

Report

	spades	soapdenovo_27	soapdenovo_49
# contigs (>= 0 bp)	1166261	44564	261294
# contigs (>= 1000 bp)	612	878	13064
# contigs (>= 5000 bp)	204	56	1269
# contigs (>= 10000 bp)	99	5	142
# contigs (>= 25000 bp)	18	0	2
# contigs (>= 50000 bp)	3	0	0
Total length (>= 0 bp)	114846363	8833082	86862967
Total length (>= 1000 bp)	3355337	2122755	29133144
Total length (>= 5000 bp)	2578595	403820	9502075
Total length (>= 10000 bp)	1858973	71105	1712941
Total length (>= 25000 bp)	620206	0	54918
Total length (>= 50000 bp)	159325	0	0
# contigs	11339	1594	33585
Largest contig	53450	19052	27938
Total length	9886584	2624604	43973845
Reference length	3380749	3380749	3380749
GC (%)	40.95	46.42	40.41
Reference GC (%)	45.32	45.32	45.32
N50	680	2245	1378
NG50	11404	1591	10035
N75	569	1189	853
NG75	5250	569	9479
L50	2660	334	6934
LG50	84	534	140
L75	6695	736	17250
LG75	196	1428	227
# misassemblies	10	16	2
# misassembled contigs	9	16	2
Misassembled contigs length	120352	34050	11980
# local misassemblies	119	105	14
# unaligned mis. contigs	0	4	0
# unaligned contigs	10863 + 3 part	165 + 24 part	32216 + 1 part
Unaligned length	6734632	139369	41055009
Genome fraction (%)	92.718	72.803	85.931
Duplication ratio	1.006	1.010	1.005
# N's per 100 kbp	0.00	2036.99	54699.83
# mismatches per 100 kbp	42.05	52.45	24.47
# indels per 100 kbp	9.51	10.81	1.34
Largest alignment	53450	19052	16563
Total aligned length	3140086	2464770	2912567
NA50	-	2184	-
NGA50	11140	1511	2587
NA75	-	1093	-
NGA75	5035	-	1097
LA50	-	342	-
LGA50	85	551	372
LA75	-	768	-
LGA75	202	-	870

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	soapdenovo_27	soapdenovo_49
# misassemblies	10	16	2
# relocations	10	16	2
# translocations	0	0	0
# inversions	0	0	0
# misassembled contigs	9	16	2
Misassembled contigs length	120352	34050	11980
# local misassemblies	119	105	14
# unaligned mis. contigs	0	4	0
# mismatches	1318	1291	711
# indels	298	266	39
# indels (<= 5 bp)	209	84	27
# indels (> 5 bp)	89	182	12
Indels length	4138	6114	659

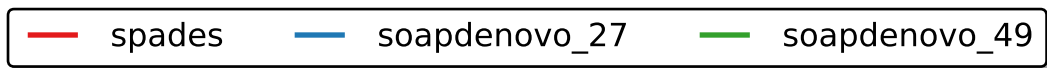
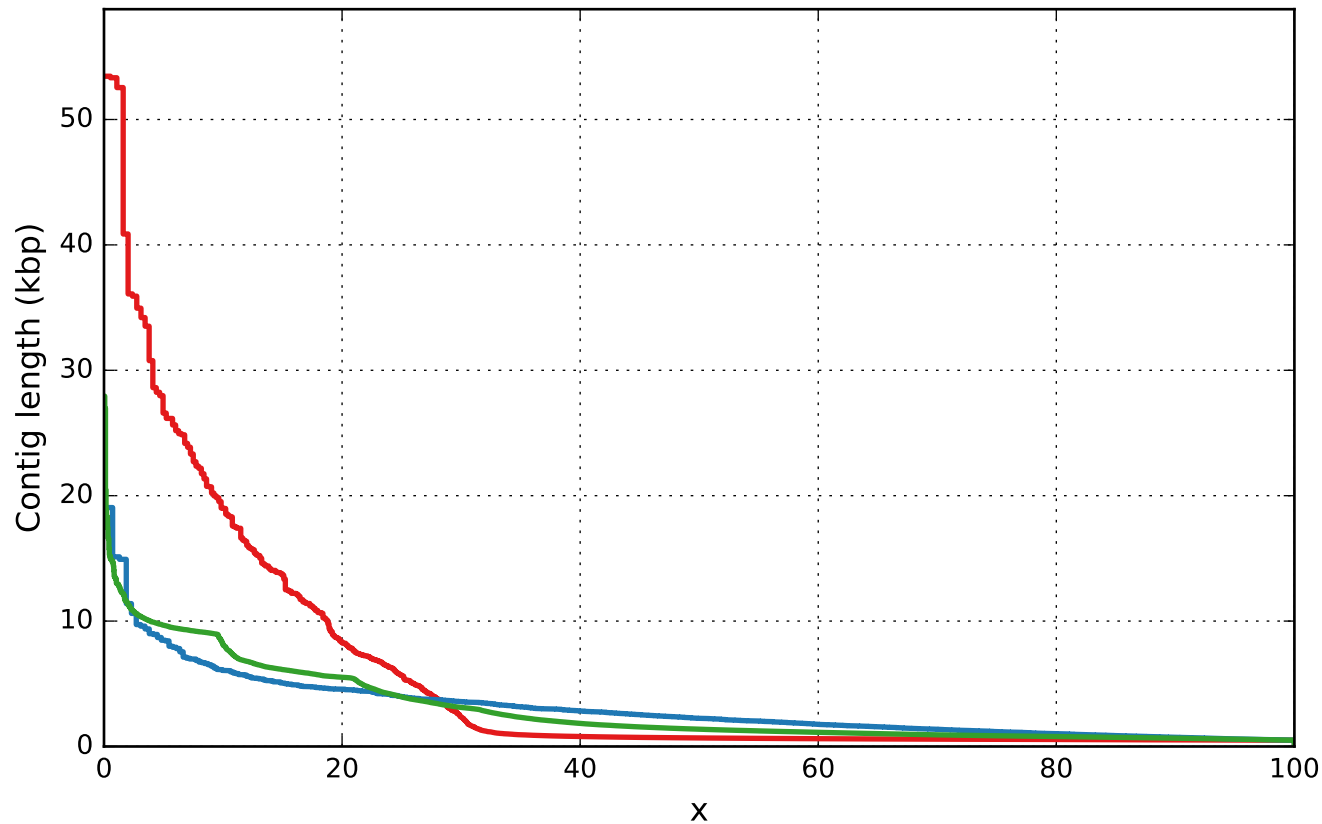
All statistics are based on contigs of size ≥ 500 bp, unless otherwise noted (e.g., "# contigs (≥ 0 bp)" and "Total length (≥ 0 bp)" include all contigs).

