

Report

	Spades_Default	Spades_Careful
# contigs (>= 0 bp)	305	322
# contigs (>= 1000 bp)	28	29
# contigs (>= 5000 bp)	21	24
# contigs (>= 10000 bp)	18	21
# contigs (>= 25000 bp)	17	19
# contigs (>= 50000 bp)	11	8
Total length (>= 0 bp)	1720704	1725382
Total length (>= 1000 bp)	1656470	1658832
Total length (>= 5000 bp)	1639109	1643537
Total length (>= 10000 bp)	1612709	1617137
Total length (>= 25000 bp)	1599461	1578815
Total length (>= 50000 bp)	1406073	1184881
# contigs	36	34
Largest contig	363181	362857
Total length	1662539	1662469
Reference length	1641481	1641481
GC (%)	30.42	30.42
Reference GC (%)	30.55	30.55
N50	142894	142894
NG50	142894	142894
N90	32795	29175
NG90	32841	29175
auN	161237.2	156897.5
auNG	163305.6	158903.6
L50	4	4
LG50	4	4
L90	14	16
LG90	13	16
# misassemblies	8	8
# misassembled contigs	5	5
Misassembled contigs length	842810	902886
# local misassemblies	5	6
# scaffold gap ext. mis.	0	0
# scaffold gap loc. mis.	0	0
# unaligned mis. contigs	0	0
# unaligned contigs	2 + 7 part	1 + 7 part
Unaligned length	51510	50800
Genome fraction (%)	98.023	98.056
Duplication ratio	1.001	1.001
# N's per 100 kbp	0.00	0.00
# mismatches per 100 kbp	376.10	374.85
# indels per 100 kbp	15.58	15.70
# genomic features	7462 + 99 part	7460 + 104 part
Largest alignment	258383	258383
Total aligned length	1611002	1611574
NA50	83240	63823
NGA50	83240	73736
NA90	23571	23676
NGA90	23571	23696
auNA	98421.2	91726.9
auNGA	99683.8	92899.8
LA50	7	8
LGA50	7	7
LA90	22	25
LGA90	22	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

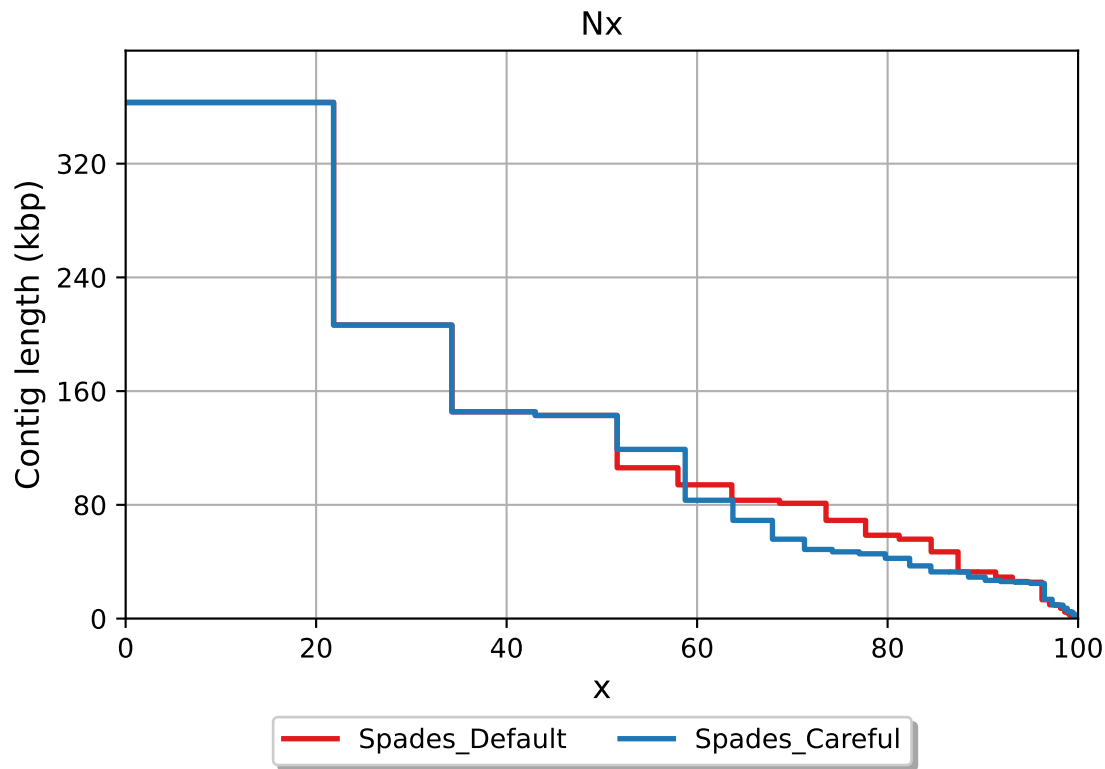
	Spades_Default	Spades_Careful
# misassemblies	8	8
# contig misassemblies	8	8
# c. relocations	8	8
# c. translocations	0	0
# c. inversions	0	0
# scaffold misassemblies	0	0
# s. relocations	0	0
# s. translocations	0	0
# s. inversions	0	0
# misassembled contigs	5	5
Misassembled contigs length	842810	902886
# local misassemblies	5	6
# scaffold gap ext. mis.	0	0
# scaffold gap loc. mis.	0	0
# unaligned mis. contigs	0	0
# mismatches	6059	6041
# indels	251	253
# indels (<= 5 bp)	225	226
# indels (> 5 bp)	26	27
Indels length	1168	1183

