

Report

	SPAdes_on_data_16_and_data_15__Scaffolds	SPAdes_on_data_16_and_data_15__Scaffolds_broken
# contigs (>= 0 bp)	646	-
# contigs (>= 1000 bp)	74	79
Total length (>= 0 bp)	8674688	-
Total length (>= 1000 bp)	8563276	8561240
# contigs	85	92
Largest contig	1014754	1014754
Total length	8570949	8569993
Reference length	4376831	4376831
GC (%)	44.54	44.54
Reference GC (%)	45.84	45.84
N50	399640	312531
NG50	652424	425453
N90	62321	62321
NG90	422477	334298
auN	445439.5	373764.7
auNG	872283.9	731844.9
L50	8	9
LG50	3	4
L90	24	28
LG90	7	8
# misassemblies	38	39
# misassembled contigs	13	16
Misassembled contigs length	3806505	3625673
# local misassemblies	33	33
# scaffold gap ext. mis.	0	-
# scaffold gap loc. mis.	1	-
# unaligned mis. contigs	3	3
# unaligned contigs	26 + 29 part	29 + 30 part
Unaligned length	4492343	4491637
Genome fraction (%)	93.360	93.359
Duplication ratio	1.001	1.001
# N's per 100 kbp	9.33	0.00
# mismatches per 100 kbp	604.12	604.12
# indels per 100 kbp	20.33	20.28
# genomic features	4178 + 111 part	4175 + 114 part
Complete BUSCO (%)	92.57	92.57
Partial BUSCO (%)	0.68	0.68
# predicted rRNA genes	3 + 1 part	3 + 1 part
Largest alignment	308191	308191
Total aligned length	4077167	4076980
NA50	-	-
NGA50	117956	114173
NA90	-	-
NGA90	11495	11495
auNA	71801.2	64962.3
auNGA	140605.1	127198.4
LA50	-	-
LGA50	11	13
LA90	-	-
LGA90	50	53

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

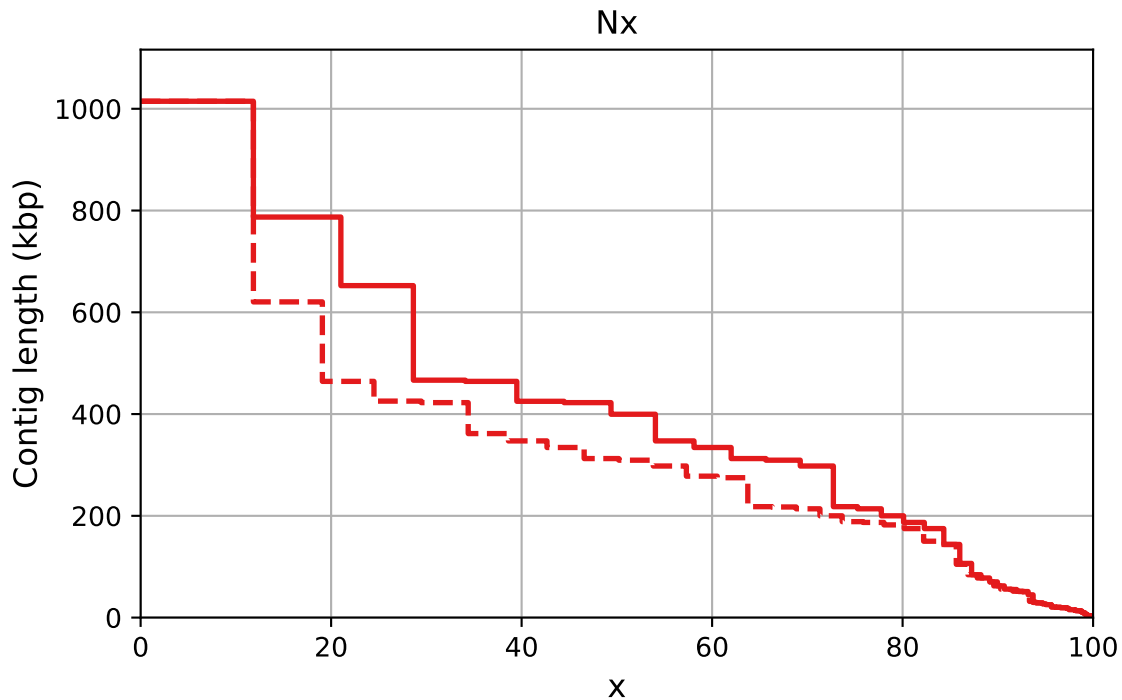
	SPAdes_on_data_16_and_data_15__Scaffolds	SPAdes_on_data_16_and_data_15__Scaffolds_broken
# misassemblies	38	39
# contig misassemblies	38	39
# c. relocations	38	39
# c. translocations	0	0
# c. inversions	0	0
# scaffold misassemblies	0	0
# s. relocations	0	0
# s. translocations	0	0
# s. inversions	0	0
# misassembled contigs	13	16
Misassembled contigs length	3806505	3625673
# local misassemblies	33	33
# scaffold gap ext. mis.	0	-
# scaffold gap loc. mis.	1	-
# unaligned mis. contigs	3	3
# mismatches	24631	24630
# indels	829	827
# indels (<= 5 bp)	707	706
# indels (> 5 bp)	122	121
Indels length	4300	3982

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_on_data_16_and_data_15__Scaffolds	SPAdes_on_data_16_and_data_15__Scaffolds_broken
# fully unaligned contigs	26	29
Fully unaligned length	707133	888902
# partially unaligned contigs	29	30
Partially unaligned length	3785210	3602735
# N's	800	0