Unaligned report

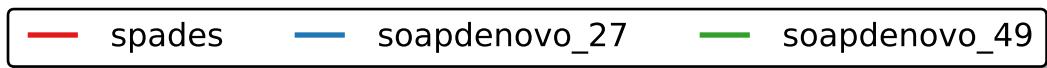
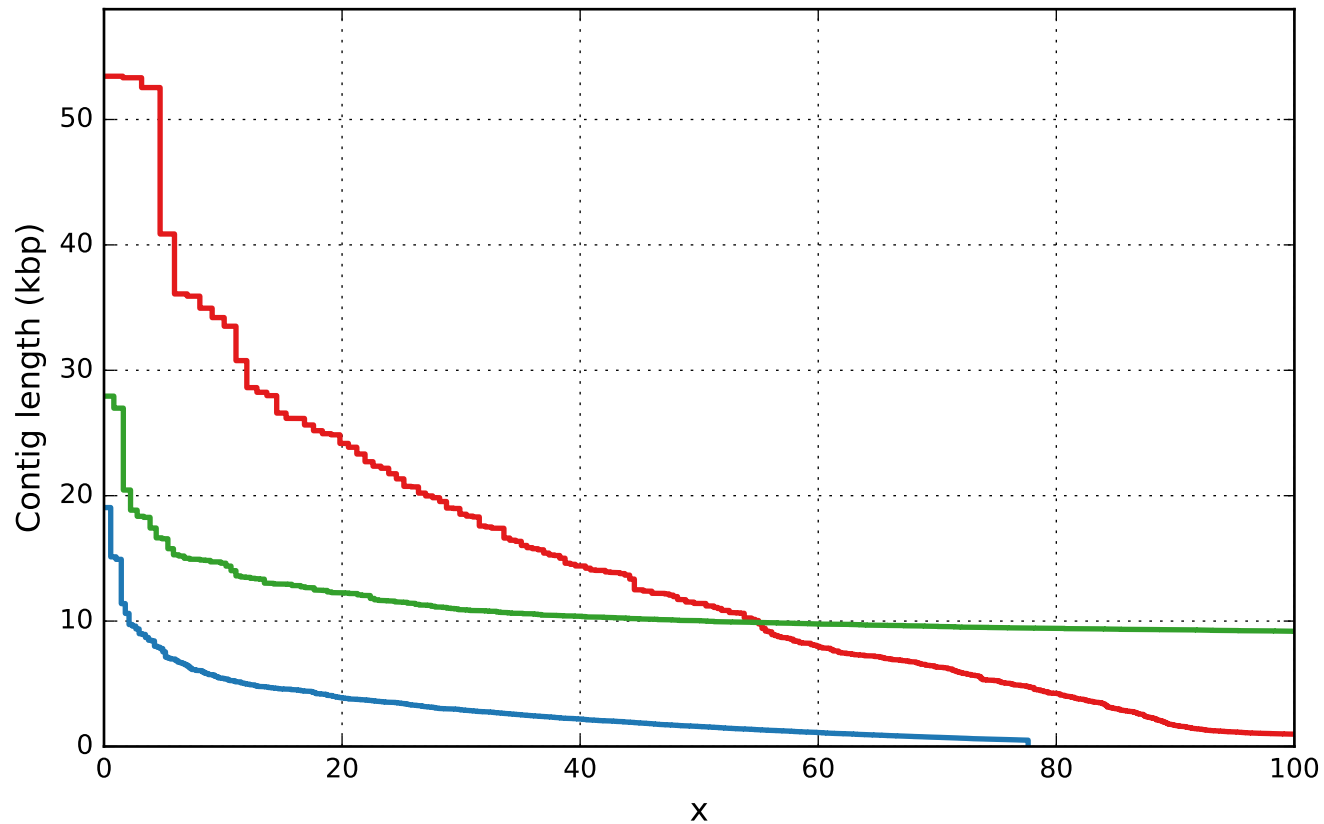
	spades	soapdenovo_27	soapdenovo_49
# fully unaligned contigs	10863	165	32216
Fully unaligned length	6731443	115554	41052036
# partially unaligned contigs	3	24	1
Partially unaligned length	3189	23815	2973
# N's	0	53463	24053618

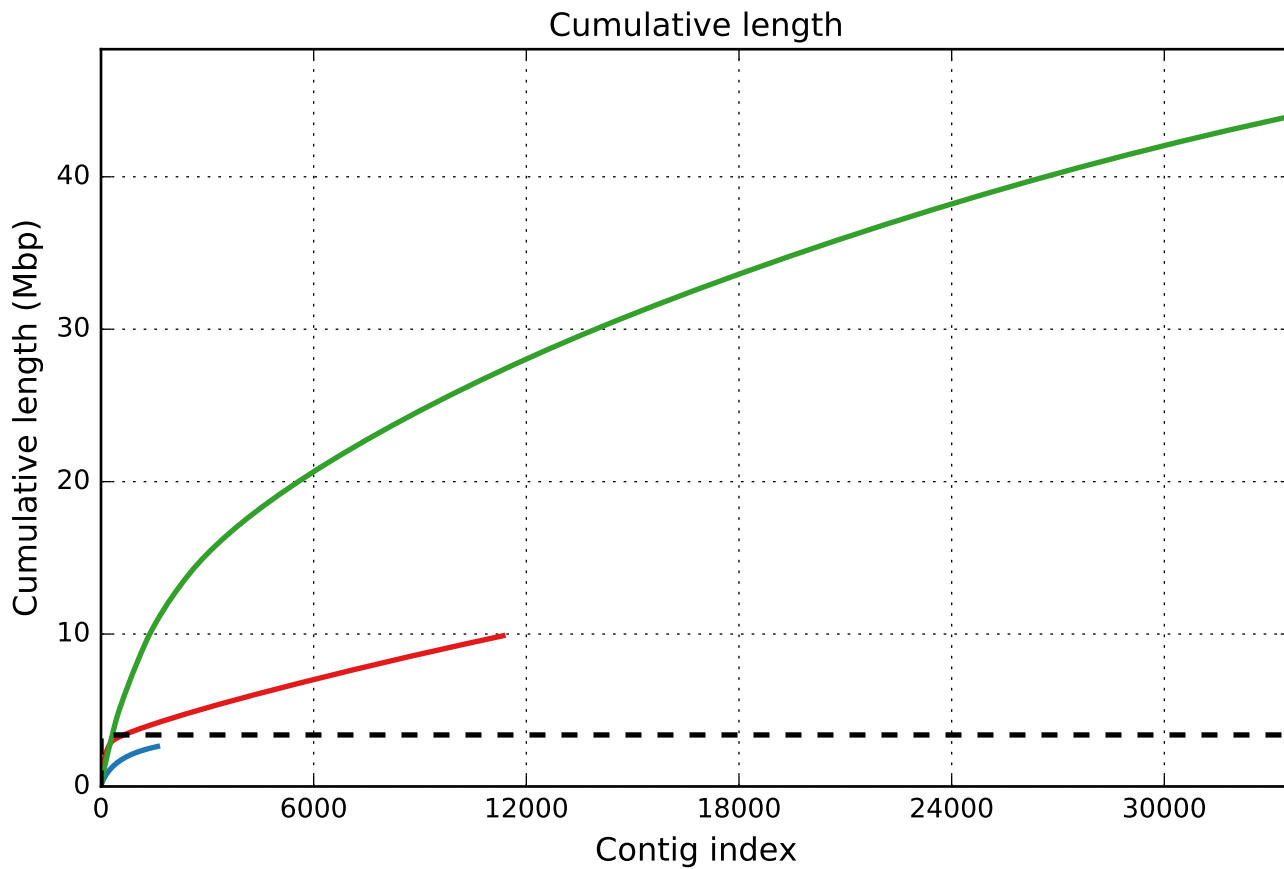
All statistics are based on contigs of size ≥ 500 bp, unless otherwise noted (e.g., "# contigs (≥ 0 bp)" and "Total length (≥ 0 bp)" include all contigs).