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

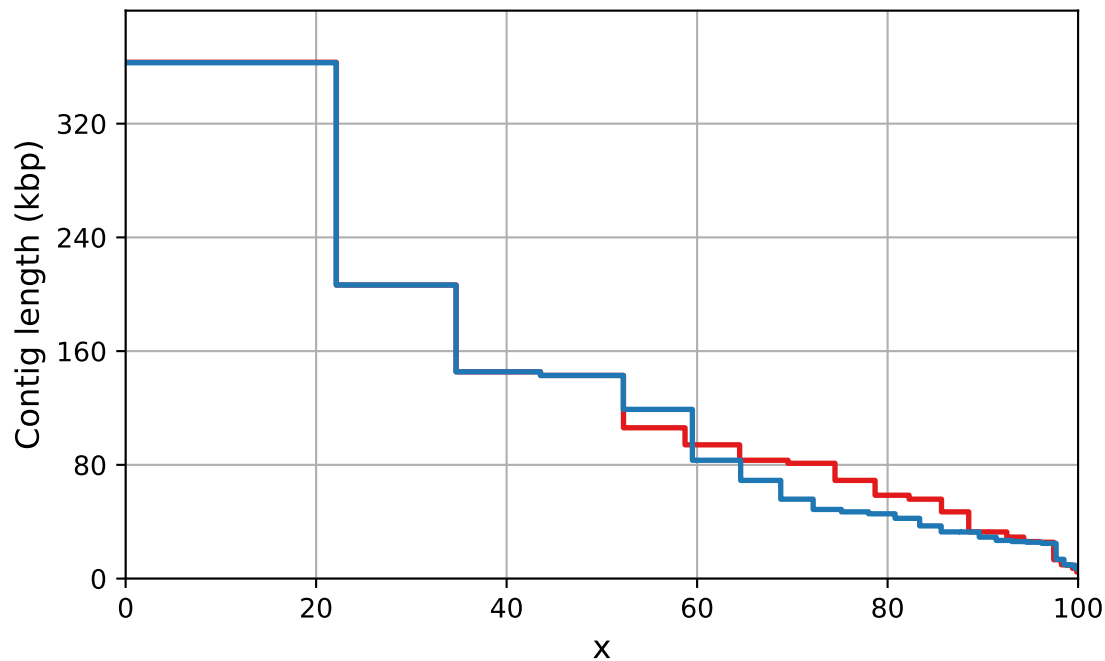
## Unaligned report

	Spades_Default	Spades_Careful
# fully unaligned contigs	2	1
Fully unaligned length	1229	646
# partially unaligned contigs	7	7
Partially unaligned length	50281	50154
# N's	0	0

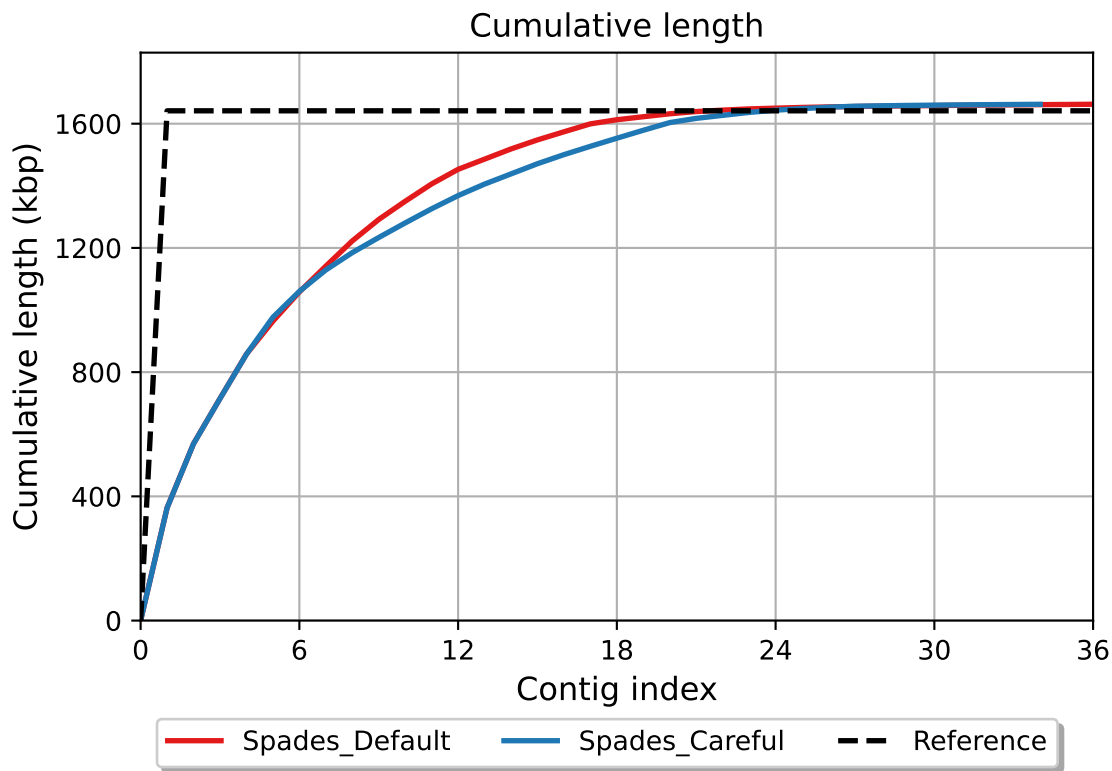
All statistics are based on contigs of size  $\geq 500$  bp, unless otherwise noted (e.g., "# contigs ( $\geq 0$  bp)" and "Total length ( $\geq 0$  bp)" include all contigs).



