Report

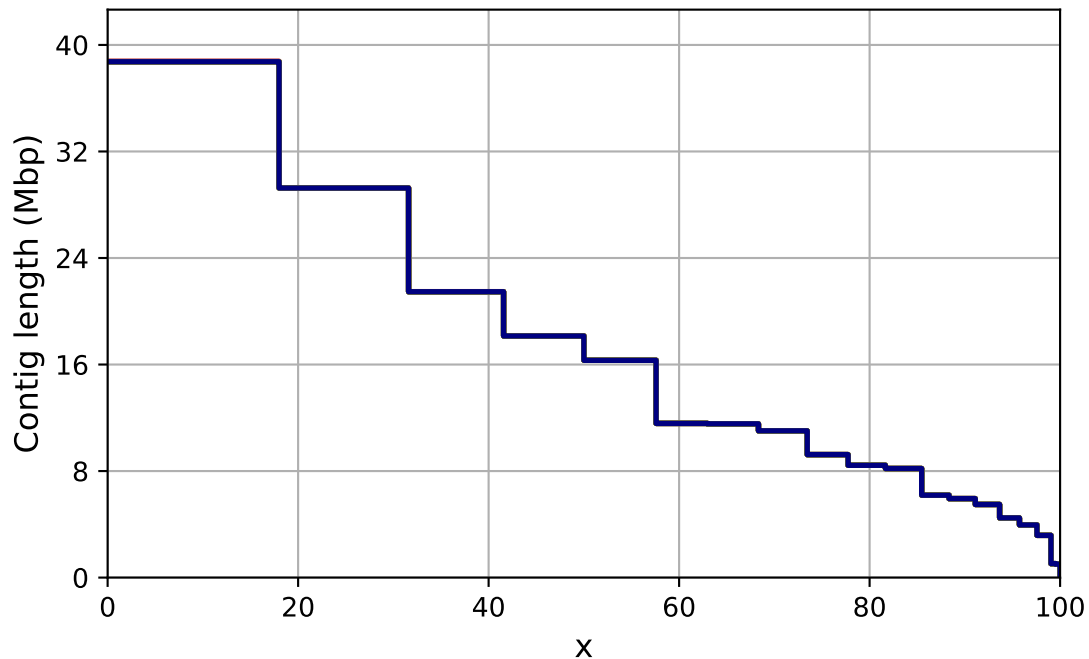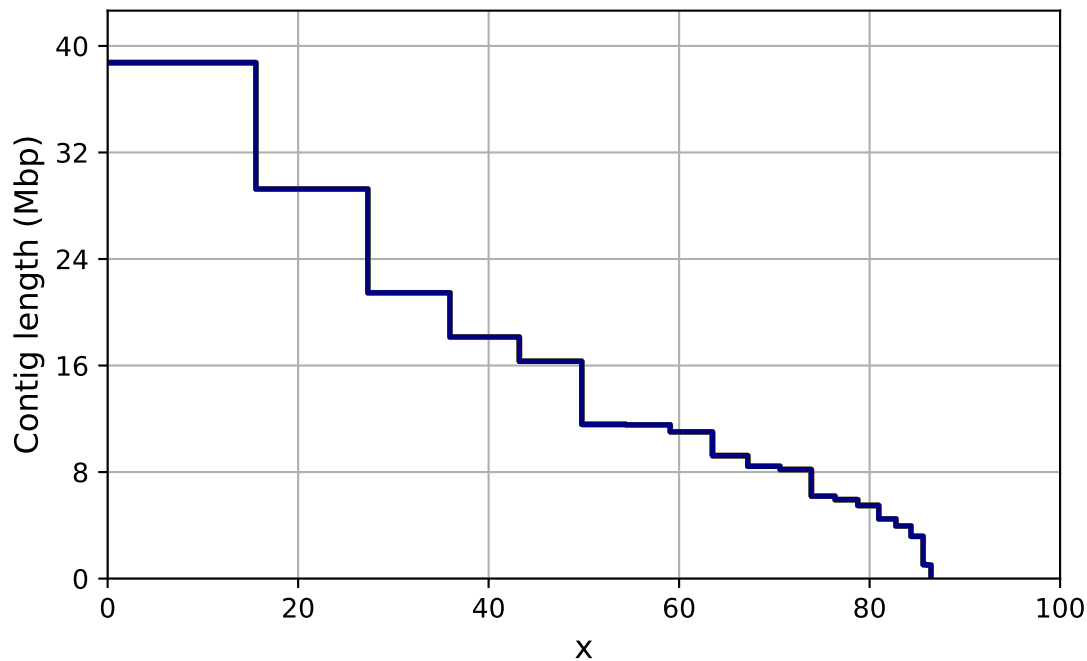|	asm.contigs	asm.contigs.nextpolishv1	asm.contigs.nextpolishv2	asm.contigs.pilonv1	asm.contigs.pilonv2	asm.contigs.pilonv3	asm.contigs.pilonv4	asm.contigs.raconv1	asm.contigs.raconv2	asm.contigs.raconv3	asm.contigs.raconv4
# contigs (>= 0 bp)	189	189	189	189	189	189	189	189	189	189	189
# contigs (>= 1000 bp)	189	189	189	189	189	189	189	189	189	189	189
# contigs (>= 5000 bp)	189	189	189	189	189	189	189	189	189	189	189
# contigs (>= 10000 bp)	188	188	188	188	188	188	188	188	188	188	188
# contigs (>= 25000 bp)	105	105	105	105	105	105	105	105	105	105	105
# contigs (>= 50000 bp)	52	52	52	52	52	52	52	52	52	52	52
Total length (>= 0 bp)	224780032	224716364	224716261	224715544	224715452	224715529	224715464	224702036	224691554	224685532	224681897
Total length (>= 1000 bp)	224780032	224716364	224716261	224715544	224715452	224715529	224715464	224702036	224691554	224685532	224681897
Total length (>= 5000 bp)	224780032	224716364	224716261	224715544	224715452	224715529	224715464	224702036	224691554	224685532	224681897
Total length (>= 10000 bp)	224773066	224709398	224709295	224708578	224708486	224708563	224708498	224695306	224685313	224679545	224675913
Total length (>= 25000 bp)	223194581	223130909	223130798	223130029	223129971	223130031	223129994	223119835	223112441	223108619	223105982
Total length (>= 50000 bp)	221504878	221441174	221441025	221440357	221440278	221440309	221440269	221432183	221425708	221422942	221421274
# contigs	19	19	19	19	19	19	19	19	19	19	19
Largest contig	38773995	38746781	38746769	38746674	38746666	38746693	38746674	38743900	38741868	38740479	38739900
Total length	215287615	215224222	215224152	215223160	215223131	215223143	215223109	215217457	215212057	215209603	215208478
Reference length	248956422	248956422	248956422	248956422	248956422	248956422	248956422	248956422	248956422	248956422	248956422
GC (%)	41.62	41.63	41.63	41.63	41.63	41.63	41.63	41.63	41.63	41.63	41.63
Reference GC (%)	41.72	41.72	41.72	41.72	41.72	41.72	41.72	41.72	41.72	41.72	41.72
N50	18149548	18145535	18145534	18145434	18145424	18145422	18145422	18145154	18144551	18144549	18144549
NG50	11579979	11578567	11578567	11578508	11578508	11578504	11578505	11578416	11578419	11578421	11578420
N75	9236438	9235729	9235729	9235656	9235655	9235655	9235655	9235738	9235734	9235734	9235734
NG75	6186682	6186462	6186462	6186423	6186425	6186425	6186425	6186475	6186477	6186477	6186476
L50	4	4	4	4	4	4	4	4	4	4	4
LG50	6	6	6	6	6	6	6	6	6	6	6
L75	9	9	9	9	9	9	9	9	9	9	9
LG75	12	12	12	12	12	12	12	12	12	12	12
# misassemblies	6	6	6	6	6	6	6	9	9	11	11
# misassembled contigs	5	5	5	5	5	5	5	8	8	8	8
Misassembled contigs length	55323237	55312360	55312337	55312076	55312088	55312089	55312089	141459995	141454614	141452158	141451272
# local misassemblies	2	2	2	2	2	2	2	24	34	38	39
# scaffold gap ext. mis.	0	0	0	0	0	0	0	0	0	0	0
# scaffold gap loc. mis.	0	0	0	0	0	0	0	0	0	0	0
# unaligned mis. contigs	0	0	0	0	0	0	0	0	0	0	0
# unaligned contigs	0 + 4 part	0 + 4 part	0 + 4 part	0 + 4 part	0 + 4 part	0 + 4 part	0 + 4 part	0 + 6 part	0 + 7 part	0 + 7 part	0 + 7 part
Unaligned length	56553	61272	61269	62646	61699	61703	61275	163683	177973	176917	193791
Genome fraction (%)	93.242	93.240	93.240	93.239	93.240	93.240	93.240	93.287	93.279	93.278	93.270
Duplication ratio	1.002	1.001	1.001	1.001	1.001	1.001	1.001	1.000	1.000	1.000	1.000
# N's per 100 kbp	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
# mismatches per 100 kbp	17.82	2.38	2.26	2.92	2.39	2.31	2.31	3.08	2.91	2.87	2.64
# indels per 100 kbp	121.45	0.81	0.71	1.60	1.36	1.28	1.25	1.97	1.16	1.08	1.00
Largest alignment	38684342	38657142	38657130	38657017	38656999	38657033	38657014	38554506	38537001	38535515	38523009
Total aligned length	214980786	214912696	214912629	214910236	214911145	214911160	214911554	215021875	214997271	214993014	214974521
NA50	14116580	14110314	14110319	14110229	14110236	14110234	14110233	14110052	14109972	14109970	14109968
NGA50	11579978	11578566	11578566	11578507	11578507	11578503	11578504	11578411	11578414	11578416	11578415
NA75	8430295	8429866	8429867	8429817	8429817	8429817	8429817	8427284	8427282	8427282	8427282
NGA75	6176186	6175966	6175966	6175927	6175929	6175929	6175929	6175979	6175981	6175981	6175980
LA50	5	5	5	5	5	5	5	5	5	5	5
LGA50	6	6	6	6	6	6	6	6	6	6	6
LA75	10	10	10	10	10	10	10	10	10	10	10
LGA75	13	13	13	13	13	13	13	13	13	13	13