Nx

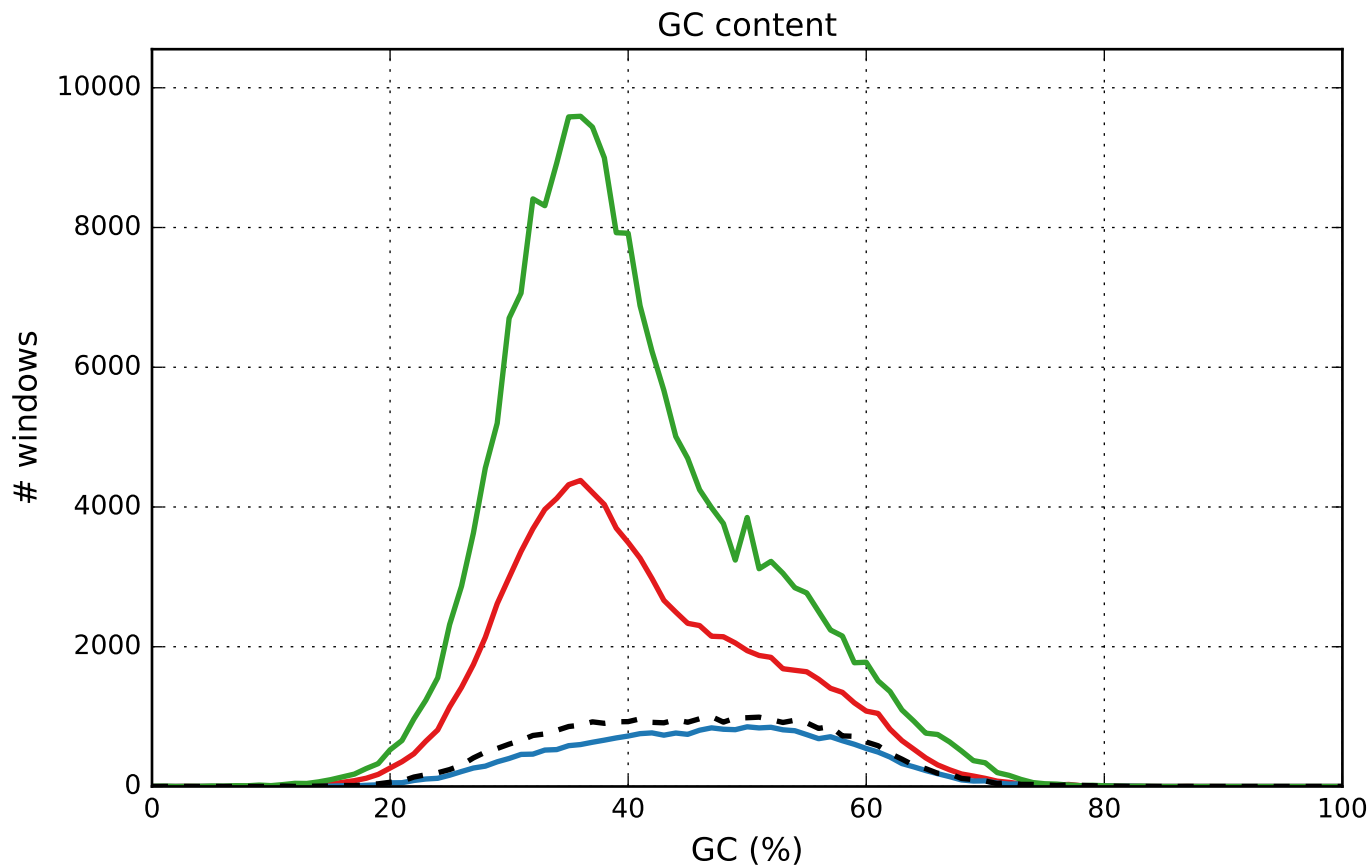


NGx



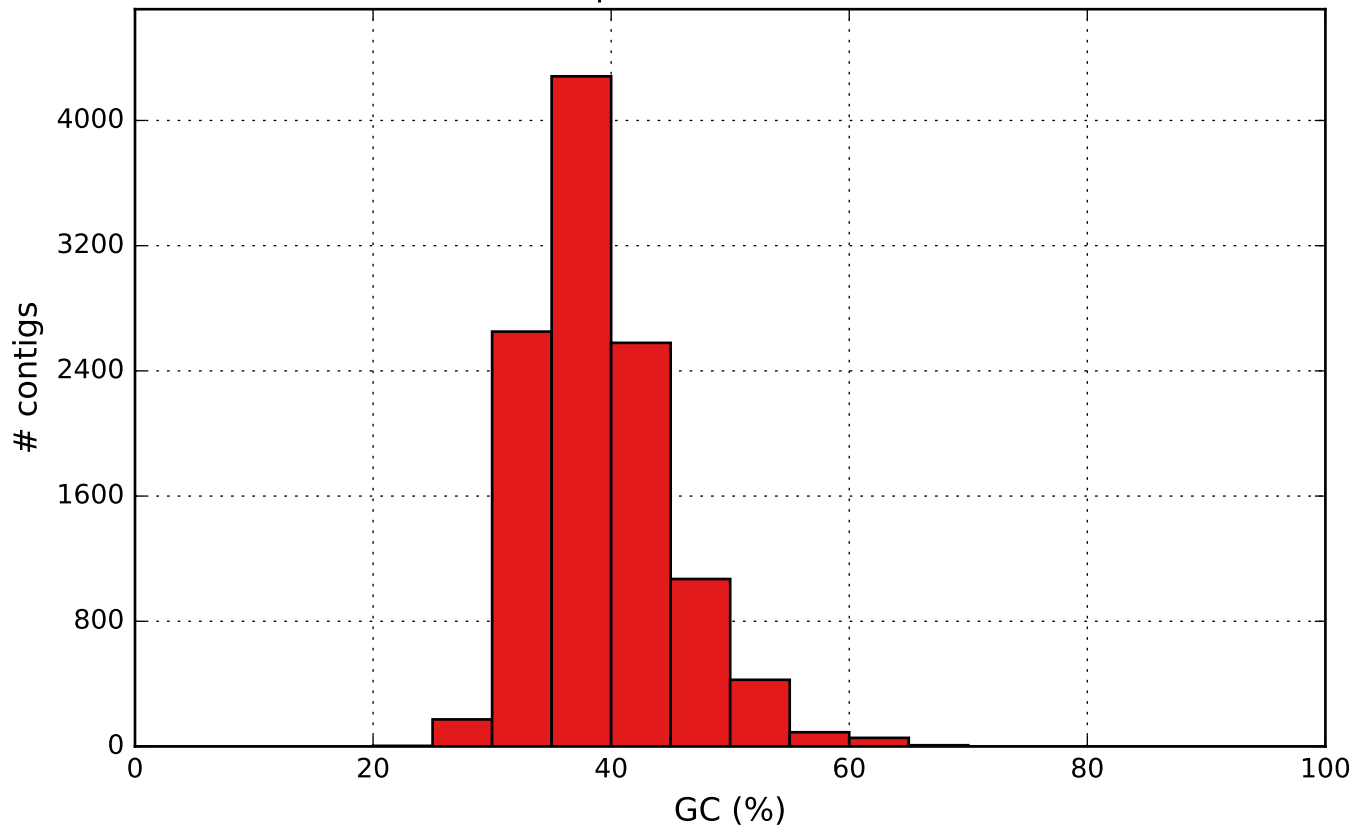


— spades — soapdenovo_49 - - Reference