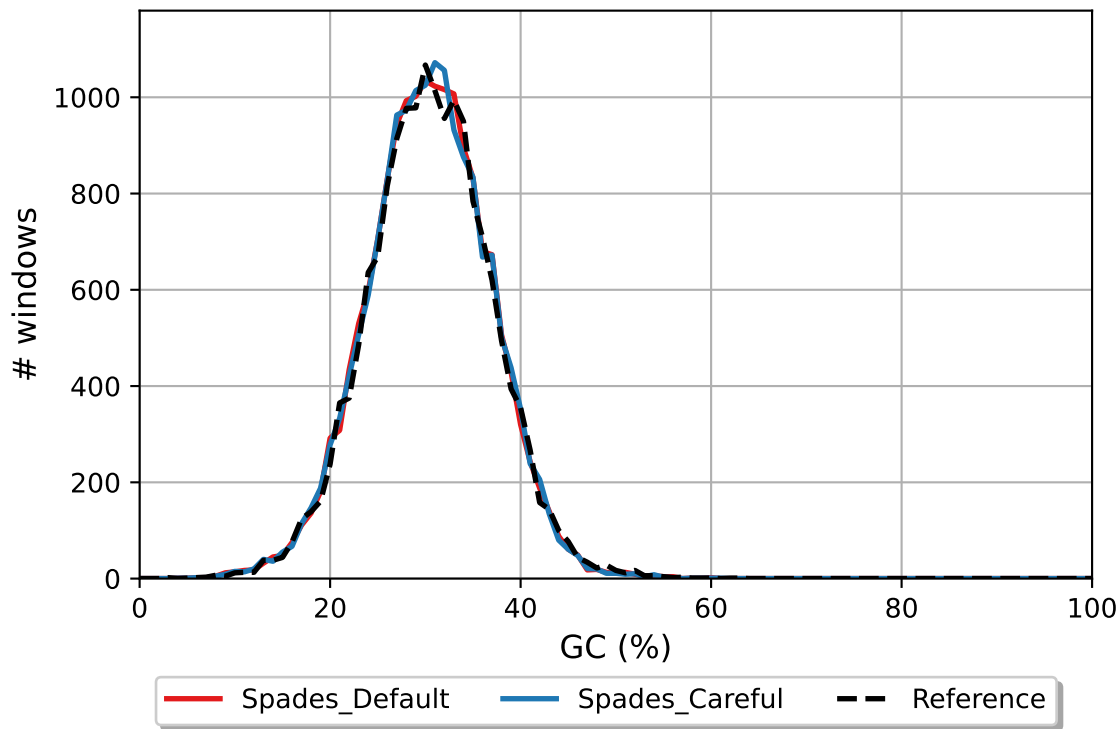
# NGx



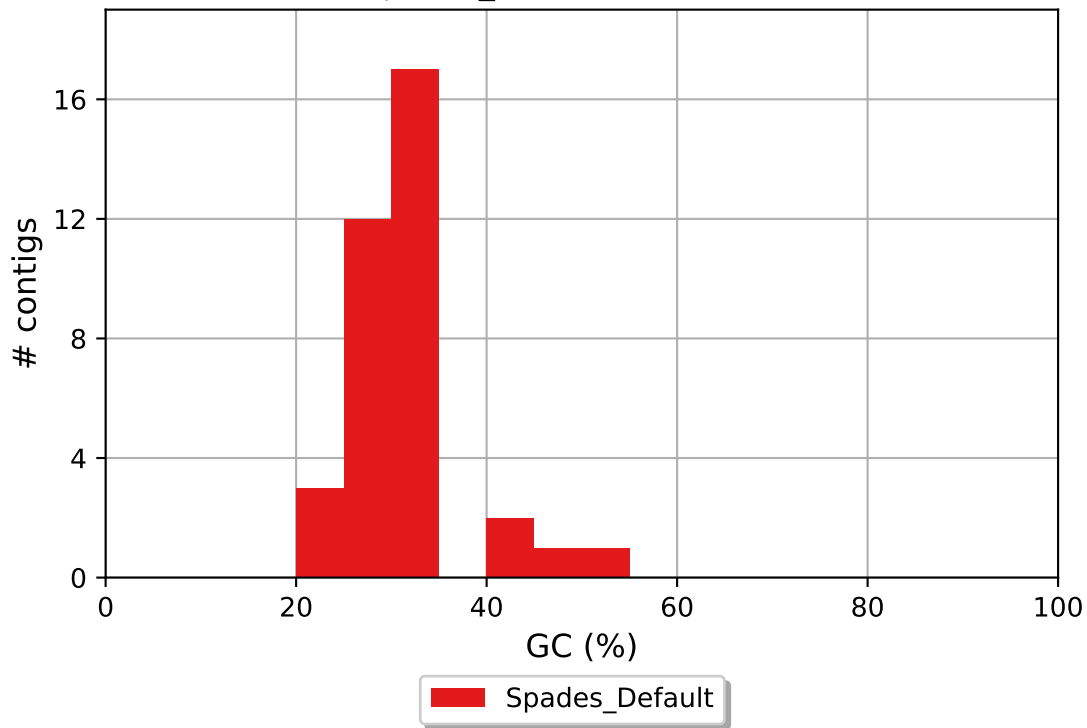
— Spades\_Default — Spades\_Careful



GC content

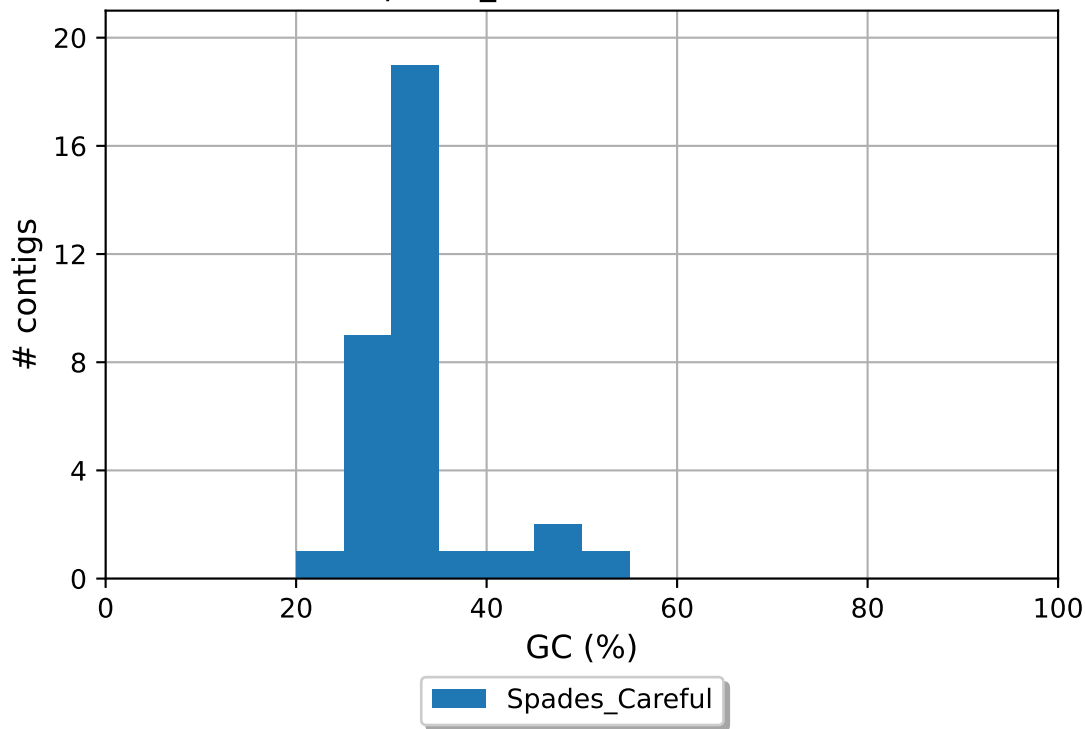