All statistics are based on contigs of size >= 1000000 bp, unless otherwise noted
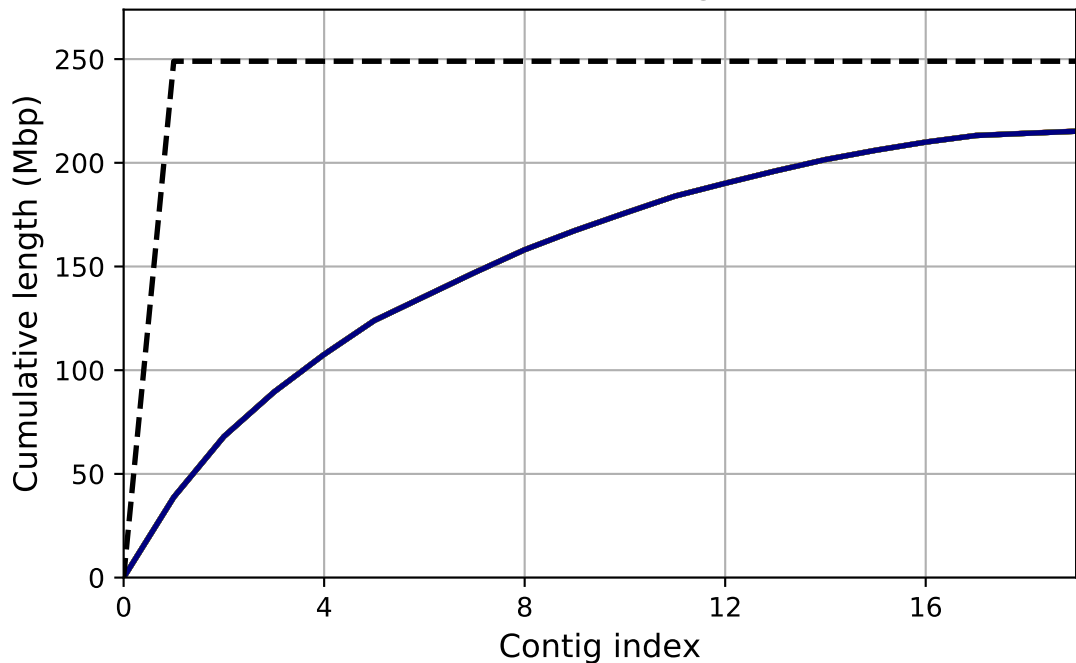(e.g., "# contigs (>= 0 bp)" and "Total length (>= 0 bp)" include all contigs).

Misassemblies report

	asm.contigs	asm.contigs.nextpolishv1	asm.contigs.nextpolishv2	asm.contigs.pilonv1	asm.contigs.pilonv2	asm.contigs.pilonv3	asm.contigs.pilonv4	asm.contigs.raconv1	asm.contigs.raconv2	asm.contigs.raconv3	asm.contigs.raconv4
# misassemblies	6	6	6	6	6	6	6	9	9	11	11
# contig misassemblies	6	6	6	6	6	6	6	9	9	11	11
# c. relocations	5	5	5	5	5	5	5	8	8	10	10
# c. translocations	0	0	0	0	0	0	0	0	0	0	0
# c. inversions	1	1	1	1	1	1	1	1	1	1	1
# scaffold misassemblies	0	0	0	0	0	0	0	0	0	0	0
# s. relocations	0	0	0	0	0	0	0	0	0	0	0
# s. translocations	0	0	0	0	0	0	0	0	0	0	0
# s. inversions	0	0	0	0	0	0	0	0	0	0	0
# misassembled contigs	5	5	5	5	5	5	5	8	8	8	8
Misassembled contigs length	55323237	55312360	55312337	55312076	55312088	55312089	55312089	141459995	141454614	141452158	141451272
# local misassemblies	2	2	2	2	2	2	2	24	34	38	39
# scaffold gap ext. mis.	0	0	0	0	0	0	0	0	0	0	0
# scaffold gap loc. mis.	0	0	0	0	0	0	0	0	0	0	0
# unaligned mis. contigs	0	0	0	0	0	0	0	0	0	0	0
# mismatches	38286	5107	4863	6275	5134	4974	4957	6625	6249	6177	5684
# indels	261011	1736	1527	3447	2917	2754	2684	4242	2494	2312	2148
# indels (<= 5 bp)	260921	1643	1435	3360	2828	2664	2594	4127	2366	2180	2020
# indels (> 5 bp)	90	93	92	87	89	90	90	115	128	132	128
Indels length	282823	4927	4664	7159	6696	6527	6513	8958	7614	7681	7201