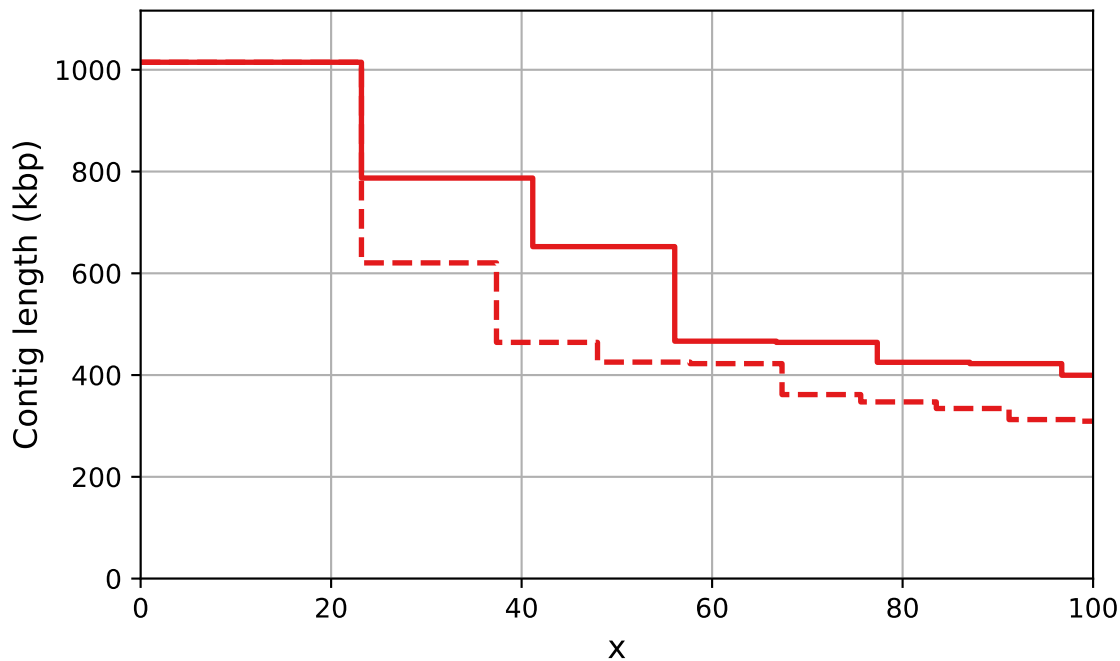
All statistics are based on contigs of size ≥ 500 bp, unless otherwise noted (e.g., "# contigs (≥ 0 bp)" and "Total length (≥ 0 bp)" include all contigs).