— soapdenovo_27



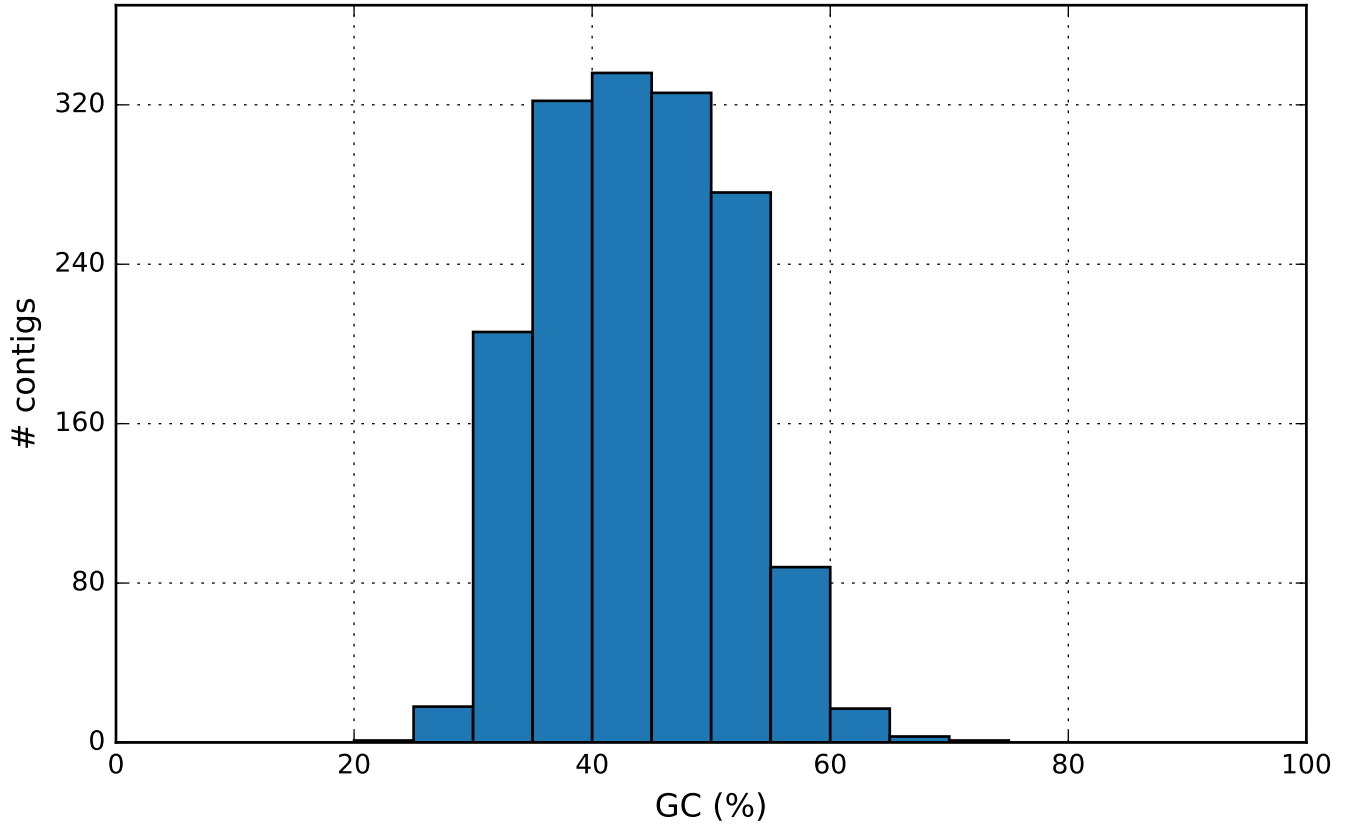
— spades — soapdenovo_49 - - Reference
— soapdenovo_27