All statistics are based on contigs of size >= 1000000 bp, unless otherwise noted
(e.g., "# contigs (>= 0 bp)" and "Total length (>= 0 bp)" include all contigs).
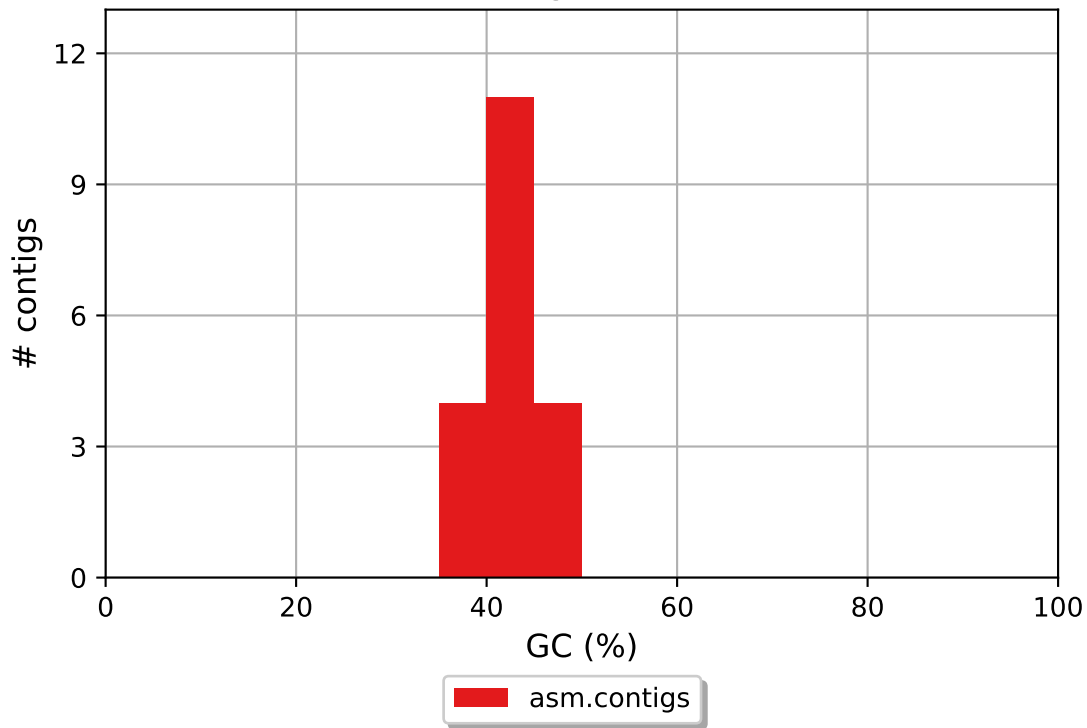
Unaligned report

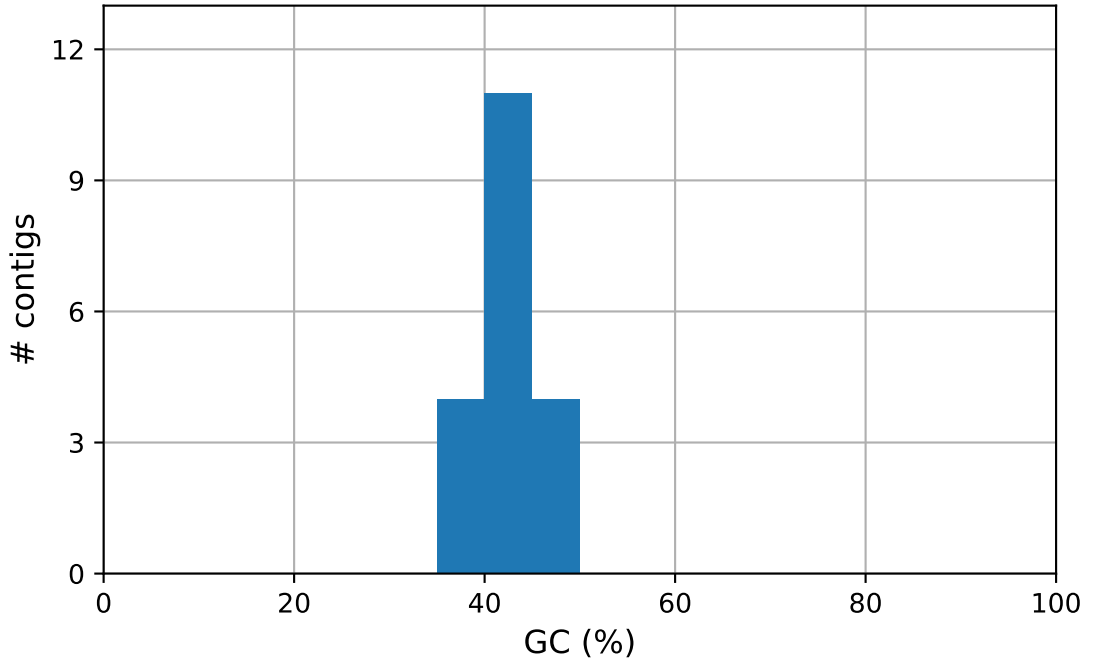|	asm.contigs	asm.contigs.nextpolishv1	asm.contigs.nextpolishv2	asm.contigs.pilonv1	asm.contigs.pilonv2	asm.contigs.pilonv3	asm.contigs.pilonv4	asm.contigs.raconv1	asm.contigs.raconv2	asm.contigs.raconv3	asm.contigs.raconv4
# fully unaligned contigs	0	0	0	0	0	0	0	0	0	0	0
Fully unaligned length	0	0	0	0	0	0	0	0	0	0	0
# partially unaligned contigs	4	4	4	4	4	4	4	6	7	7	7
Partially unaligned length	56553	61272	61269	62646	61699	61703	61275	163683	177973	176917	193791
# N's	0	0	0	0	0	0	0	0	0	0	0

All statistics are based on contigs of size >= 1000000 bp, unless otherwise noted
(e.g., "# contigs (>= 0 bp)" and "Total length (>= 0 bp)" include all contigs).

Nx

— asm.contigs	— asm.contigs.pilonv2	— asm.contigs.raconv2
— asm.contigs.nextpolishv1	— asm.contigs.pilonv3	— asm.contigs.raconv3
— asm.contigs.nextpolishv2	— asm.contigs.pilonv4	— asm.contigs.raconv4
— asm.contigs.pilonv1	— asm.contigs.raconv1	

NGx

	asm.contigs		asm.contigs.pilonv2		asm.contigs.raconv2
	asm.contigs.nextpolishv1		asm.contigs.pilonv3		asm.contigs.raconv3
	asm.contigs.nextpolishv2		asm.contigs.pilonv4		asm.contigs.raconv4
	asm.contigs.pilonv1		asm.contigs.raconv1		

Cumulative length

asm.contigs	asm.contigs.pilonv2	asm.contigs.raconv2
asm.contigs.nextpolishv1	asm.contigs.pilonv3	asm.contigs.raconv3
asm.contigs.nextpolishv2	asm.contigs.pilonv4	asm.contigs.raconv4
asm.contigs.pilonv1	asm.contigs.raconv1	Reference