des_on_data_16_and_data_15_Scaffolds

--- SPAdes_on_data_16_and_data_15_Scaffolds

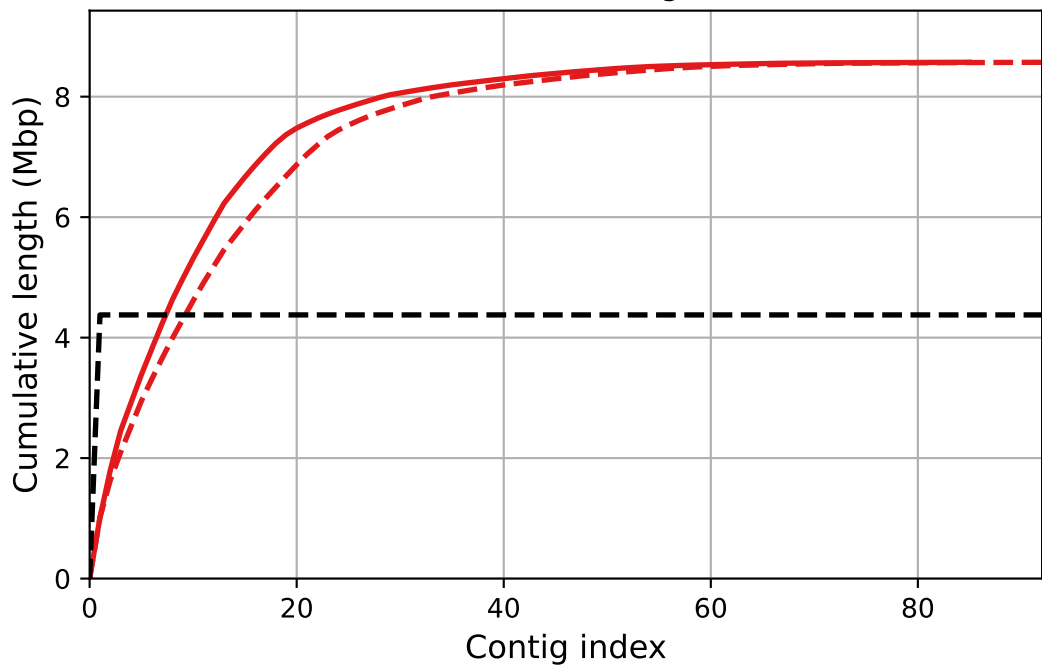
NGx



des_on_data_16_and_data_15_Scaffolds

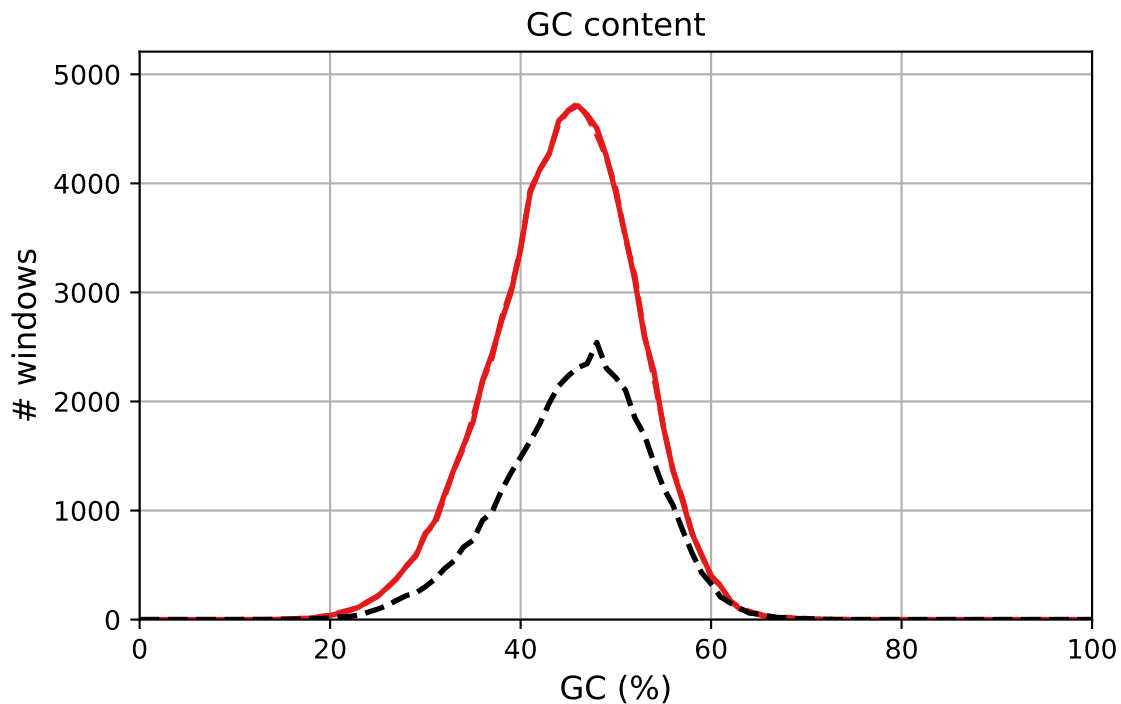
-- SPAdes_on_data_16_and_data_15_Scaffolds

Cumulative length



data_16_and_data_15__Scaffolds

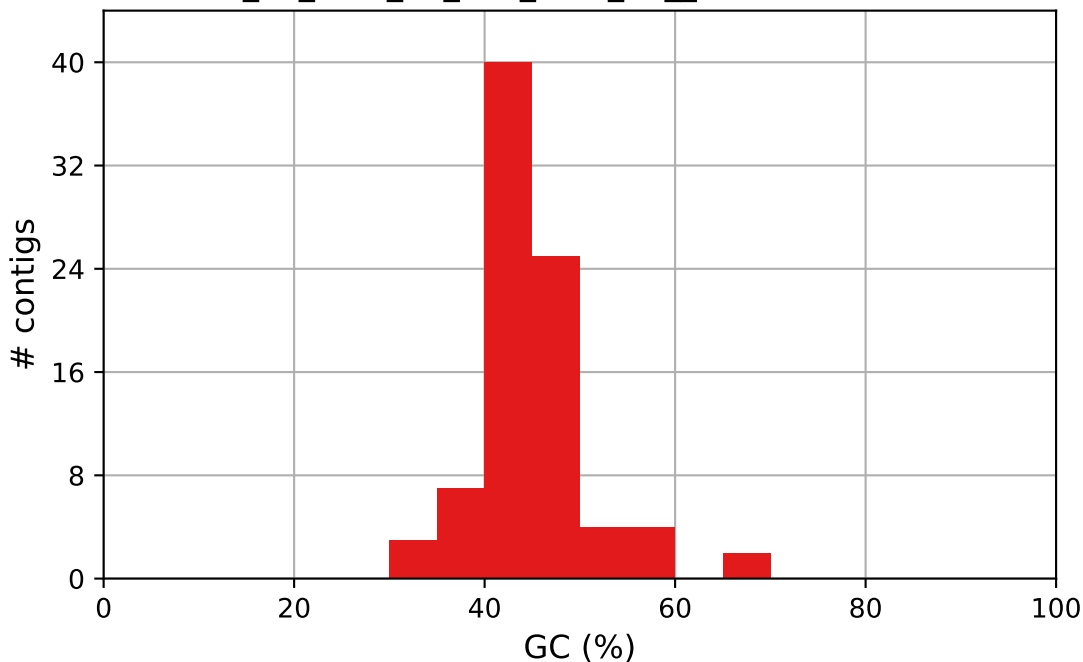
-- SPAdes_on_data_16_and_data_15__Scaffolds_broken



data_16_and_data_15_Scaffolds

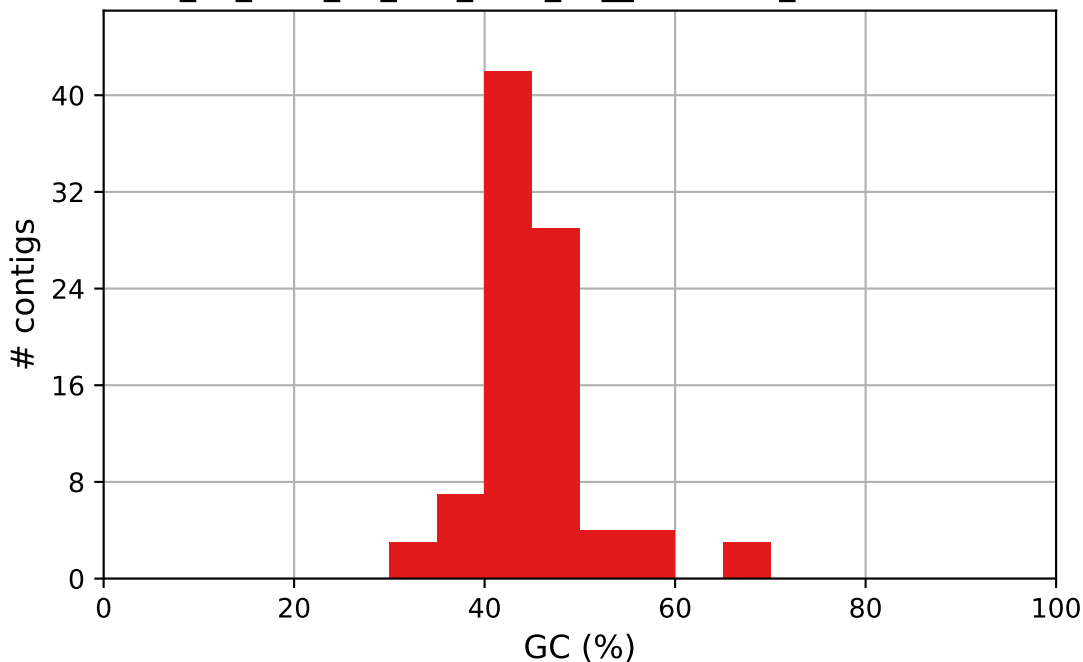
SPAdes_on_data_16_and_data_15_Scaffolds_broken