spades GC content



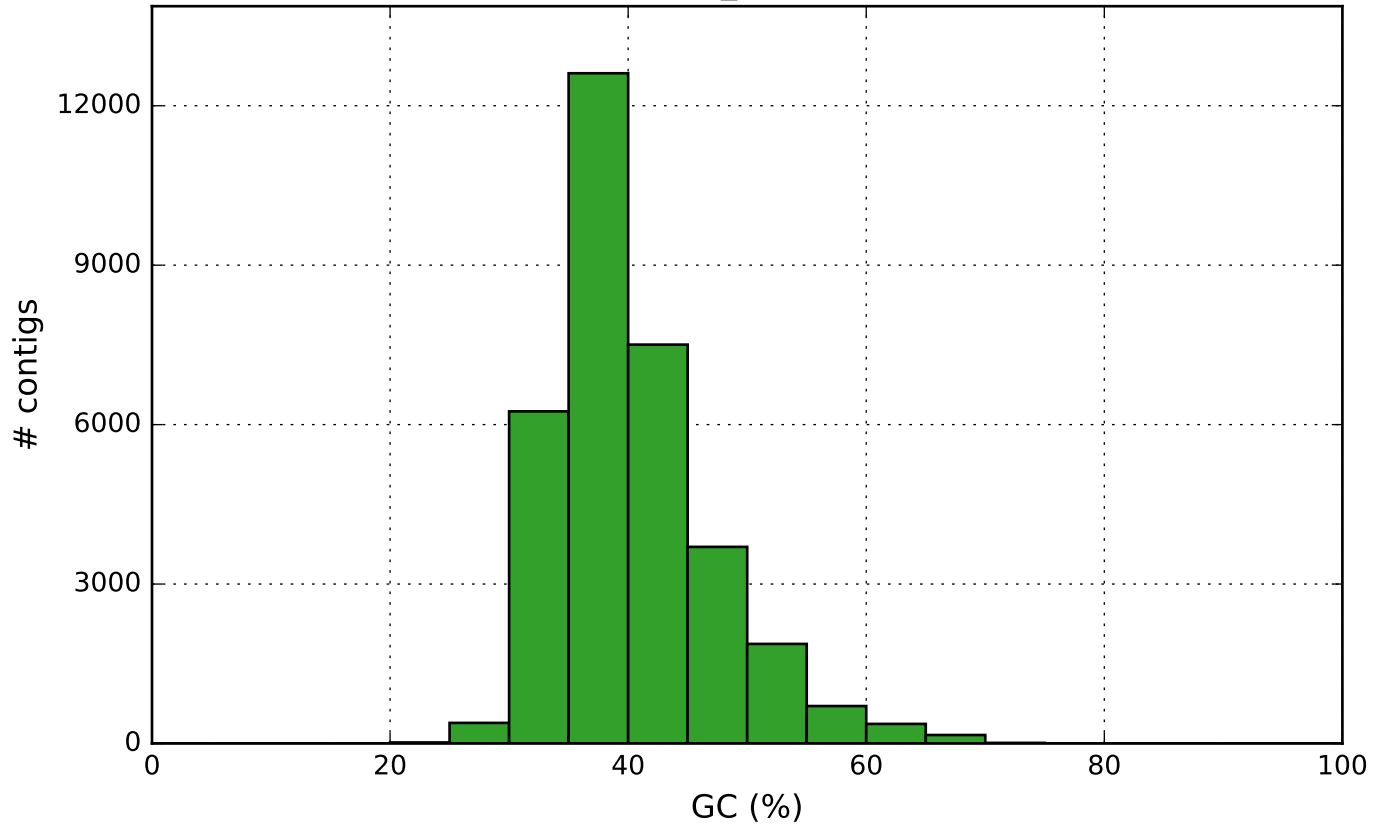
spades

soapdenovo_27 GC content



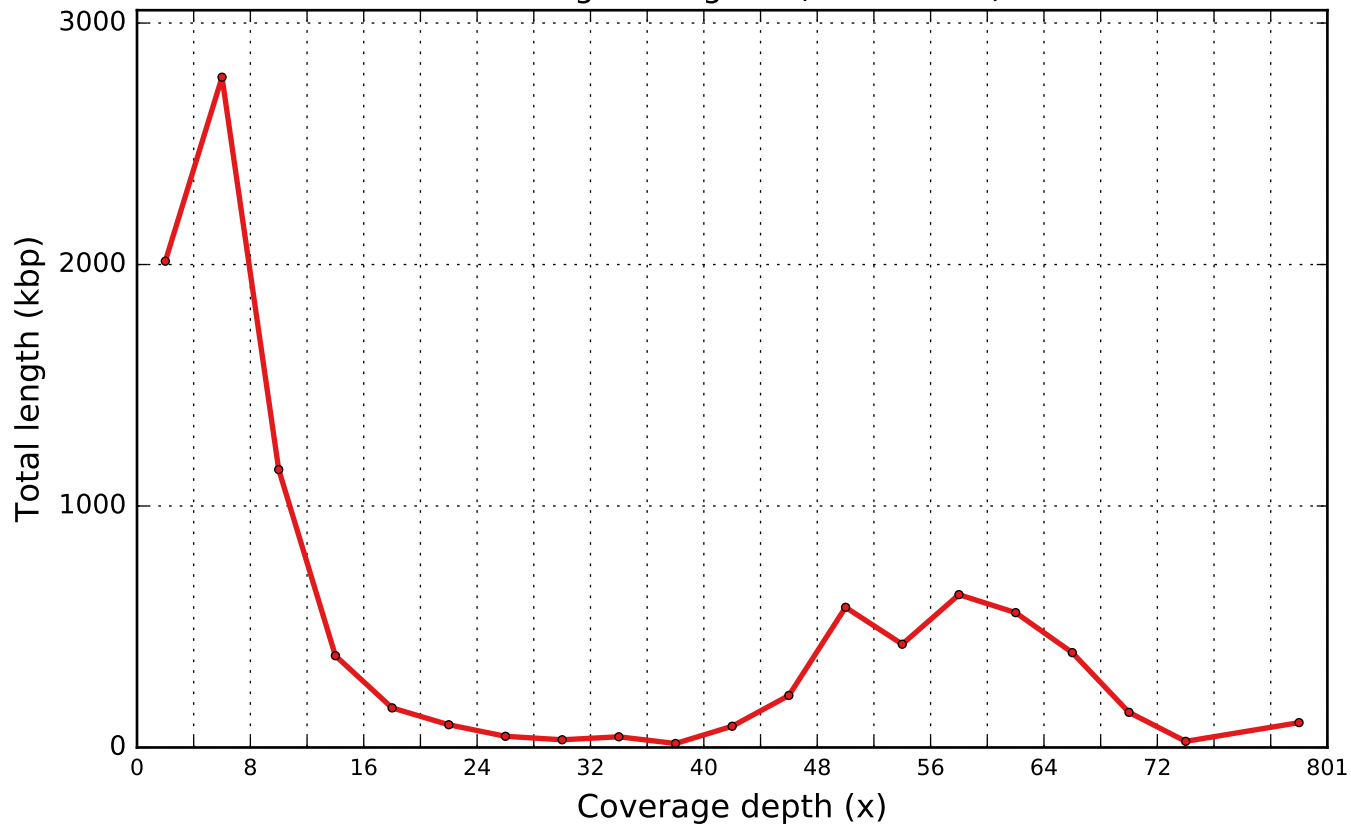