GC content
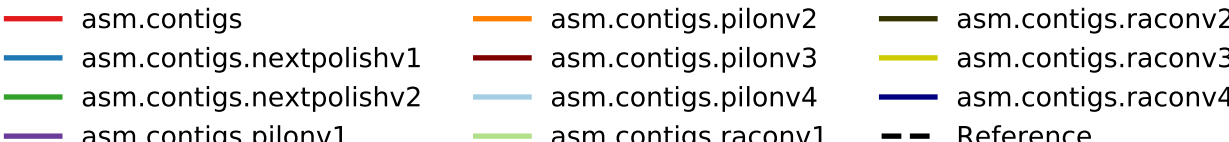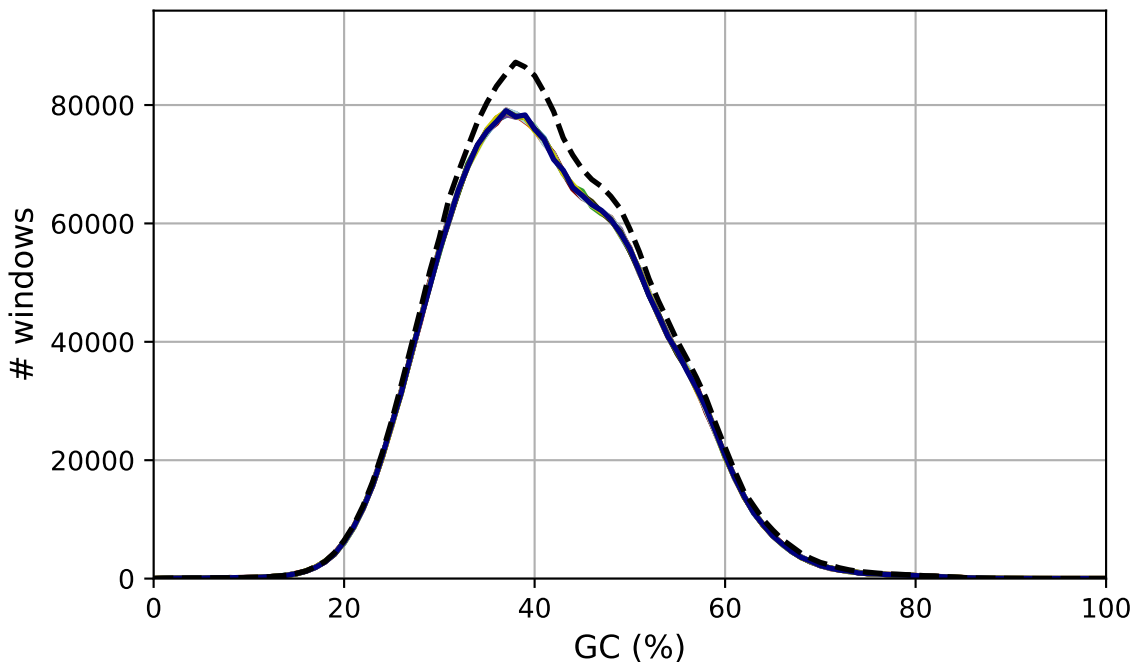
—— asm.contigs	—— asm.contigs.pilonv2	—— asm.contigs.raconv2
—— asm.contigs.nextpolishv1	—— asm.contigs.pilonv3	—— asm.contigs.raconv3
—— asm.contigs.nextpolishv2	—— asm.contigs.pilonv4	—— asm.contigs.raconv4
—— asm.contigs.pilonv1	—— asm.contigs.raconv1	- - Reference

