

Report

	il_com_contigs	il_com_k51_contigs	il_com_k61_contigs	il_for_contigs	il_for_k51_contigs	il_rev_contigs	il_rev_k51contigs	np_canu_1000l_80x_contigs
# contigs (>= 0 bp)	32	21	17	14	11	20	13	26
# contigs (>= 1000 bp)	9	7	6	7	7	8	6	19
# contigs (>= 5000 bp)	6	3	3	3	4	6	3	11
# contigs (>= 10000 bp)	4	2	2	2	3	3	2	7
# contigs (>= 25000 bp)	1	2	2	2	2	2	2	0
# contigs (>= 50000 bp)	0	1	1	1	0	1	1	0
Total length (>= 0 bp)	129852	121150	118577	119176	113821	143911	115715	166328
Total length (>= 1000 bp)	117111	113178	111789	115185	111405	137122	111652	161203
Total length (>= 5000 bp)	106941	101539	101782	100705	101316	129213	101290	138044
Total length (>= 10000 bp)	93679	93916	94145	93293	93891	111256	93916	109873
Total length (>= 25000 bp)	35695	93916	94145	93293	69957	89470	93916	0
Total length (>= 50000 bp)	0	58114	56148	57128	0	51598	58114	0
# contigs	32	21	17	14	11	20	13	26
Largest contig	35695	58114	56148	57128	35802	51598	58114	23789
Total length	129852	121150	118577	119176	113821	143911	115715	166328
Reference length	134226	134226	134226	134226	134226	134226	134226	134226
GC (%)	54.91	54.99	55.32	56.01	55.96	55.34	55.70	55.50
Reference GC (%)	56.23	56.23	56.23	56.23	56.23	56.23	56.23	56.23
N50	21008	35802	37997	36165	34155	37872	58114	11672
NG50	21008	35802	37997	36165	34155	37872	35802	12234
N75	7619	35802	37997	36165	23934	21786	35802	6883
NG75	7619	7623	7637	7412	7425	21786	7374	10359
L50	3	2	2	2	2	2	1	5
LG50	3	2	2	2	2	2	2	4
L75	5	2	2	2	3	3	2	10
LG75	5	3	3	3	4	3	3	7
# misassemblies	0	0	0	0	0	0	0	0
# misassembled contigs	0	0	0	0	0	0	0	0
Misassembled contigs length	0	0	0	0	0	0	0	0
# local misassemblies	4	3	4	3	2	1	3	0
# scaffold gap ext. mis.	0	0	0	0	0	0	0	0
# scaffold gap loc. mis.	0	0	0	0	0	0	0	0
# unaligned mis. contigs	0	0	0	0	0	0	0	0
# unaligned contigs	20 + 0 part	12 + 0 part	8 + 0 part	5 + 0 part	2 + 0 part	9 + 0 part	5 + 0 part	0 + 0 part
Unaligned length	10910	6594	4440	2738	1038	4762	2650	0
Genome fraction (%)	83.478	84.107	84.583	86.801	83.918	83.769	83.977	71.534
Duplication ratio	1.062	1.015	1.005	0.999	1.001	1.238	1.003	1.732
# N's per 100 kbp	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
# mismatches per 100 kbp	1118.26	1017.77	992.67	1078.89	995.21	1195.30	1077.01	1593.47
# indels per 100 kbp	88.35	94.78	93.37	81.54	88.78	102.28	84.28	533.24
# genomic features	208 + 32 part	219 + 20 part	223 + 19 part	219 + 32 part	214 + 25 part	222 + 22 part	215 + 24 part	156 + 34 part
Largest alignment	35695	57962	55918	56651	35802	51598	57962	23783
Total aligned length	118303	114288	113475	115892	112505	139022	112576	166193
NA50	20550	35802	37988	36129	33998	37863	57962	11672
NGA50	20550	35802	37988	36129	33998	37863	35802	12232
NA75	7609	35802	37988	36129	23934	21786	35802	6878
NGA75	7609	7618	7631	4815	7425	21786	7364	10359
LA50	3	2	2	2	2	2	1	5
LGA50	3	2	2	2	2	2	2	4
LA75	5	2	2	2	3	3	2	10
LGA75	5	3	3	4	4	3	3	7

All statistics are based on contigs of size >= 50 bp, unless otherwise noted (e.g., "# contigs (>= 0 bp)" and "Total length (>= 0 bp)" include all contigs).