Spades\_Default GC content

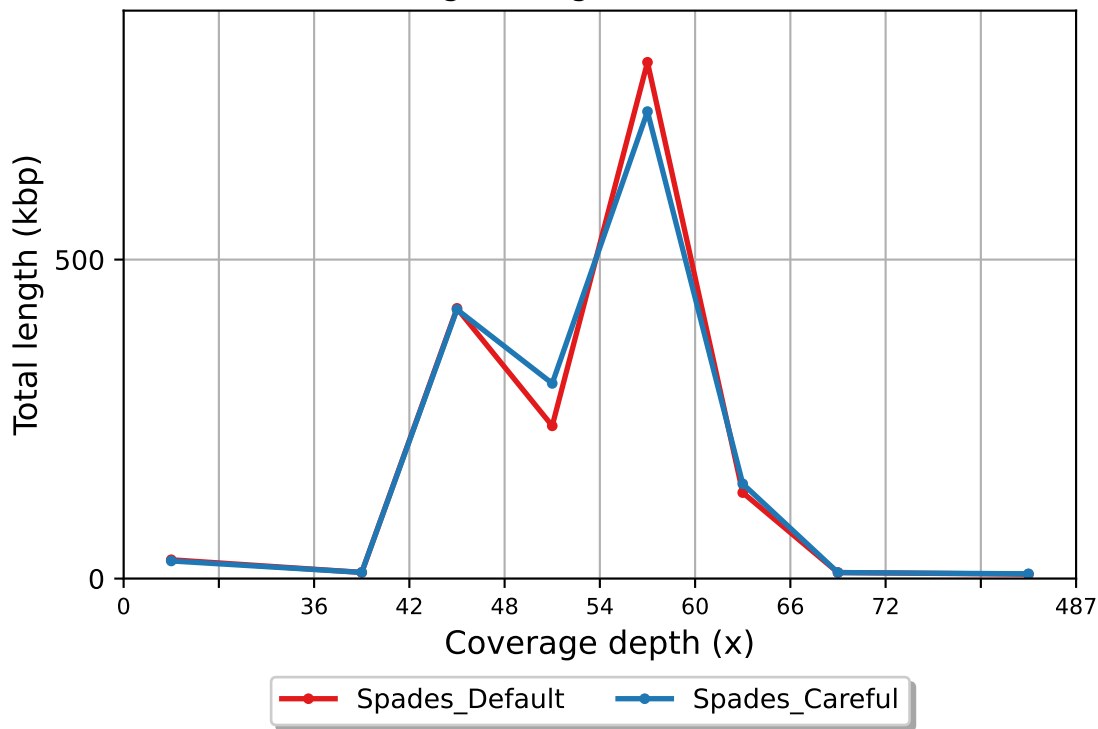




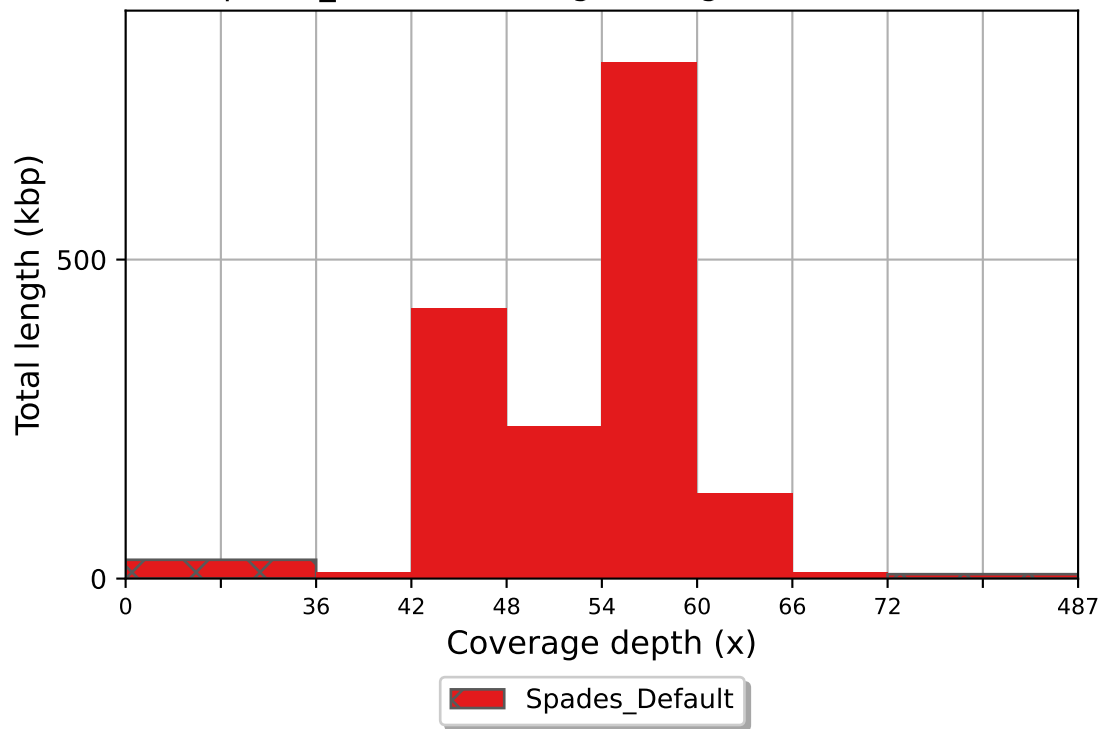
Spades\_Careful GC content



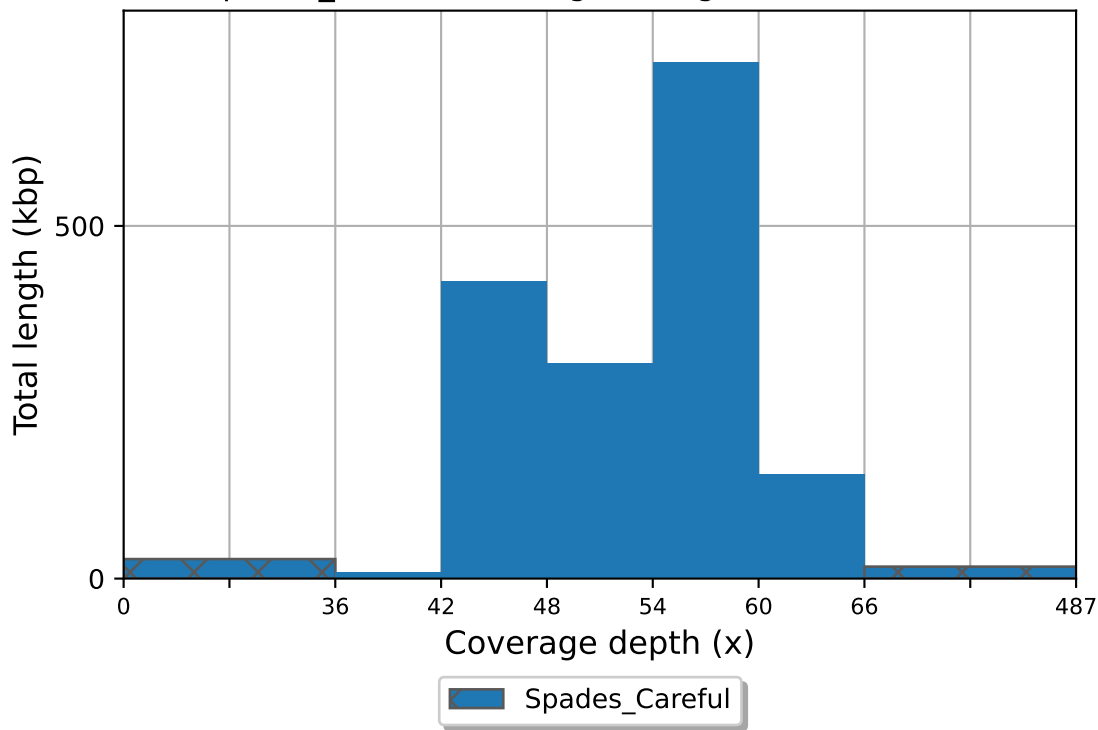
Coverage histogram (bin size: 6x)



