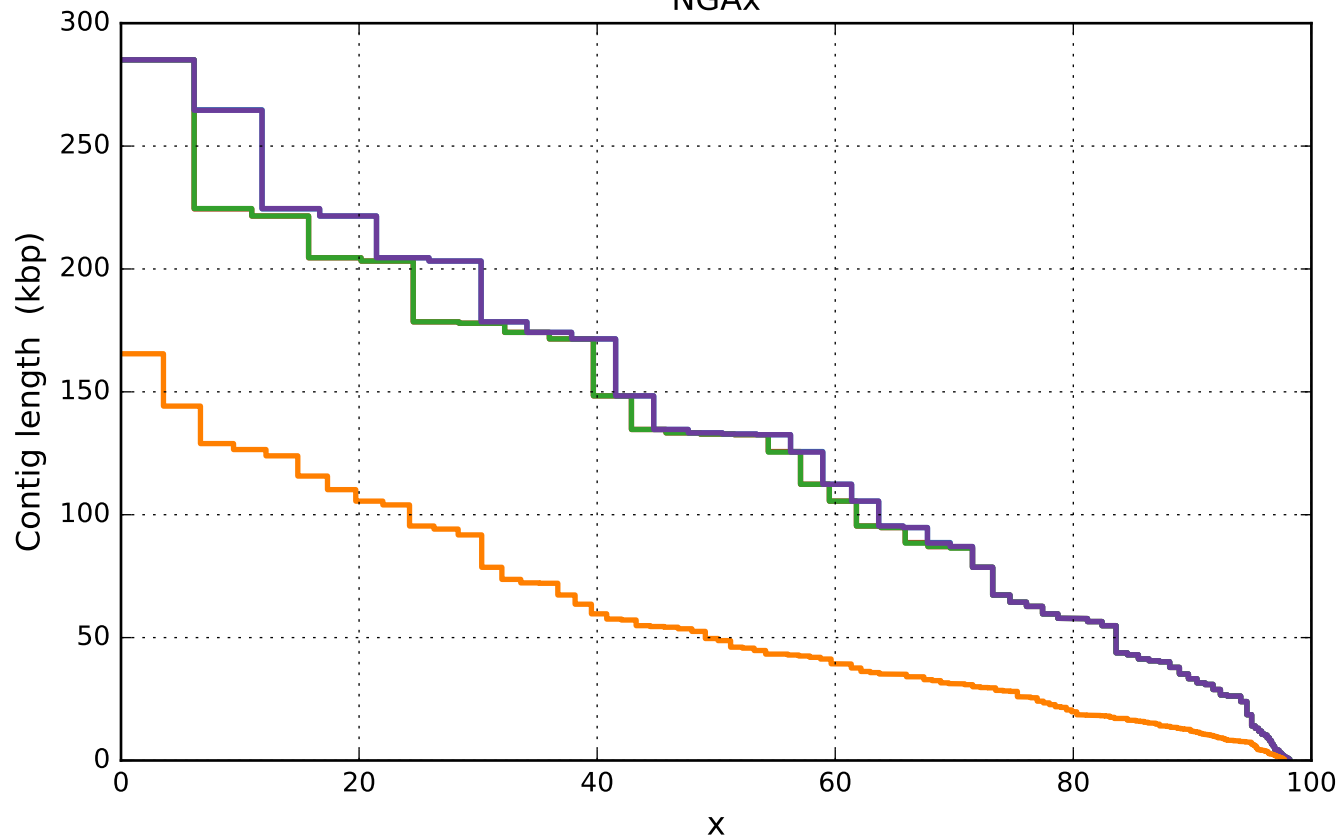
Cumulative length (aligned contigs)