Misassemblies report

	il_com_contigs	il_com_k51_contigs	il_com_k61_contigs	il_for_contigs	il_for_k51_contigs	il_rev_contigs	il_rev_k51contigs	np_canu_1000l_80x_contigs
# misassemblies	0	0	0	0	0	0	0	0
# contig misassemblies	0	0	0	0	0	0	0	0
# c. relocations	0	0	0	0	0	0	0	0
# c. translocations	0	0	0	0	0	0	0	0
# c. inversions	0	0	0	0	0	0	0	0
# scaffold misassemblies	0	0	0	0	0	0	0	0
# s. relocations	0	0	0	0	0	0	0	0
# s. translocations	0	0	0	0	0	0	0	0
# s. inversions	0	0	0	0	0	0	0	0
# misassembled contigs	0	0	0	0	0	0	0	0
Misassembled contigs length	0	0	0	0	0	0	0	0
# local misassemblies	4	3	4	3	2	1	3	0
# scaffold gap ext. mis.	0	0	0	0	0	0	0	0
# scaffold gap loc. mis.	0	0	0	0	0	0	0	0
# unaligned mis. contigs	0	0	0	0	0	0	0	0
# mismatches	1253	1149	1127	1257	1121	1344	1214	1530
# indels	99	107	106	95	100	115	95	512
# indels (<= 5 bp)	94	98	95	89	93	106	85	506
# indels (> 5 bp)	5	9	11	6	7	9	10	6
Indels length	226	494	466	832	460	562	505	847

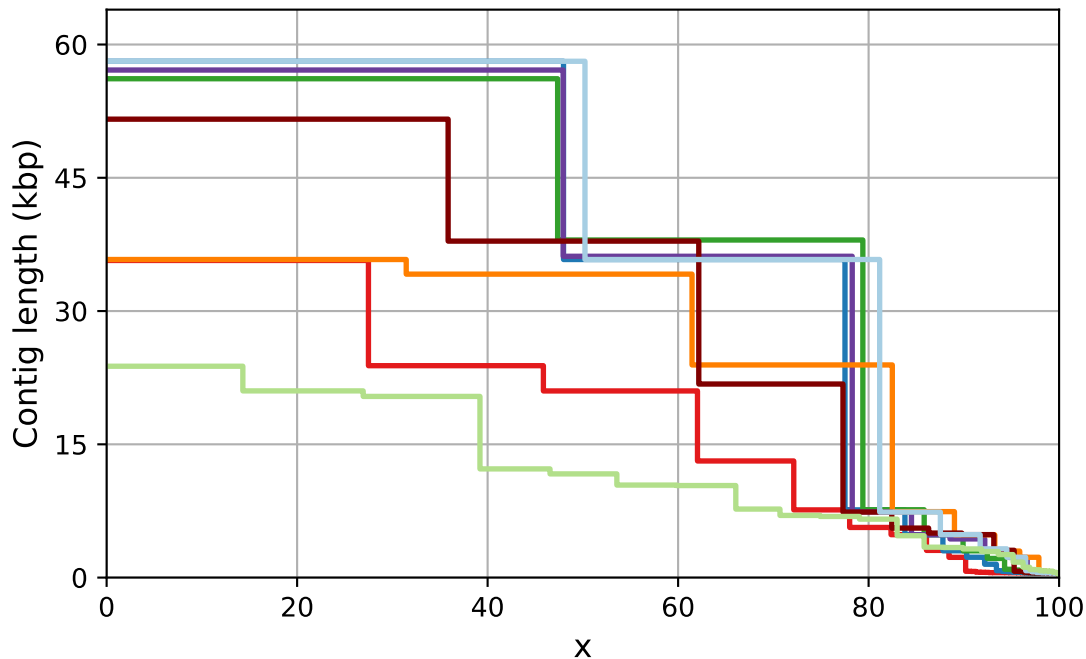
All statistics are based on contigs of size ≥ 50 bp, unless otherwise noted (e.g., "# contigs (≥ 0 bp)" and "Total length (≥ 0 bp)" include all contigs).