asm.contigs.nextpolishv2 GC content
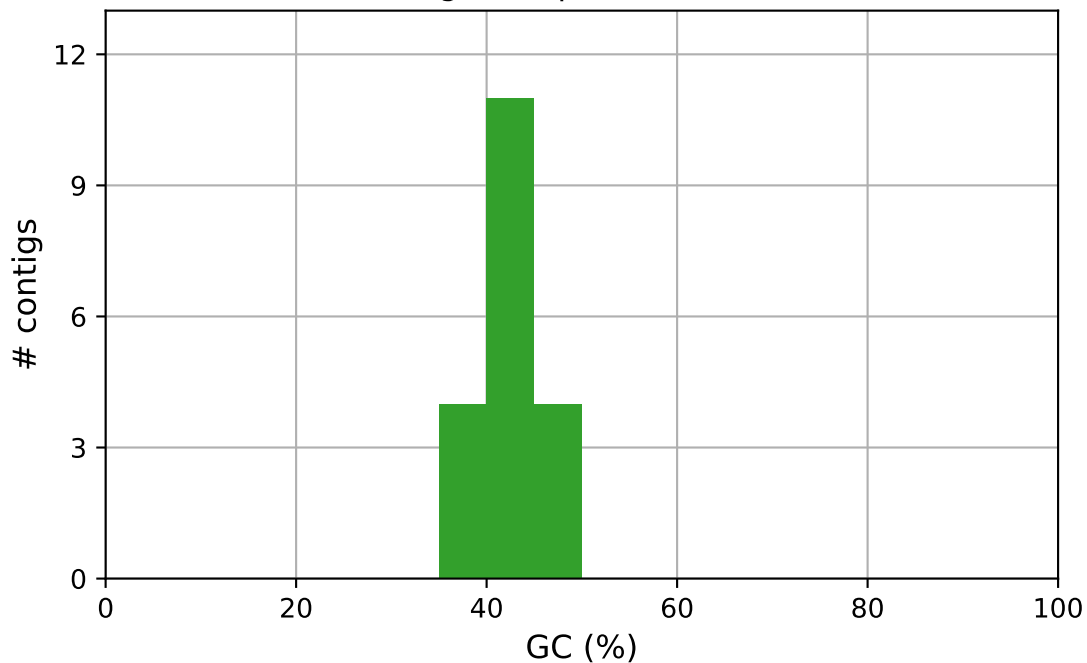
asm.contigs.pilonv1 GC content
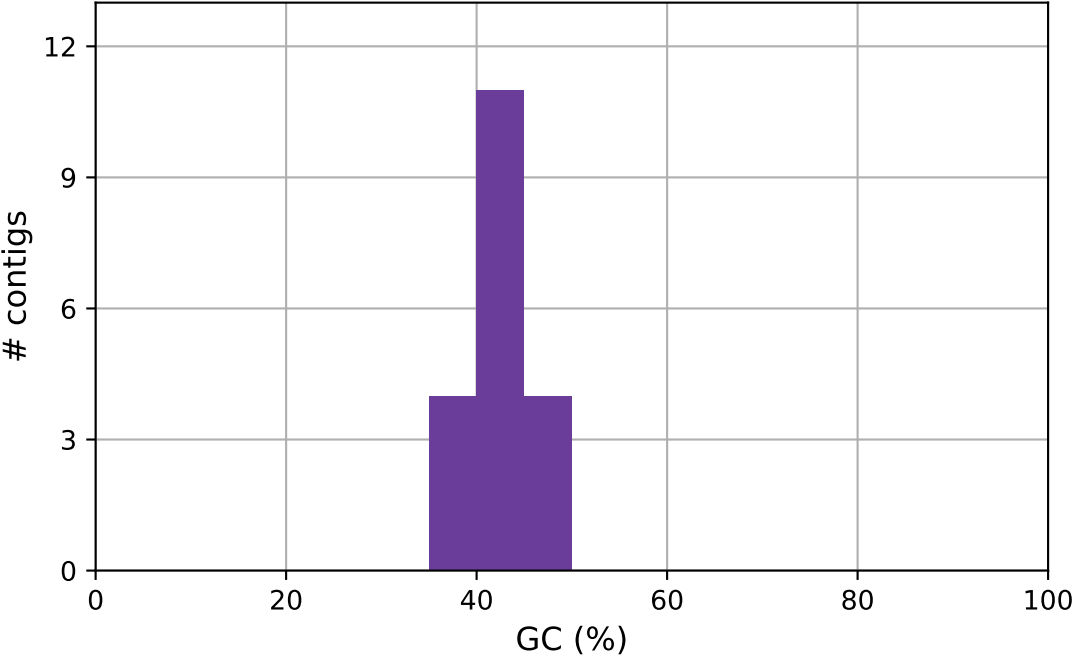
asm.contigs.pilonv2 GC content
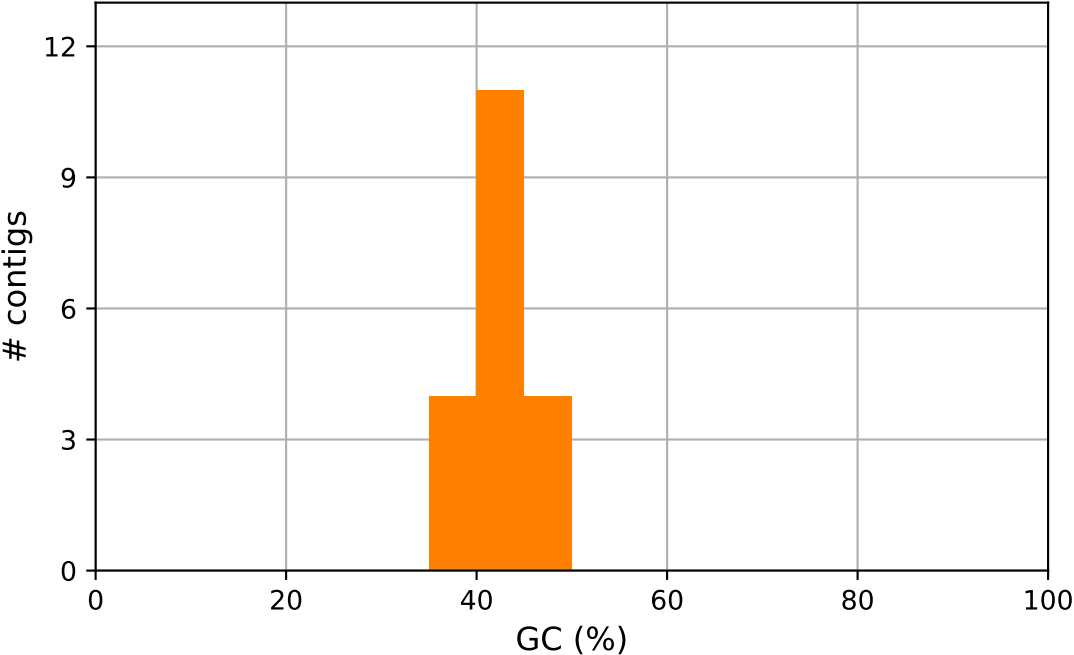
asm.contigs.pilonv3 GC content
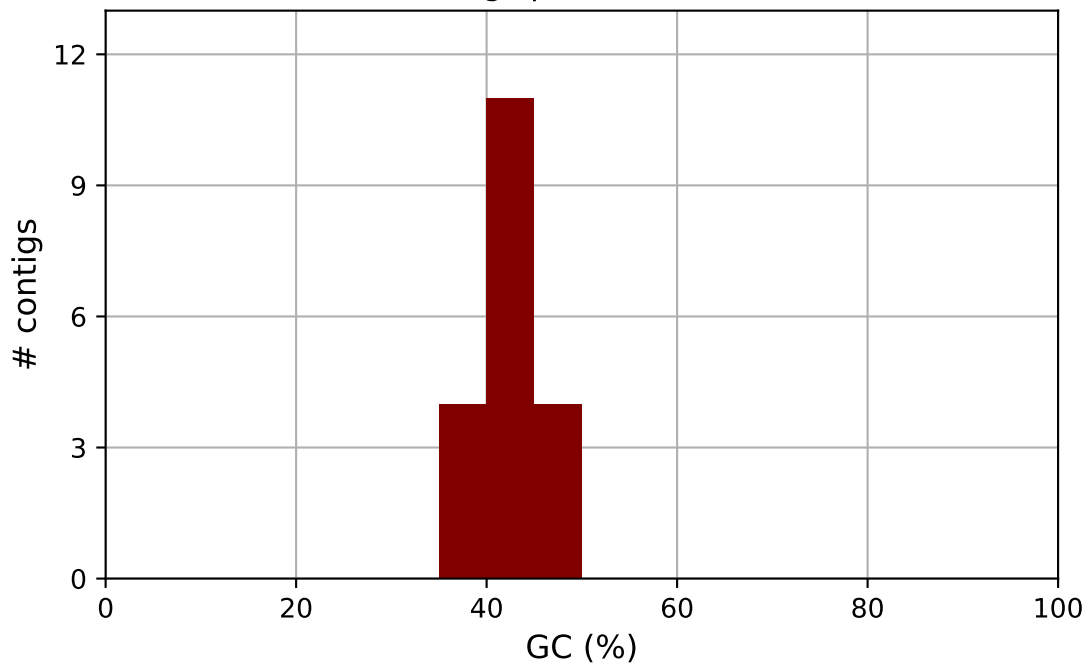
asm.contigs.pilonv4 GC content
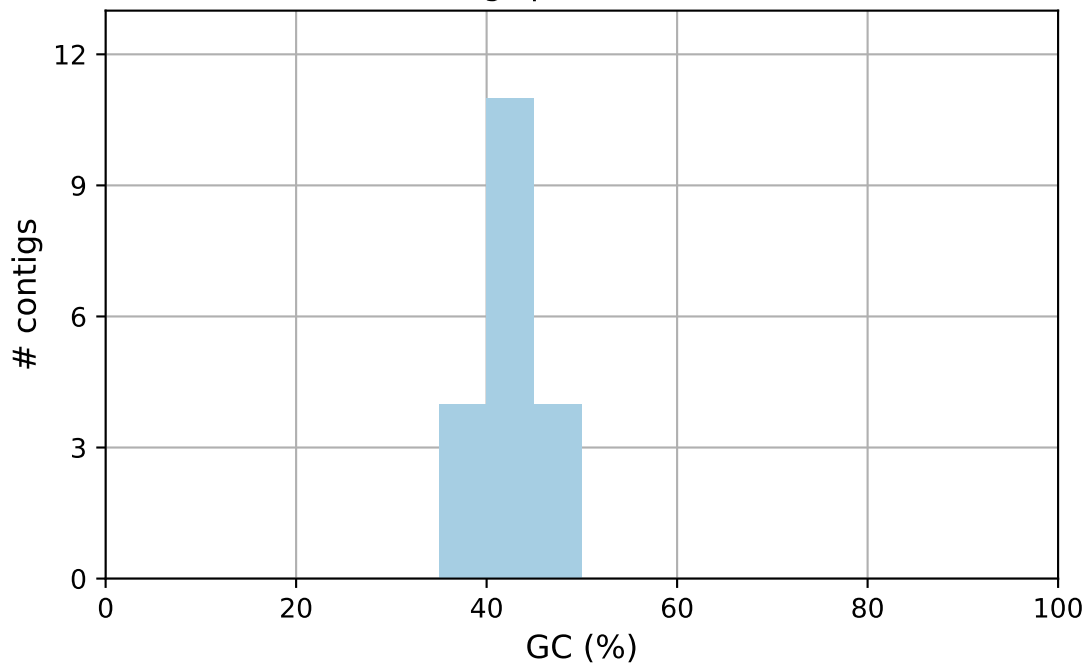