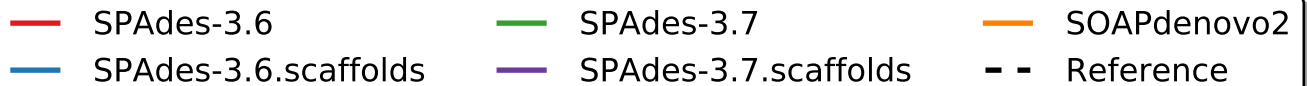
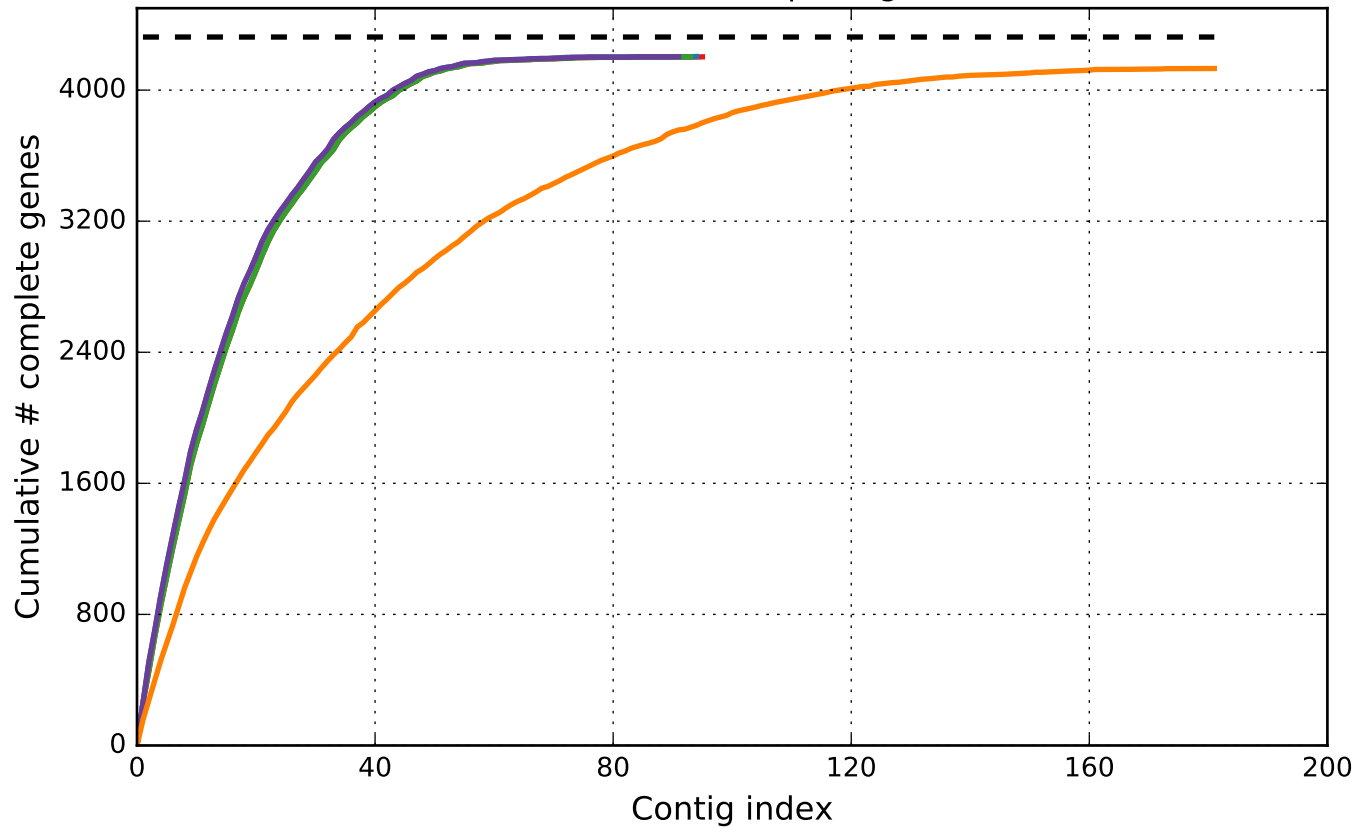
NAx



NGAx



Cumulative # complete genes



complete genes