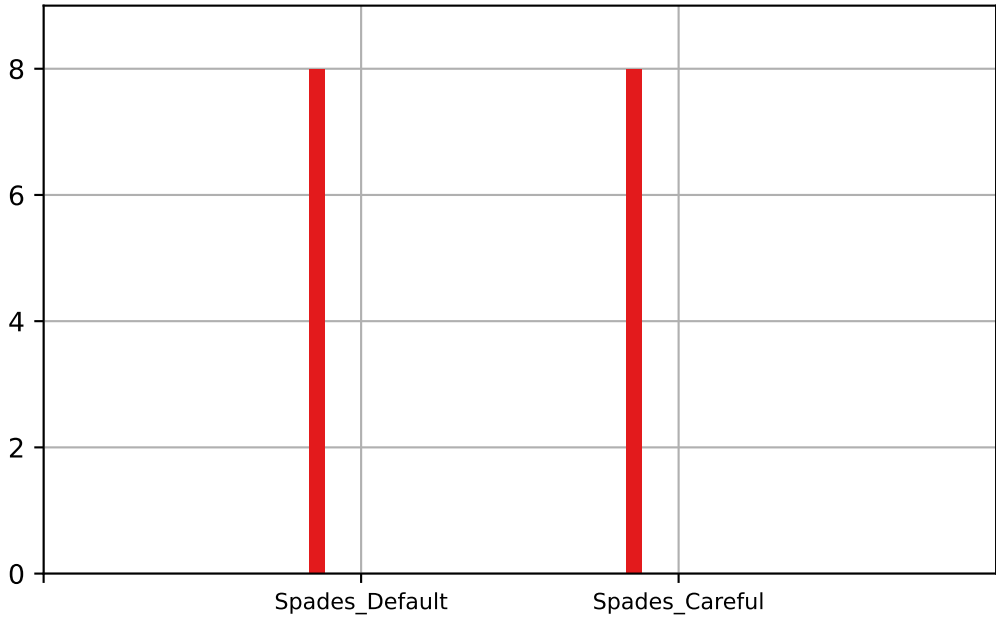
Spades\_Default coverage histogram (bin size: 6x)



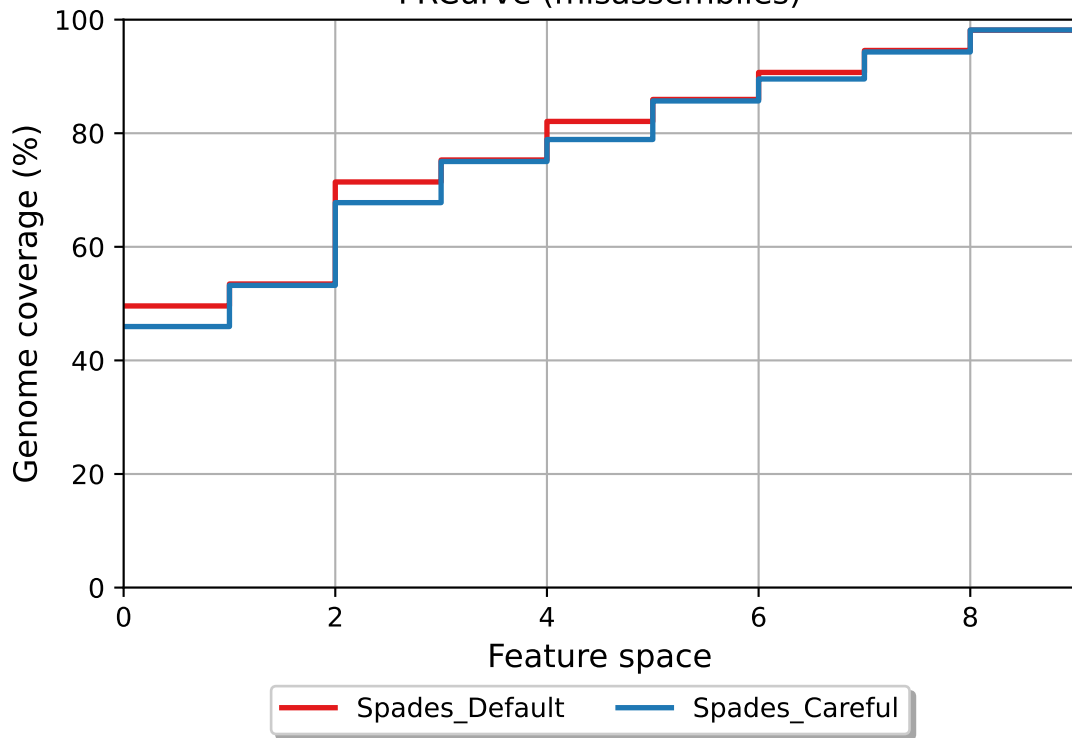
Spades\_Careful coverage histogram (bin size: 6x)