SPAdes_on_data_16_and_data_15__Scaffolds GC content



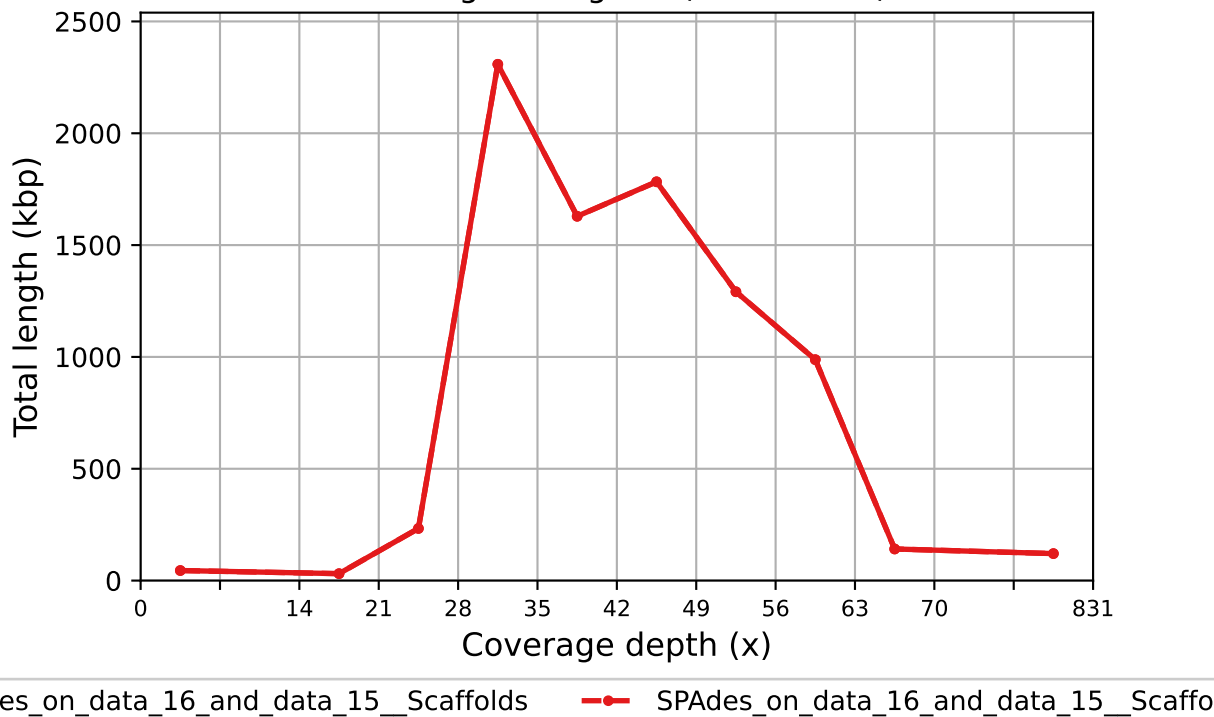
SPAdes_on_data_16_and_data_15__Scaffolds

SPAdes_on_data_16_and_data_15__Scaffolds_broken GC content

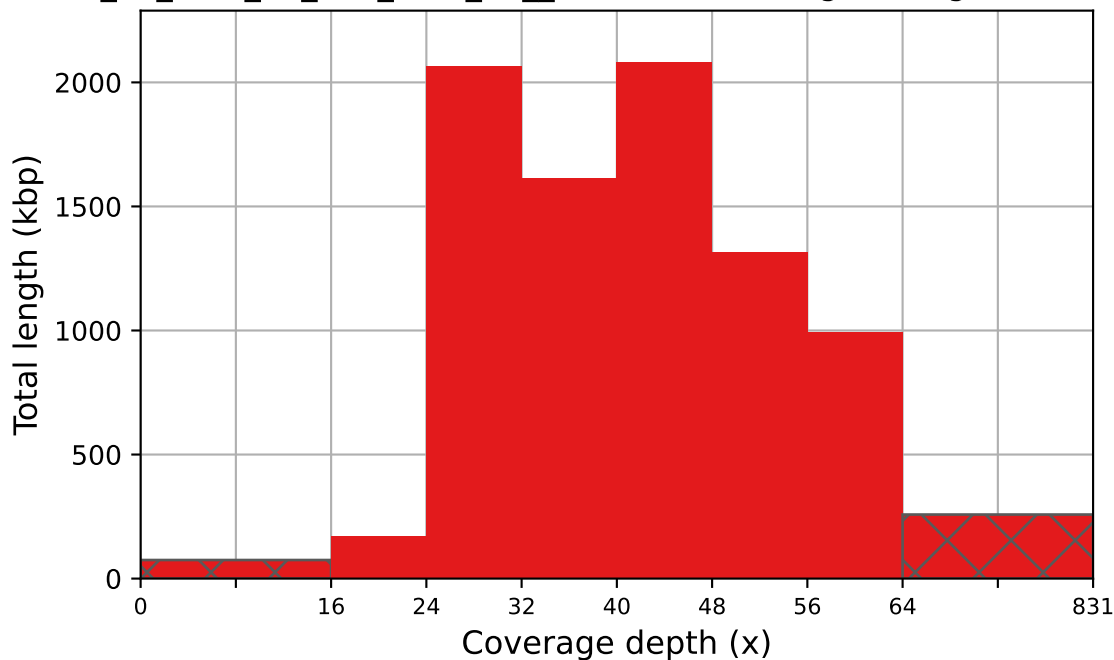


SPAdes_on_data_16_and_data_15__Scaffolds_broken

Coverage histogram (bin size: 7x)