Unaligned report

	ll_com_contigs	il_com_k51_contigs	il_com_k61_contigs	ll_for_contigs	il_for_k51_contigs	il_rev_contigs	il_rev_k51contigs	np_canu_1000l_80x_contigs
# fully unaligned contigs	20	12	8	5	2	9	5	0
Fully unaligned length	10910	6594	4440	2738	1038	4762	2650	0
# partially unaligned contigs	0	0	0	0	0	0	0	0
Partially unaligned length	0	0	0	0	0	0	0	0
# N's	0	0	0	0	0	0	0	0

All statistics are based on contigs of size ≥ 50 bp, unless otherwise noted (e.g., "# contigs (≥ 0 bp)" and "Total length (≥ 0 bp)" include all contigs).

Nx



il_com_contigs

il_for_contigs

il_rev_k51contigs

il_com_k51_contigs

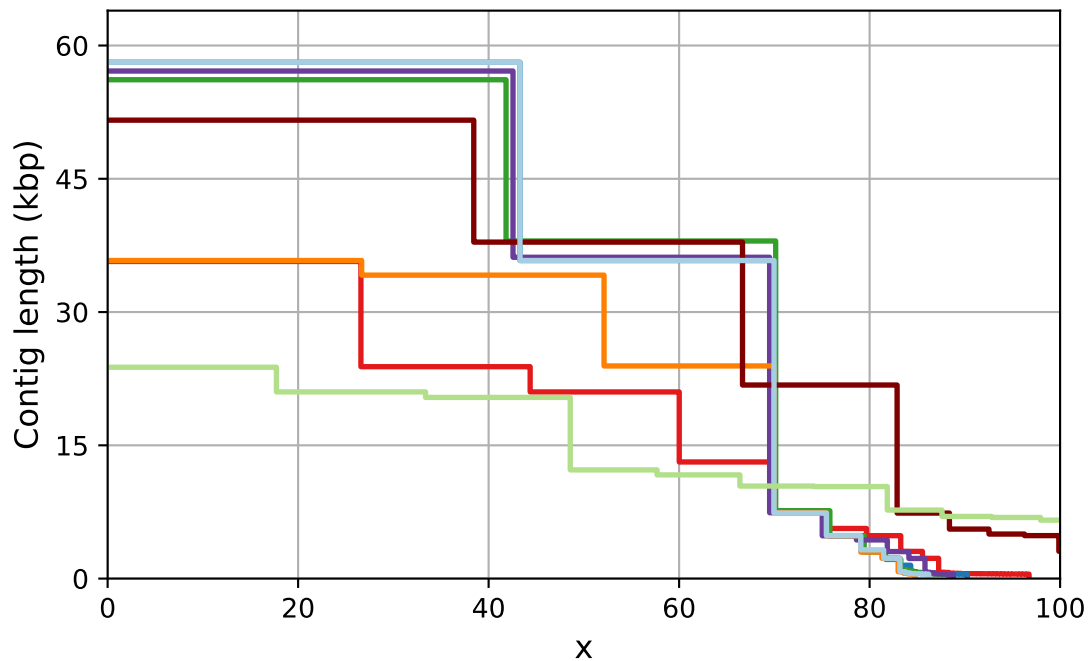
il_for_k51_contigs

np_canu_1000l_80x_contigs

il_com_k61_contigs

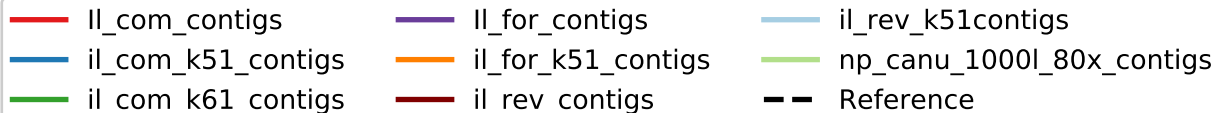
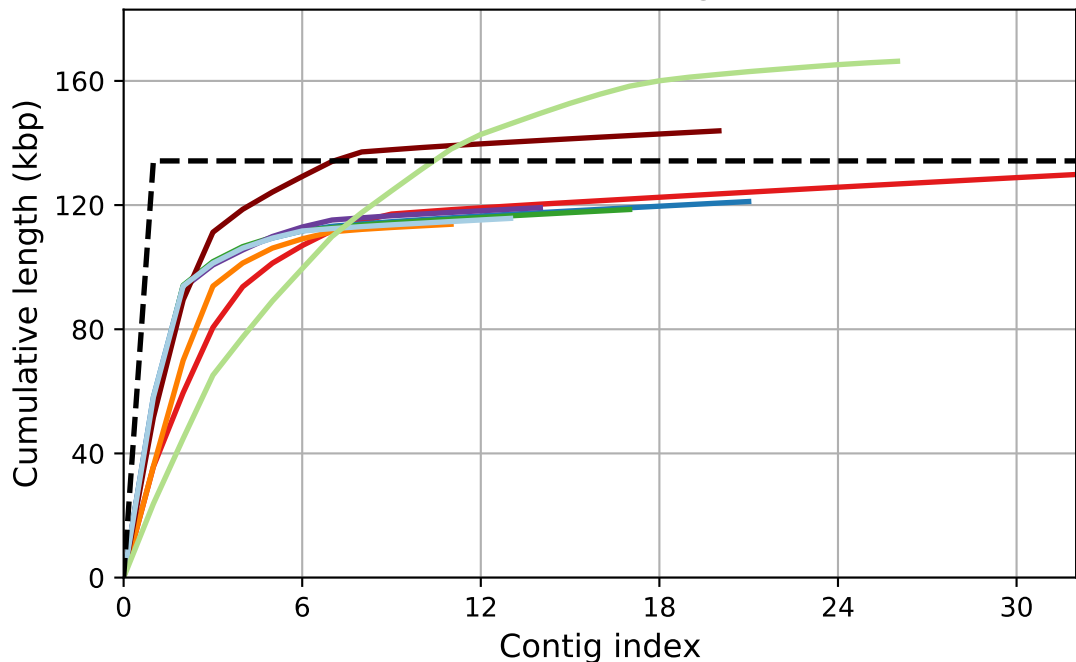
il_rev_contigs

NGx

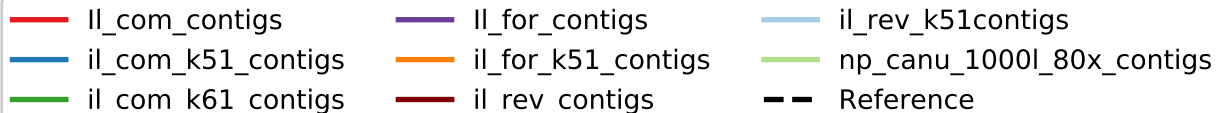
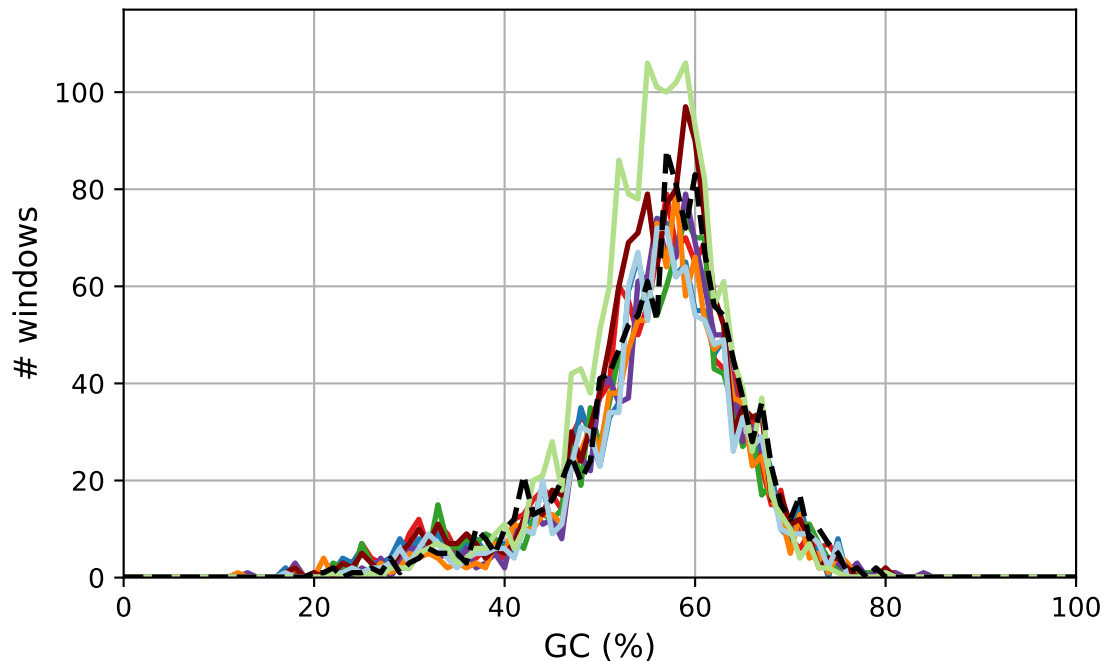