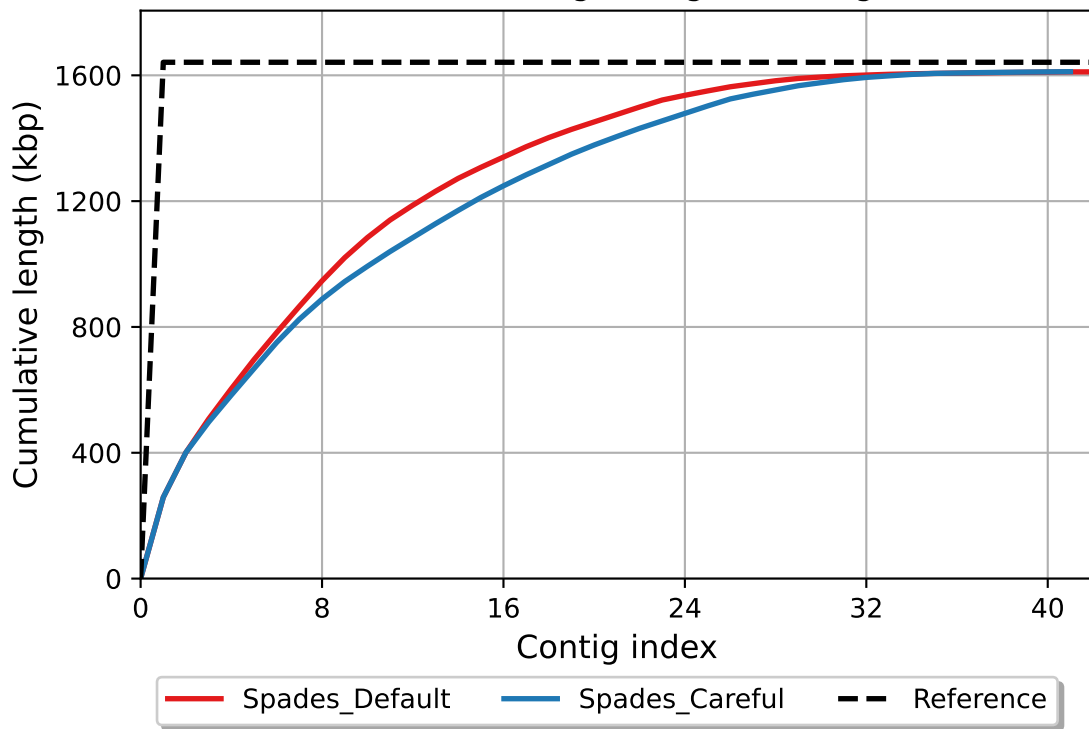
## Misassemblies



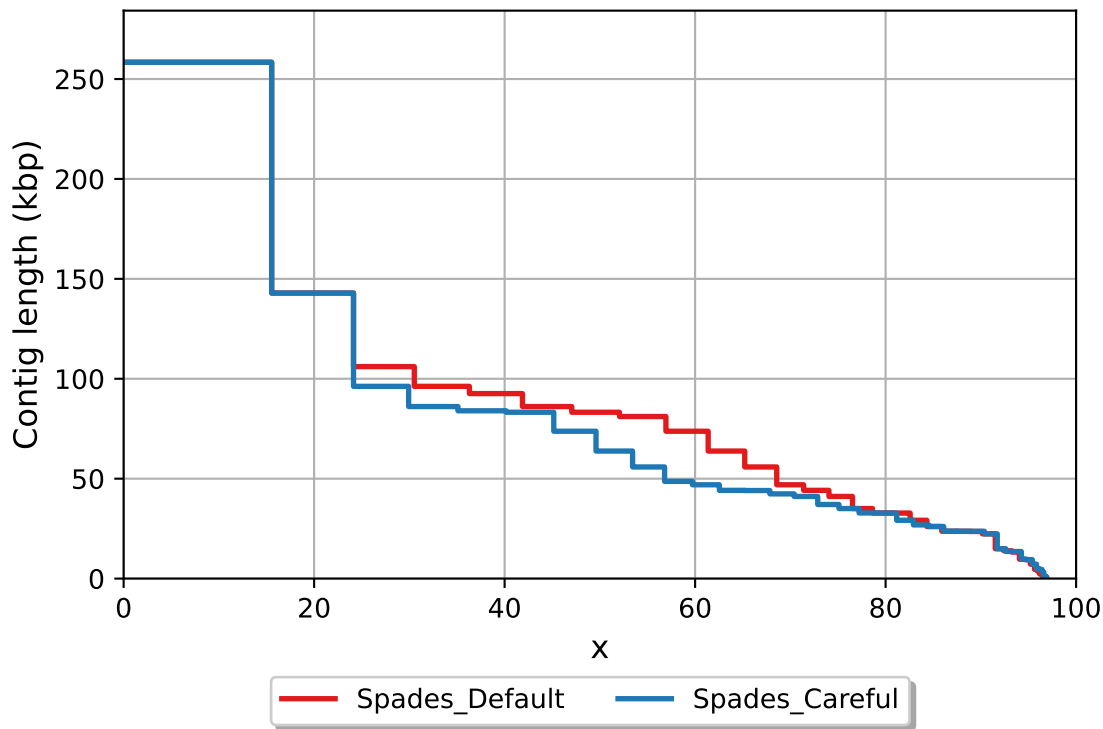
FRCurve (misassemblies)