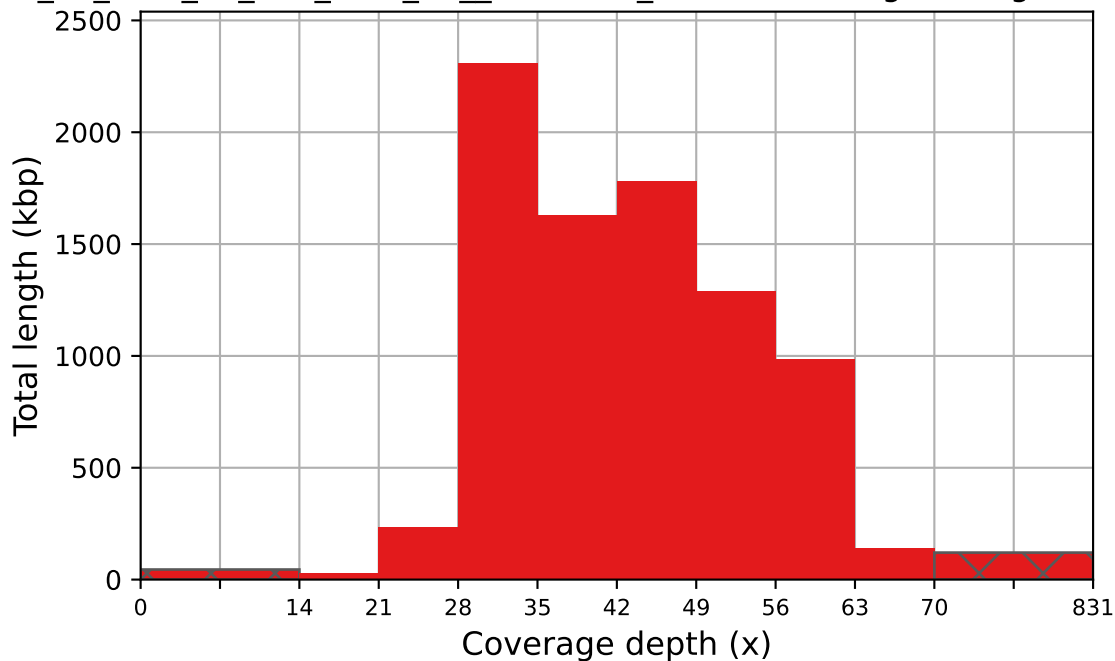


SPAdes_on_data_16_and_data_15__Scaffolds coverage histogram (bin size: 8



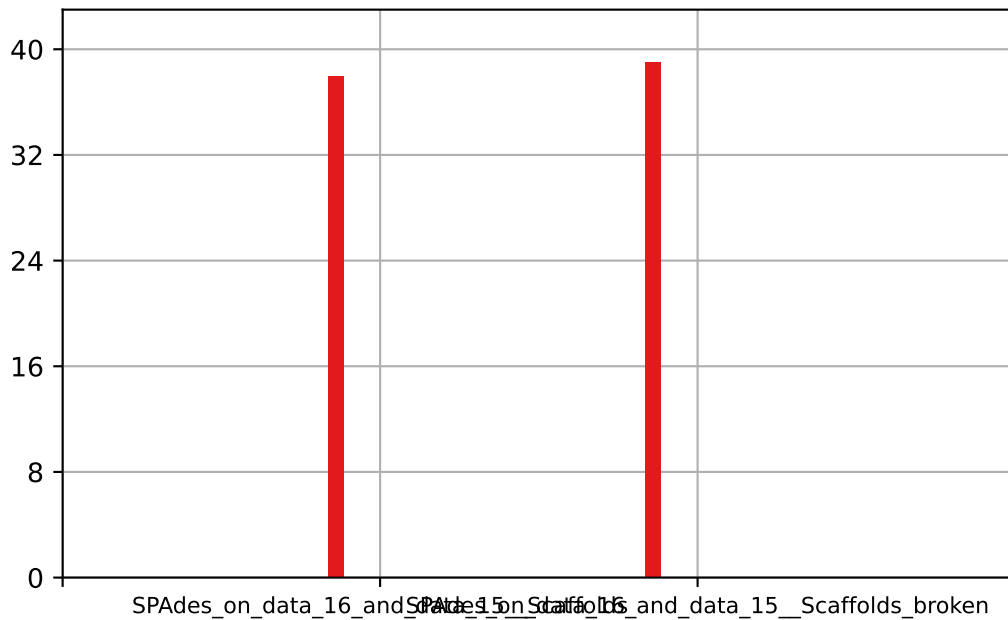
SPAdes_on_data_16_and_data_15__Scaffolds

des_on_data_16_and_data_15__Scaffolds_broken coverage histogram (bin size 7)