- | | | |
|---|--|---|
| — il_com_contigs | — il_for_contigs | — il_rev_k51contigs |
| — il_com_k51_contigs | — il_for_k51_contigs | — np_canu_1000l_80x_contigs |
| — il_com_k61_contigs | — il_rev_contigs | |

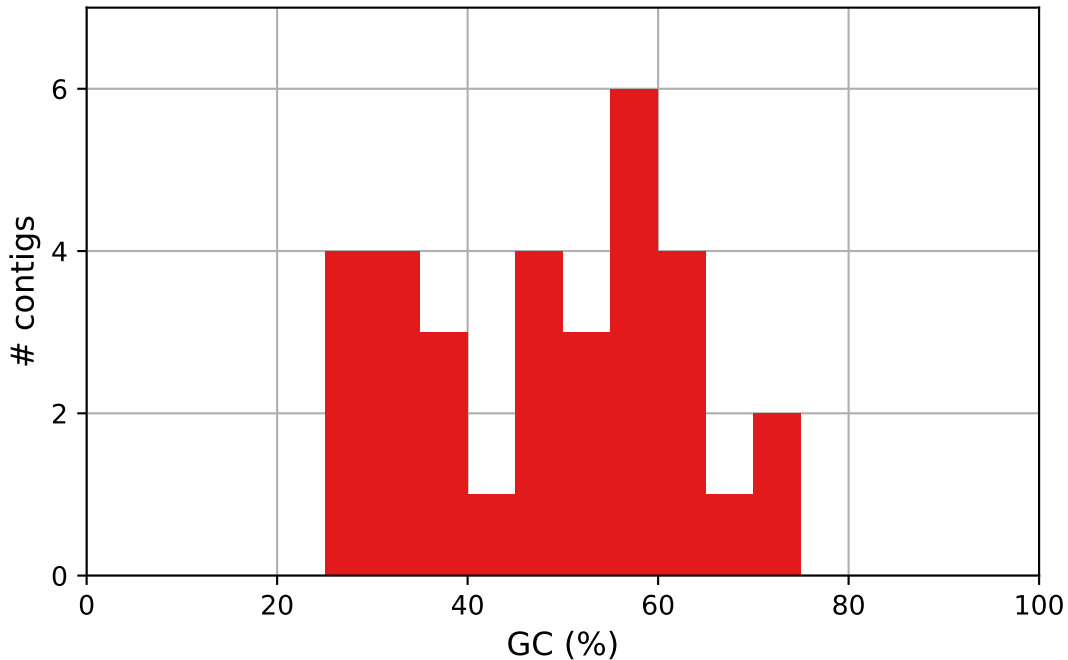
Cumulative length



GC content

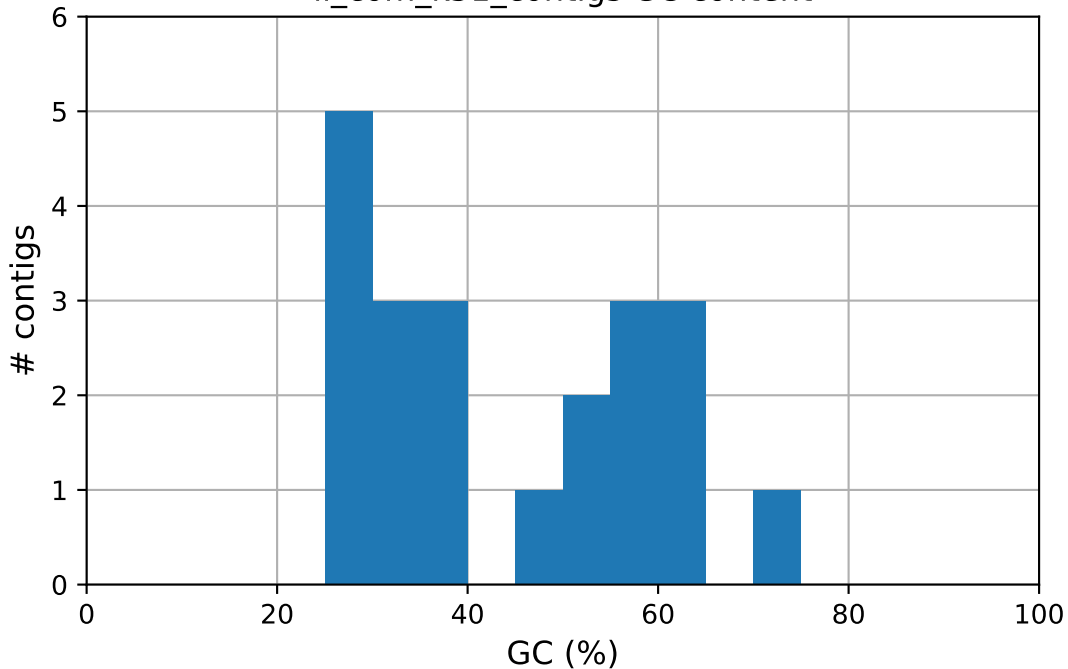


Il_com_contigs GC content