Cumulative length (aligned contigs)

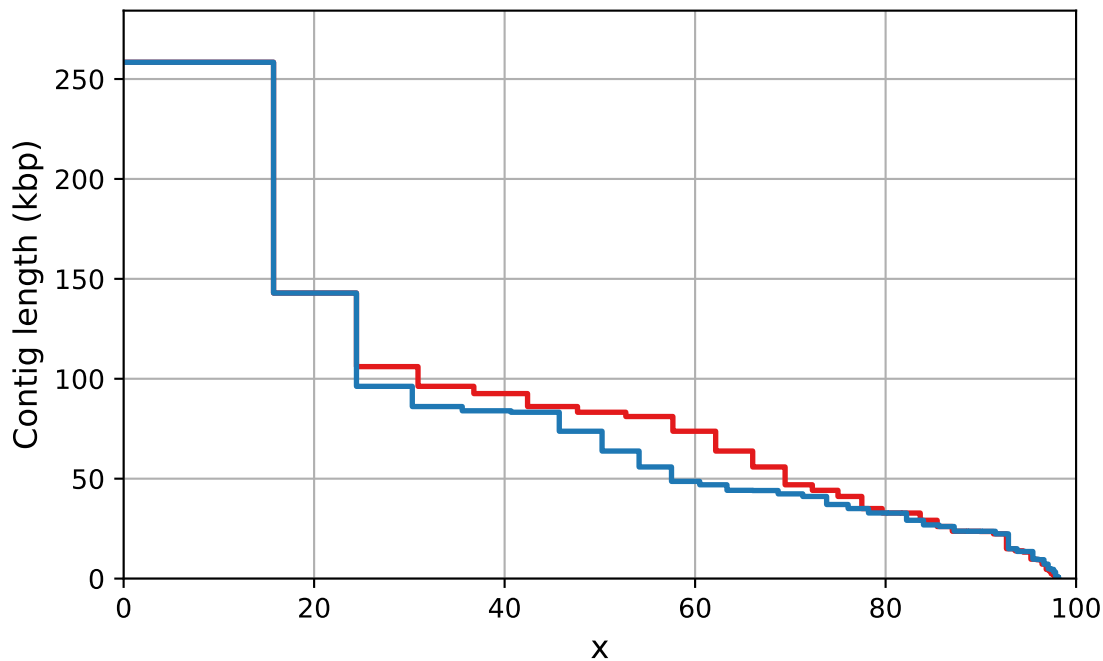


# NAx



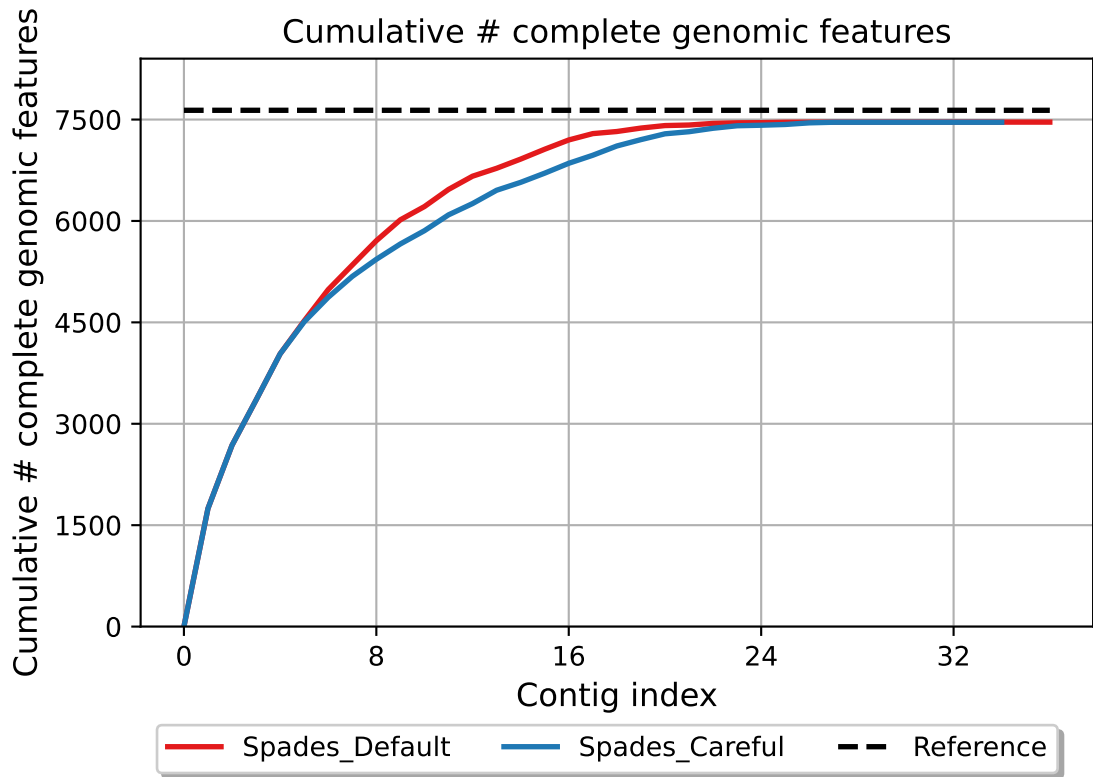


# NGAx

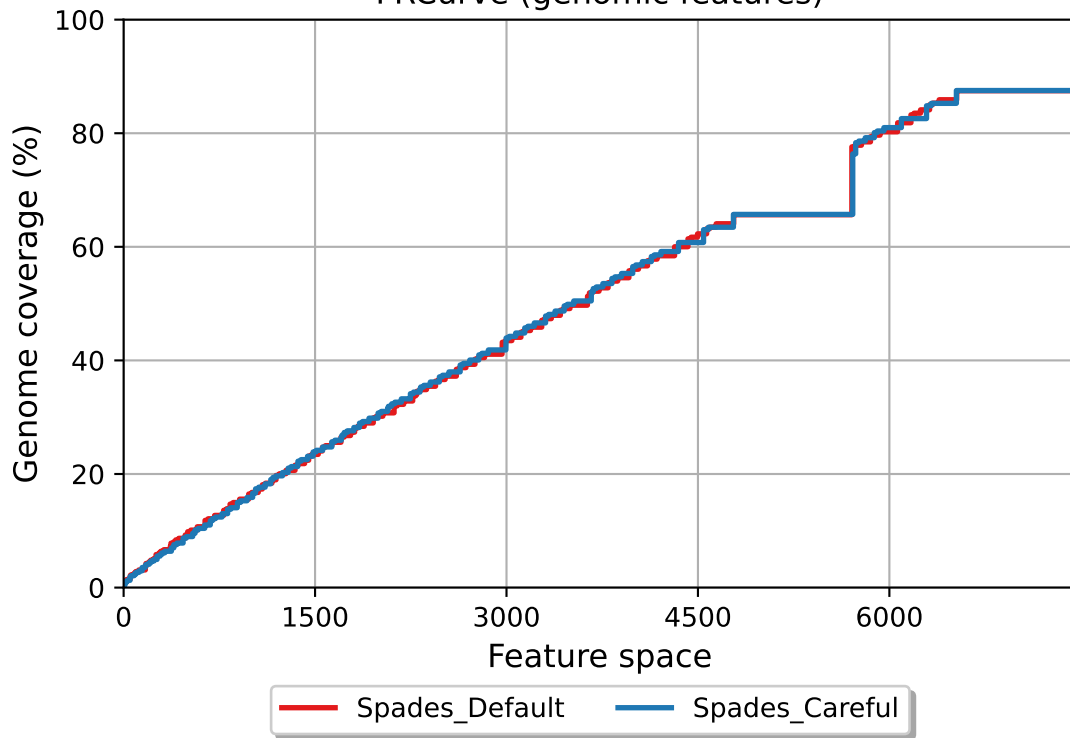


— Spades\_Default

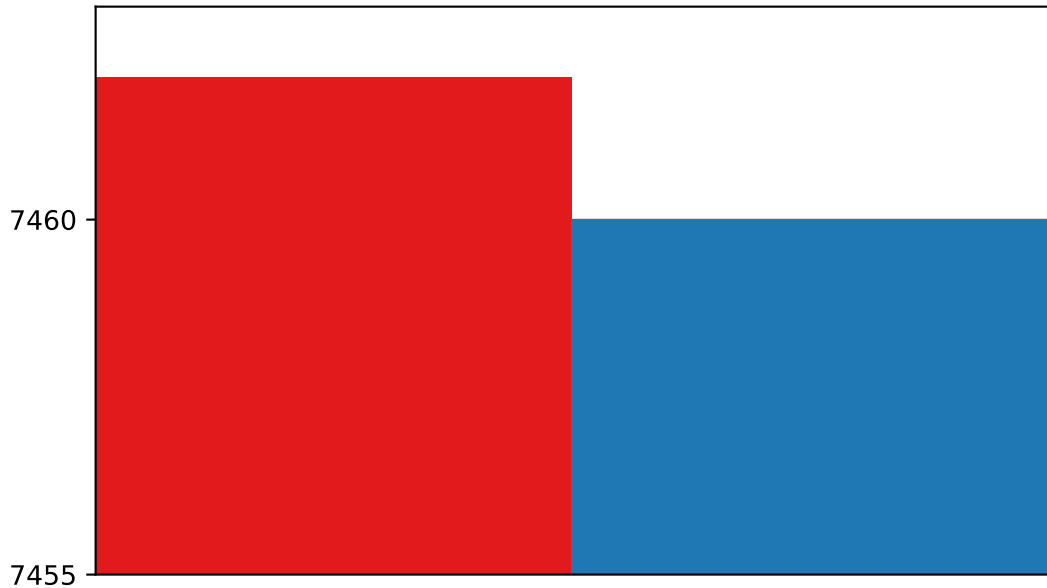