soapdenovo_27

soapdenovo_49 GC content



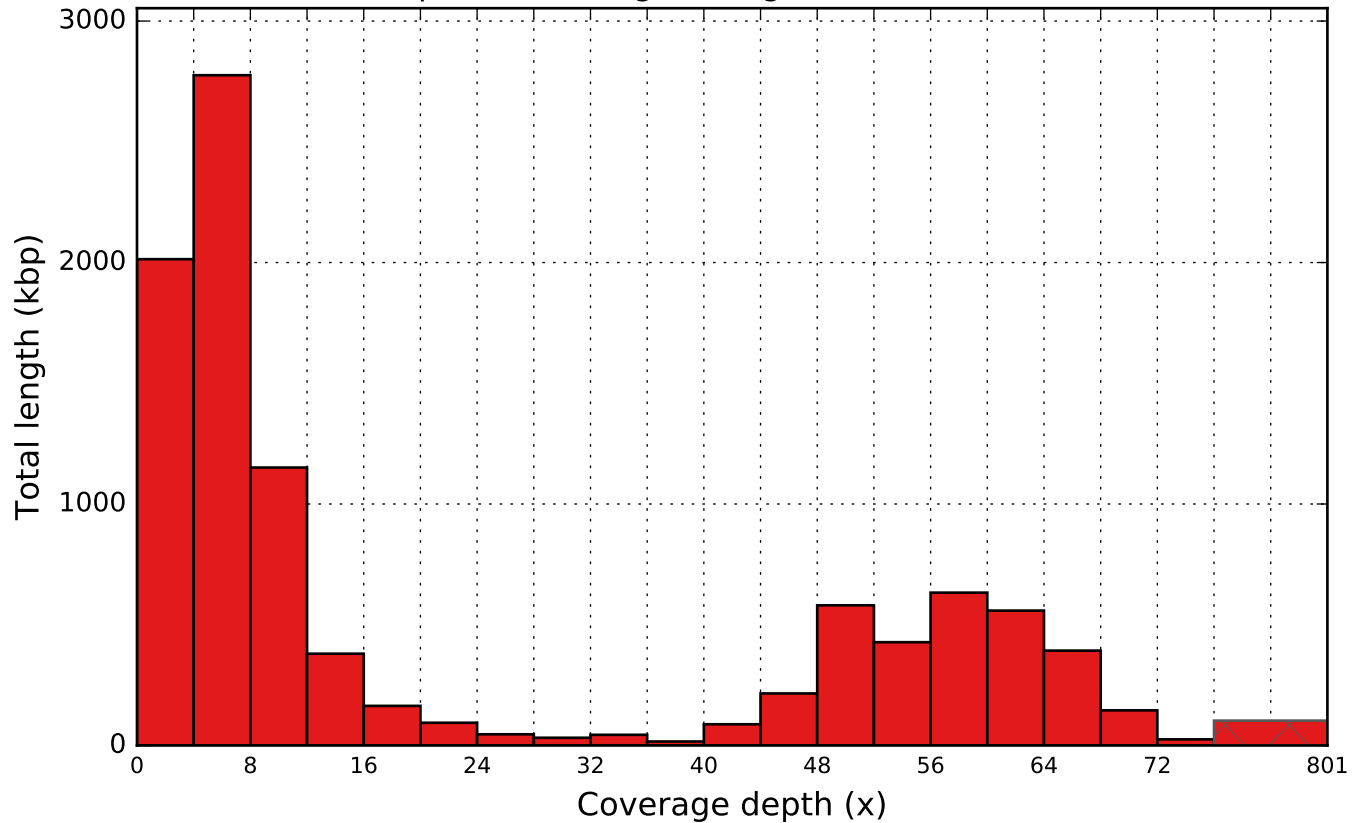
■ soapdenovo_49

Coverage histogram (bin size: 4x)