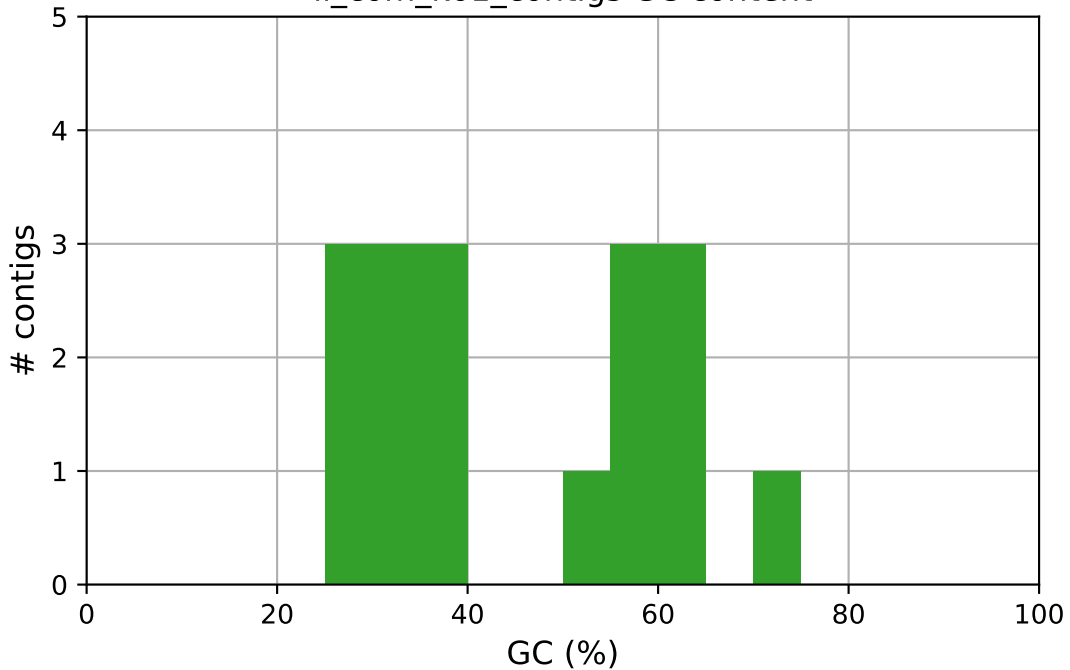
Il_com_contigs

il_com_k51_contigs GC content



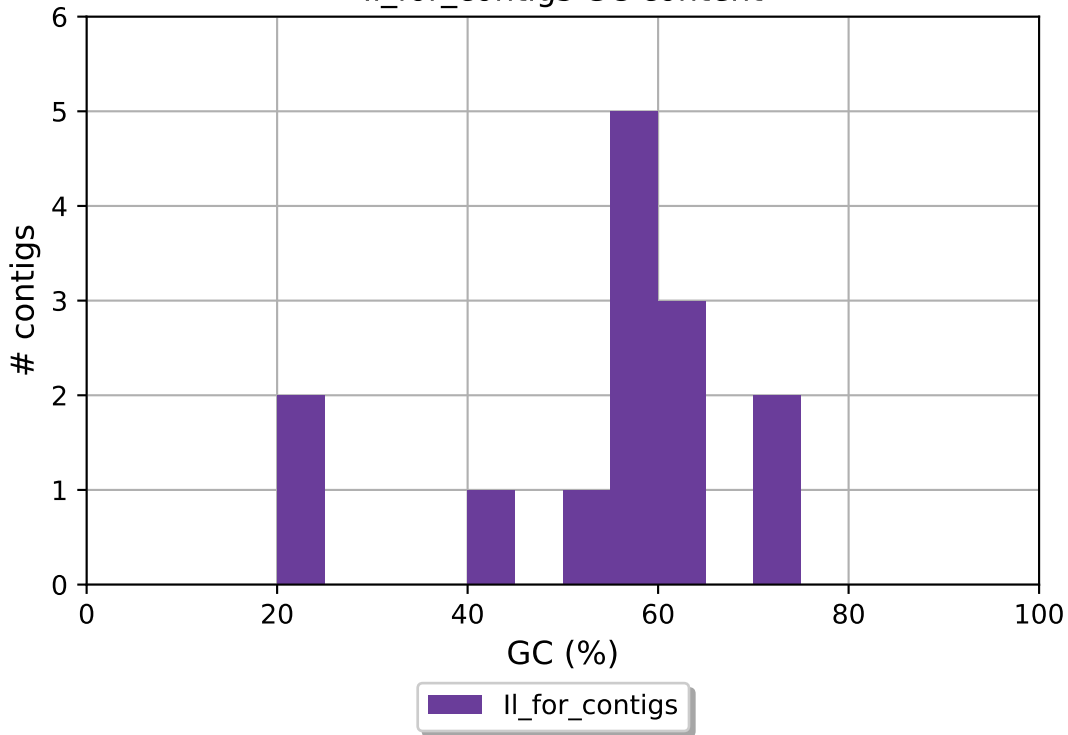
il_com_k51_contigs

il_com_k61_contigs GC content