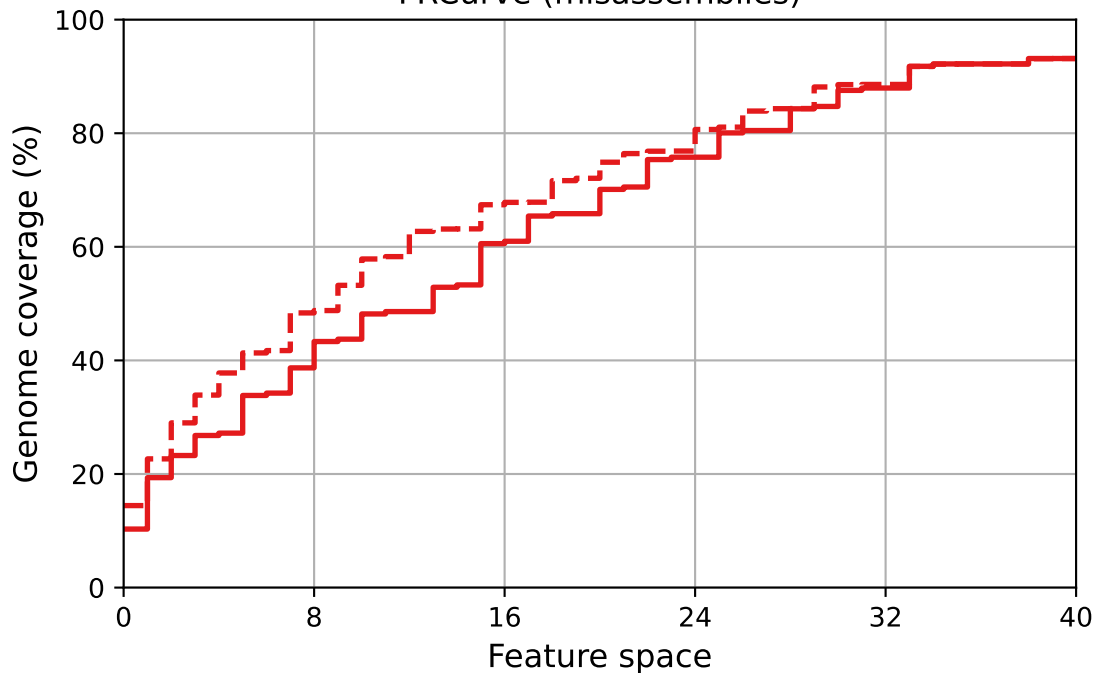


SPAdes_on_data_16_and_data_15__Scaffolds_broken

Misassemblies



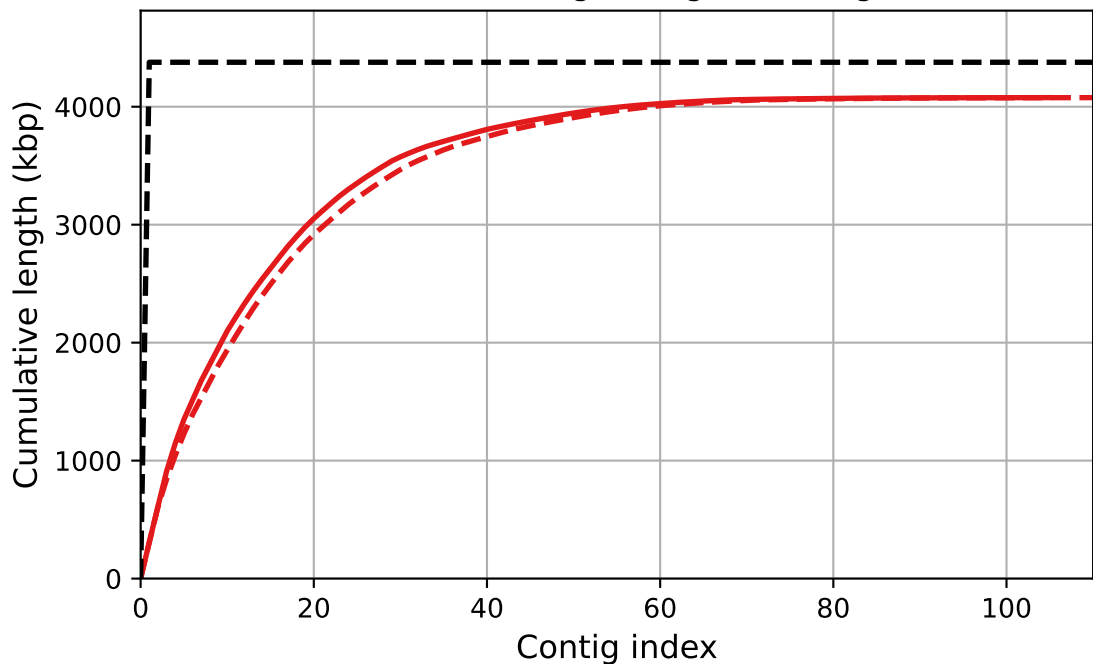
FRCurve (misassemblies)