asm.contigs.raconv1 GC content
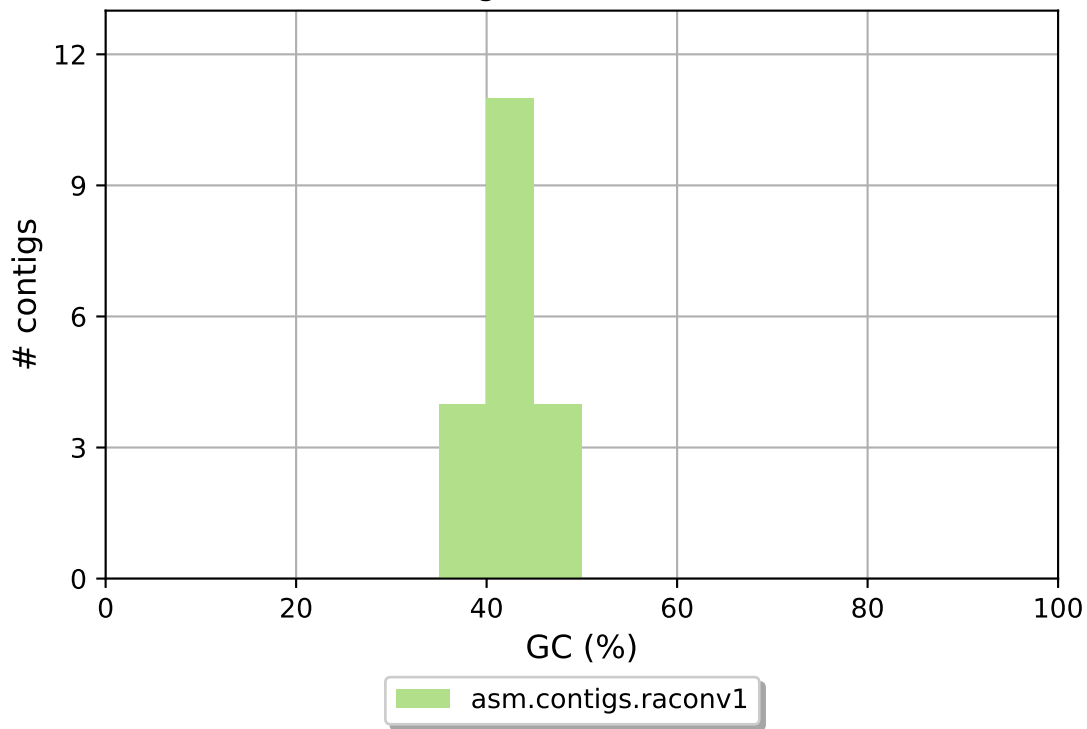
asm.contigs.raconv2 GC content
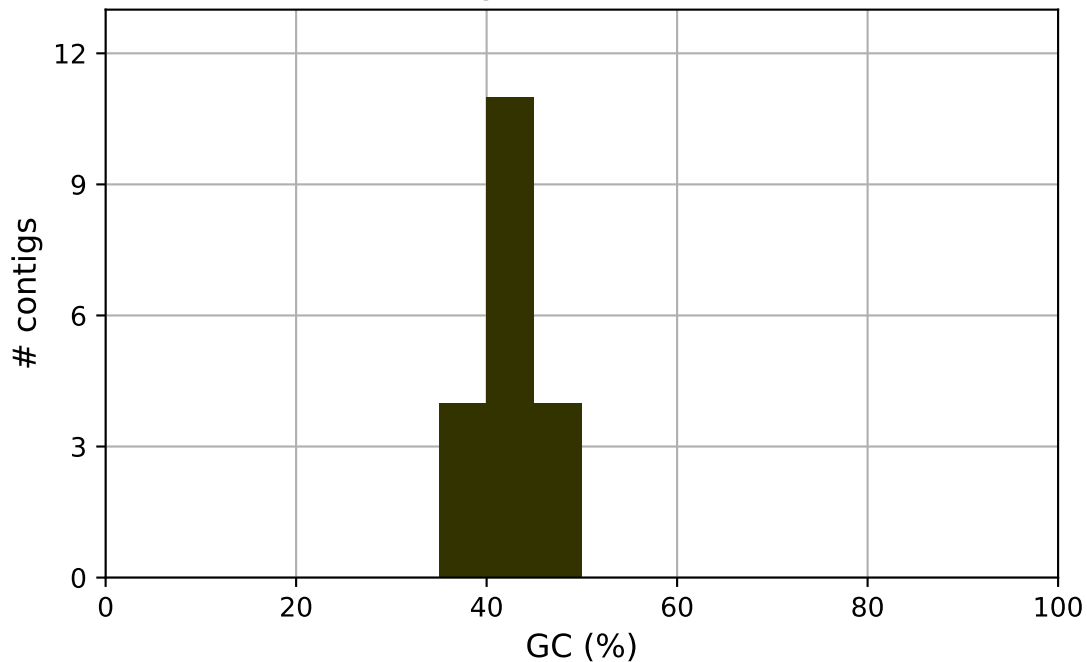
asm.contigs.raconv3 GC content
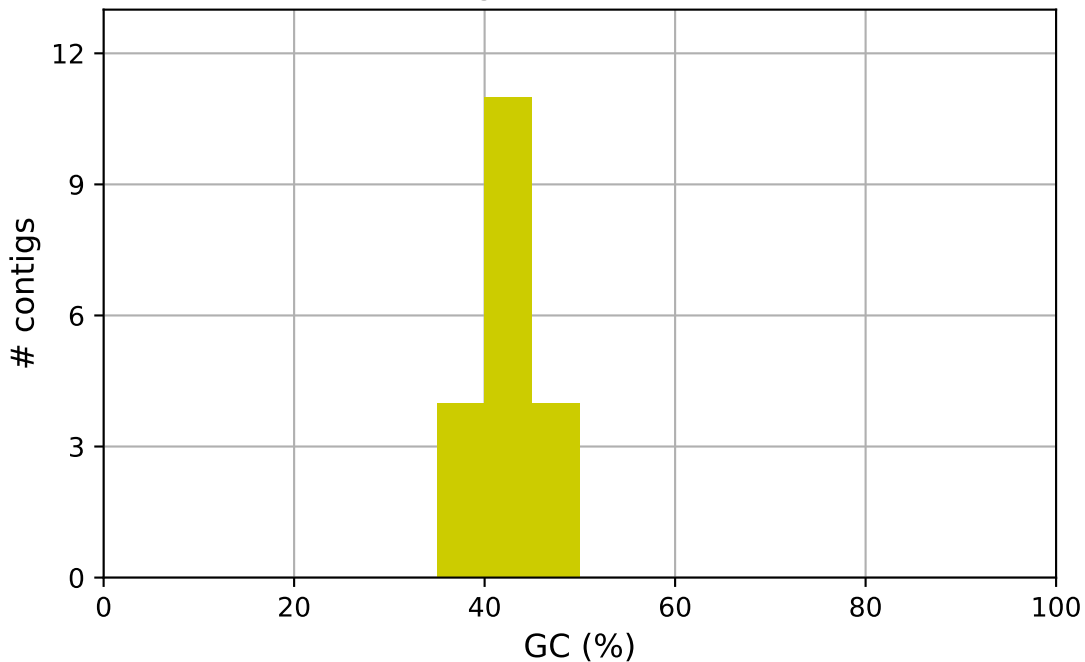
asm.contigs.raconv4 GC content
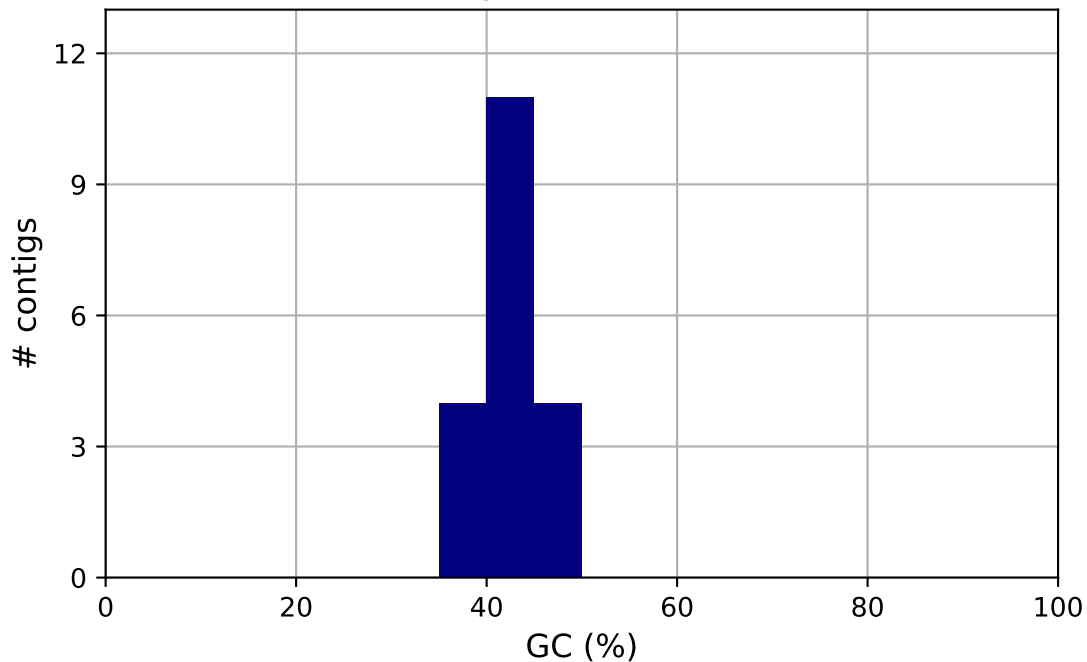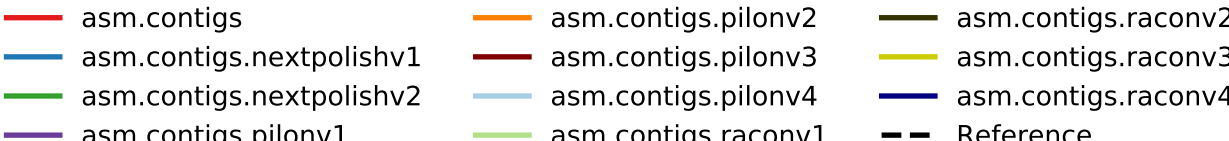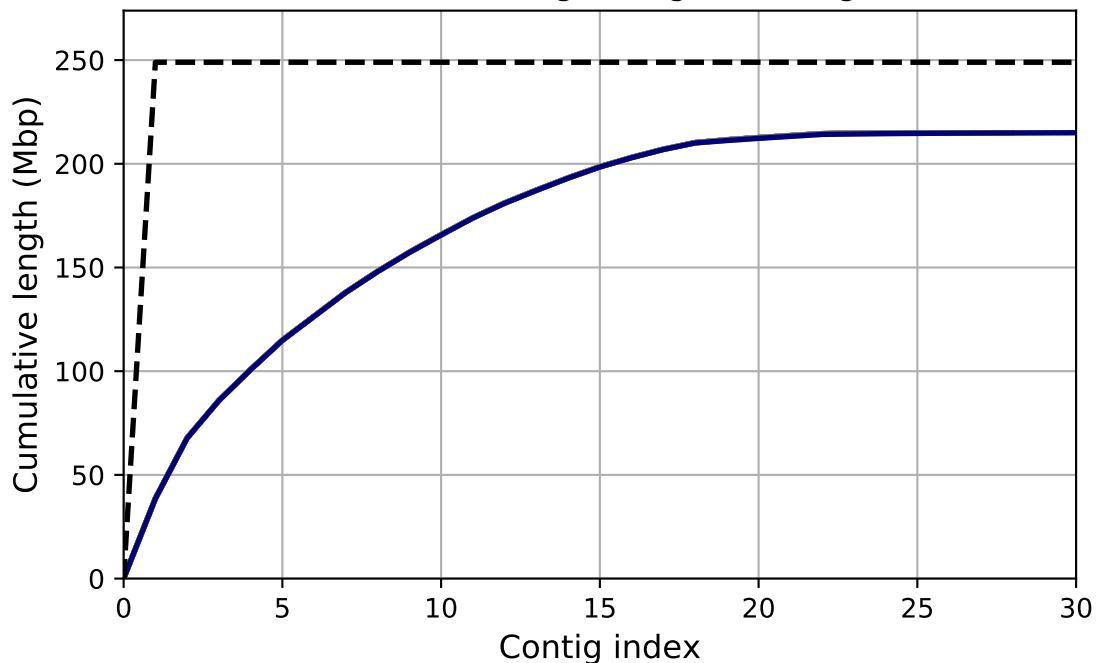
Misassemblies