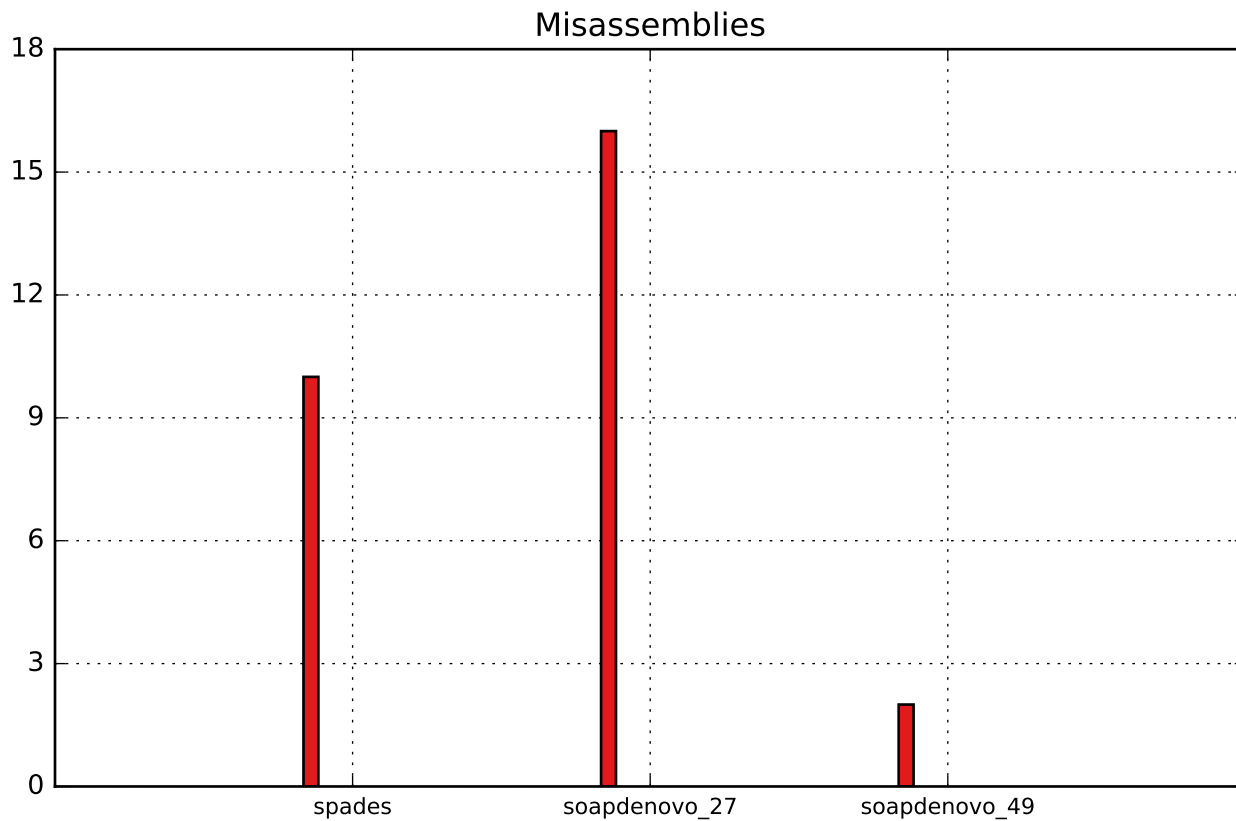


spades

spades coverage histogram (bin size: 4x)

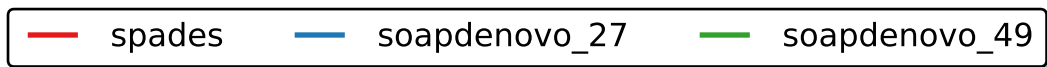
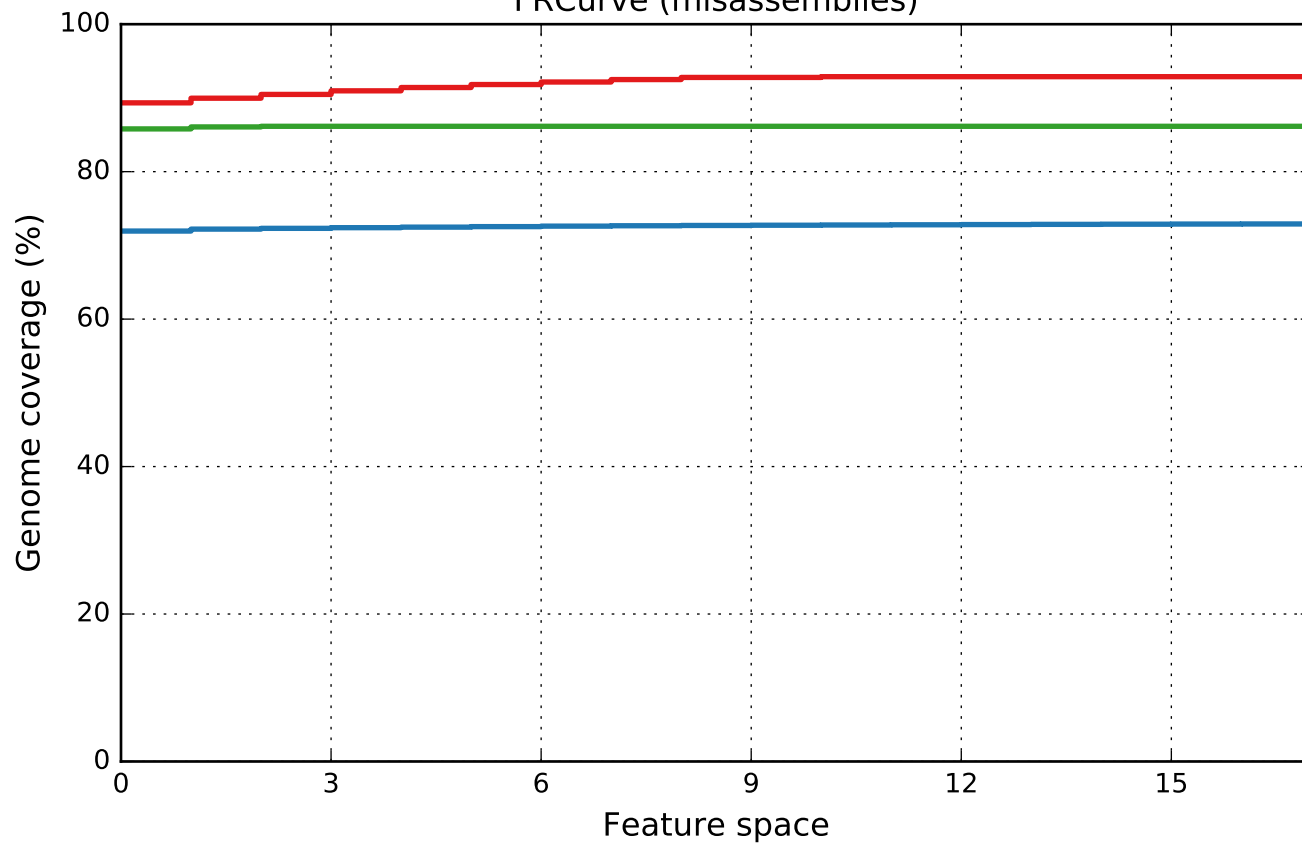