des_on_data_16_and_data_15_Scaffolds

-- SPAdes_on_data_16_and_data_15_Scaffolds

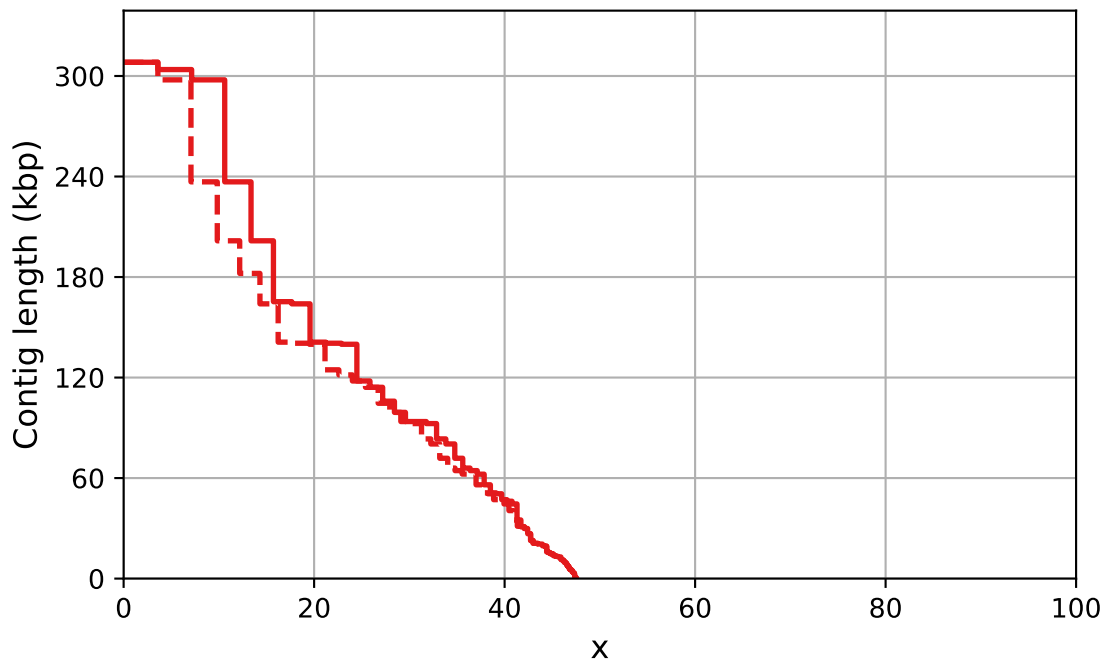
Cumulative length (aligned contigs)