relocations   # inversions
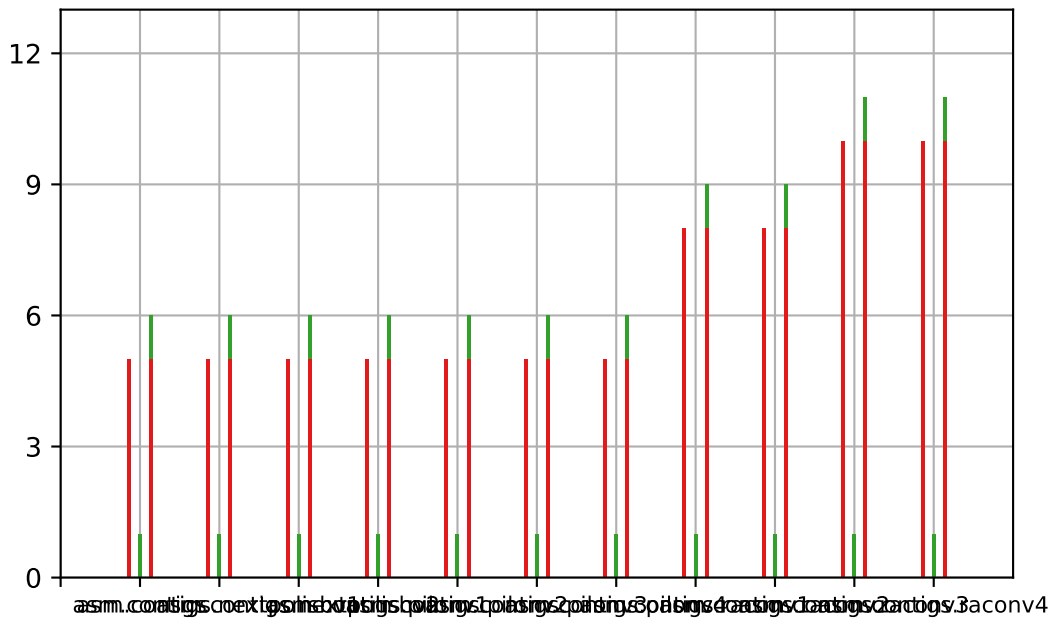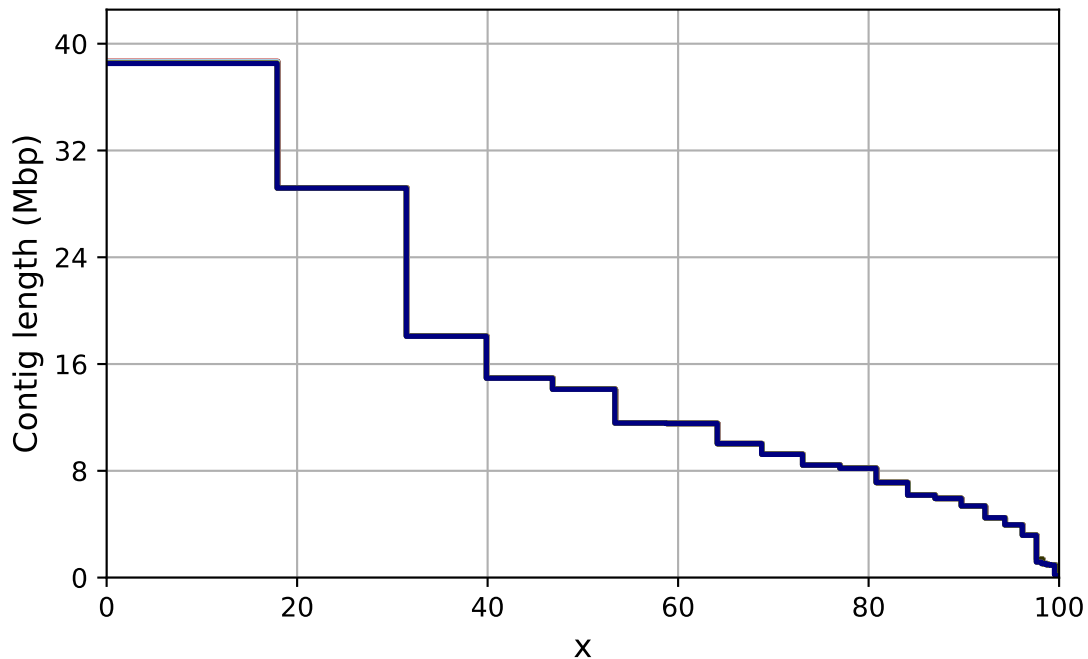
FRCurve (misassemblies)