— Spades\_Careful



FRCurve (genomic features)



# complete genomic features

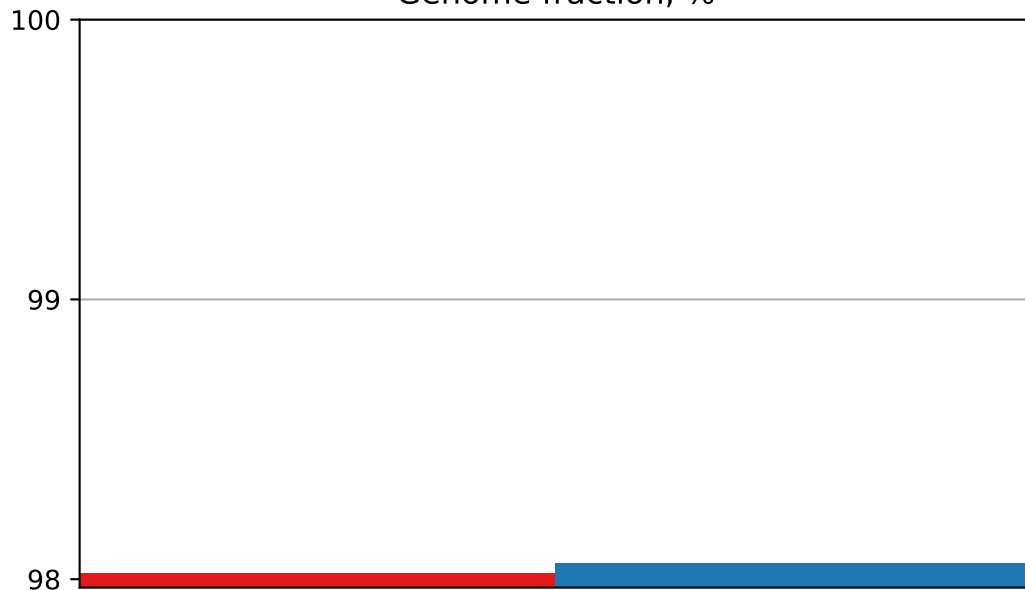


Spades\_Default



Spades\_Careful

Genome fraction, %



Spades\_Default



Spades\_Careful