data_16_and_data_15__Scaffolds

SPAdes_on_data_16_and_data_15__Scaffolds_broken

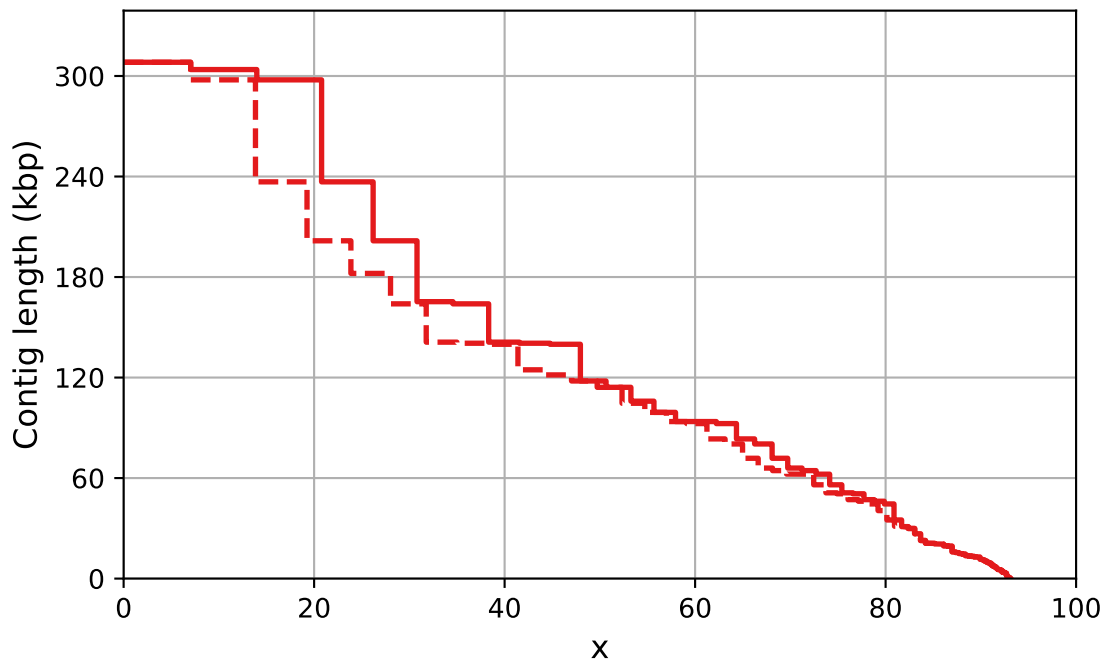
NAx



des_on_data_16_and_data_15_Scaffolds

-- SPAdes_on_data_16_and_data_15_Scaffolds

NGAx

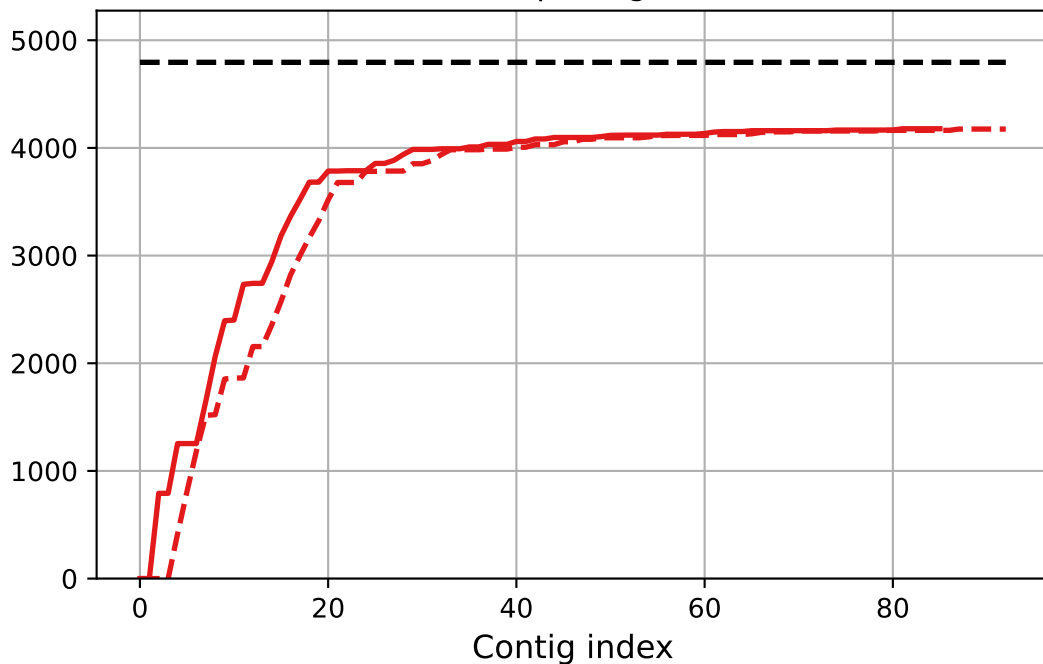


des_on_data_16_and_data_15_Scaffolds

-- SPAdes_on_data_16_and_data_15_Scaffolds

Cumulative # complete genomic features

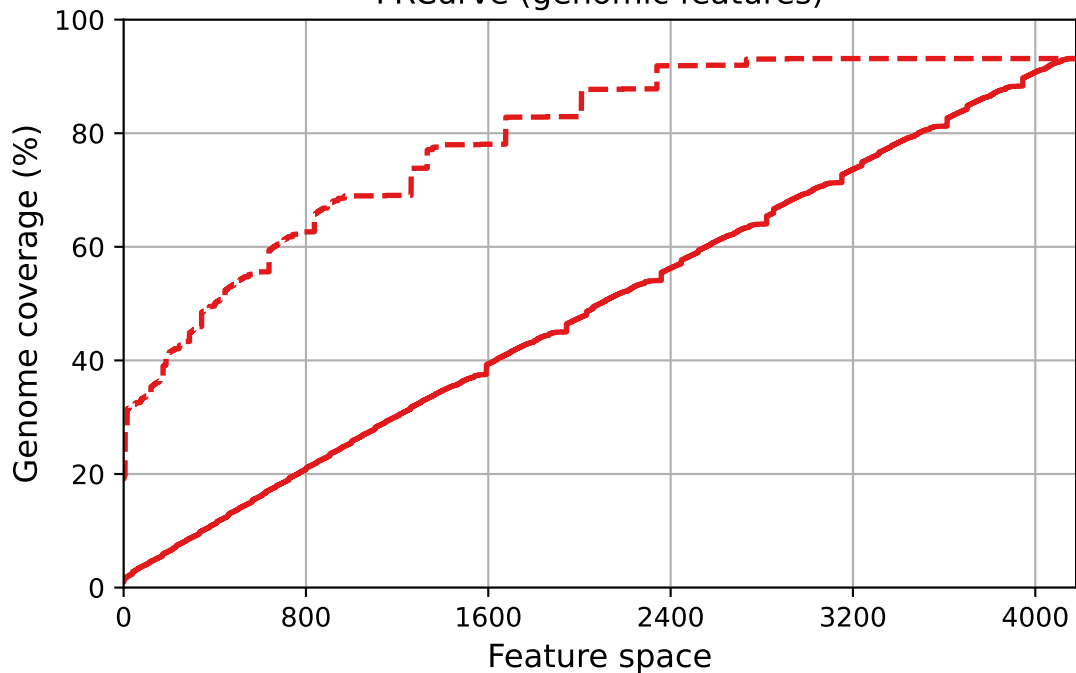
Cumulative # complete genomic features



data_16_and_data_15__Scaffolds

SPAdes_on_data_16_and_data_15__Scaffolds_broken

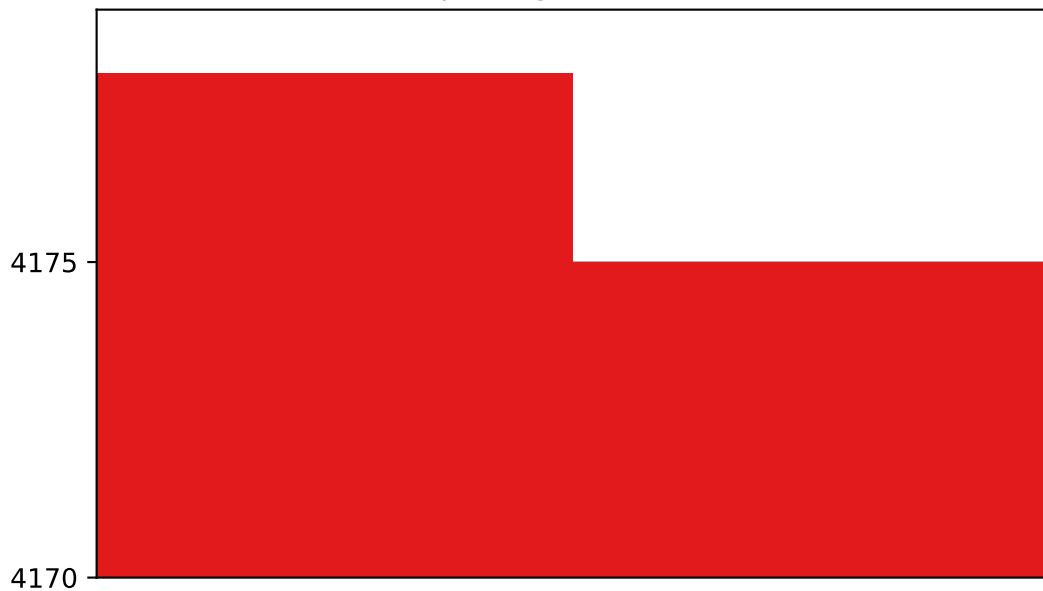
FRCurve (genomic features)



des_on_data_16_and_data_15_Scaffolds

-- SPAdes_on_data_16_and_data_15_Scaffolds

complete genomic features



des_on_data_16_and_data_15_Scaffolds



SPAdes_on_data_16_and_data_15_Scaffolds

Genome fraction, %

100

95

des_on_data_16_and_data_15__Scaffolds



SPAdes_on_data_16_and_data_15__Scaffolds