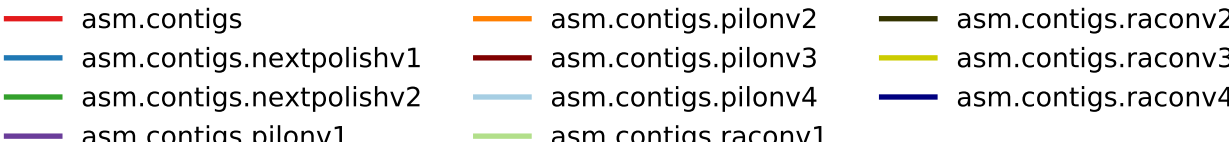|		
── asm.contigs	── asm.contigs.pilonv2	── asm.contigs.raconv2
── asm.contigs.nextpolishv1	── asm.contigs.pilonv3	── asm.contigs.raconv3
── asm.contigs.nextpolishv2	── asm.contigs.pilonv4	── asm.contigs.raconv4
── asm.contigs.pilonv1	── asm.contigs.raconv1	

Cumulative length (aligned contigs)
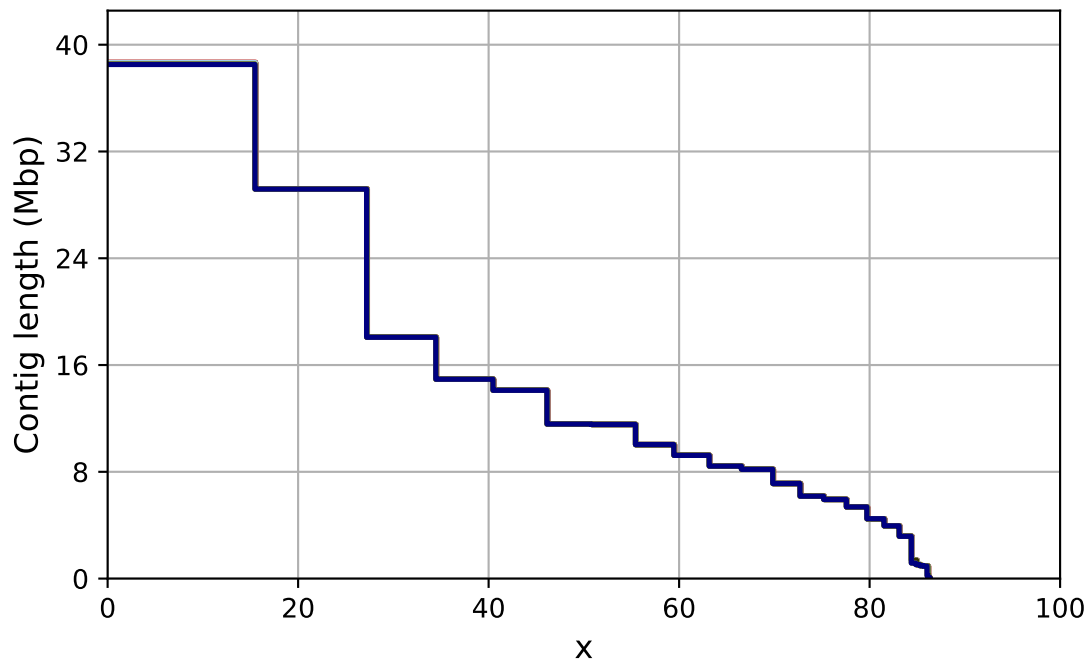
Legend		
asm.contigs	asm.contigs.pilonv2	asm.contigs.raconv2
asm.contigs.nextpolishv1	asm.contigs.pilonv3	asm.contigs.raconv3
asm.contigs.nextpolishv2	asm.contigs.pilonv4	asm.contigs.raconv4
asm.contigs.pilonv1	asm.contigs.raconv1	Reference

NAx

Contig length (Mbp) vs x

Legend:
- asm.contigs
- asm.contigs.nextpolishv1
- asm.contigs.nextpolishv2
- asm.contigs.pilonv1
- asm.contigs.pilonv2
- asm.contigs.pilonv3
- asm.contigs.pilonv4
- asm.contigs.raconv1
- asm.contigs.raconv2
- asm.contigs.raconv3
- asm.contigs.raconv4

NGAx

▬ asm.contigs	▬ asm.contigs.pilonv2	▬ asm.contigs.raconv2
▬ asm.contigs.nextpolishv1	▬ asm.contigs.pilonv3	▬ asm.contigs.raconv3
▬ asm.contigs.nextpolishv2	▬ asm.contigs.pilonv4	▬ asm.contigs.raconv4
▬ asm.contigs.pilonv1	▬ asm.contigs.raconv1	

Genome fraction, %

100

95

■ asm.contigs	■ asm.contigs.pilonv2 ■ asm.contigs.raconv2
■ asm.contigs.nextpolishv1	■ asm.contigs.pilonv3 ■ asm.contigs.raconv3
■ asm.contigs.nextpolishv2	■ asm.contigs.pilonv4 ■ asm.contigs.raconv4
■ asm.contigs.pilonv1	■ asm.contigs.raconv1 |