spades

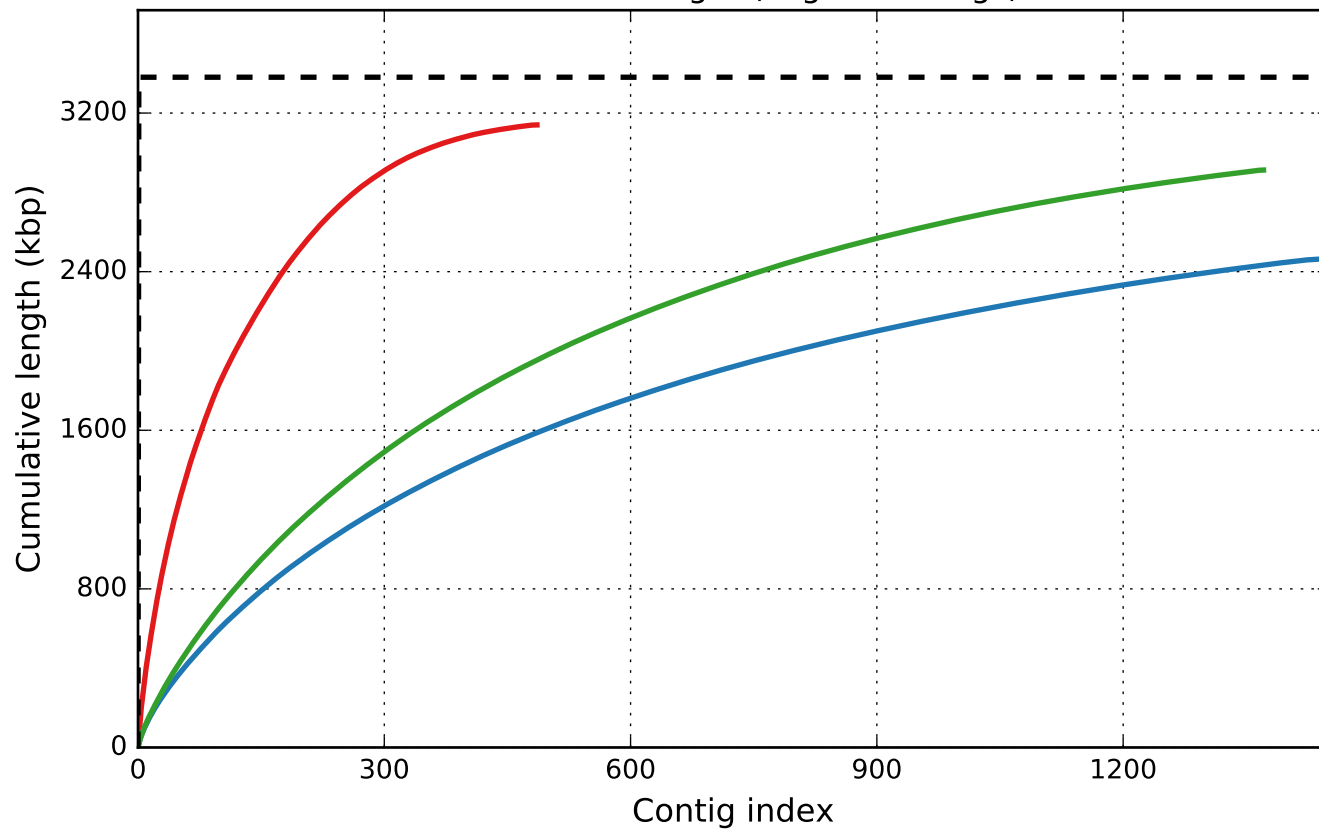


 # relocations

FRCurve (misassemblies)

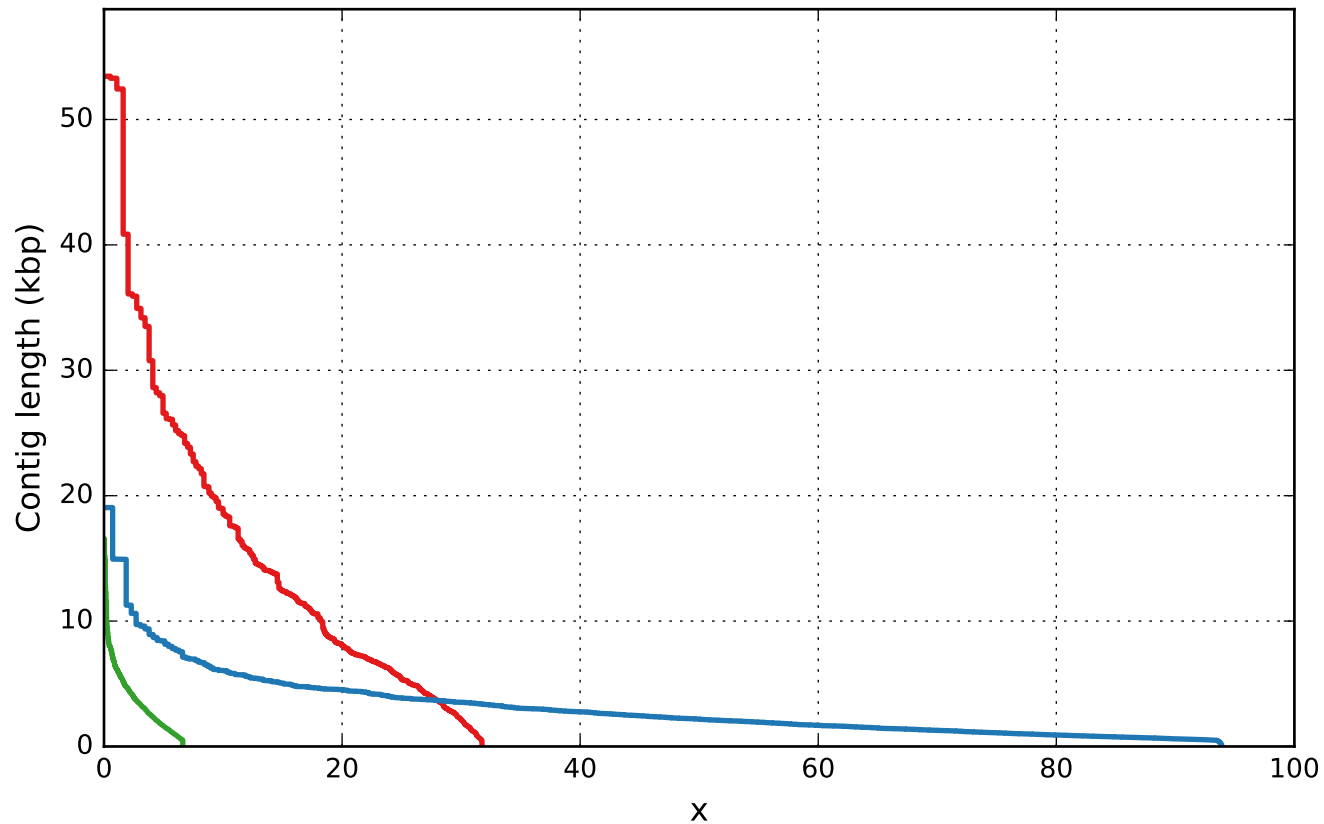


Cumulative length (aligned contigs)



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NAx



NGAx