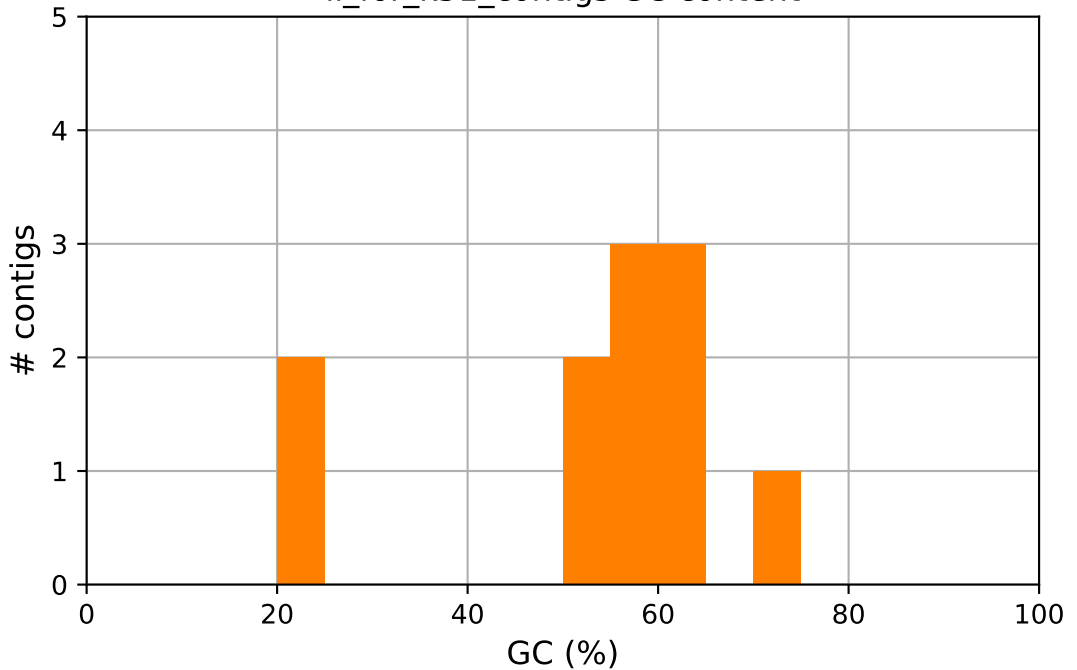


il_com_k61_contigs

Il_for_contigs GC content

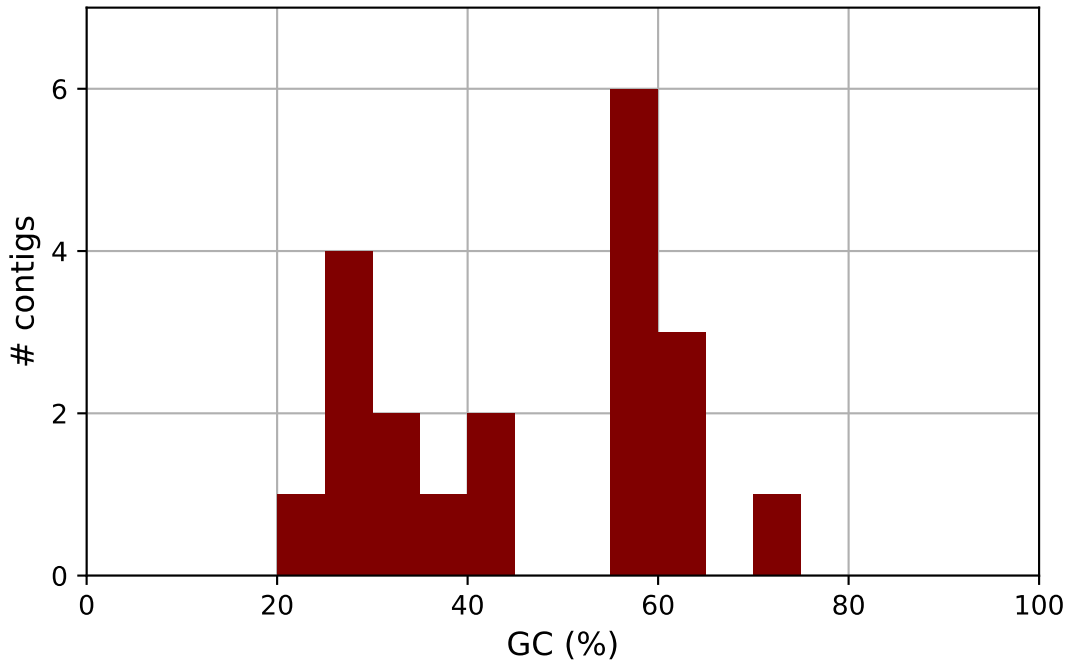


il_for_k51_contigs GC content



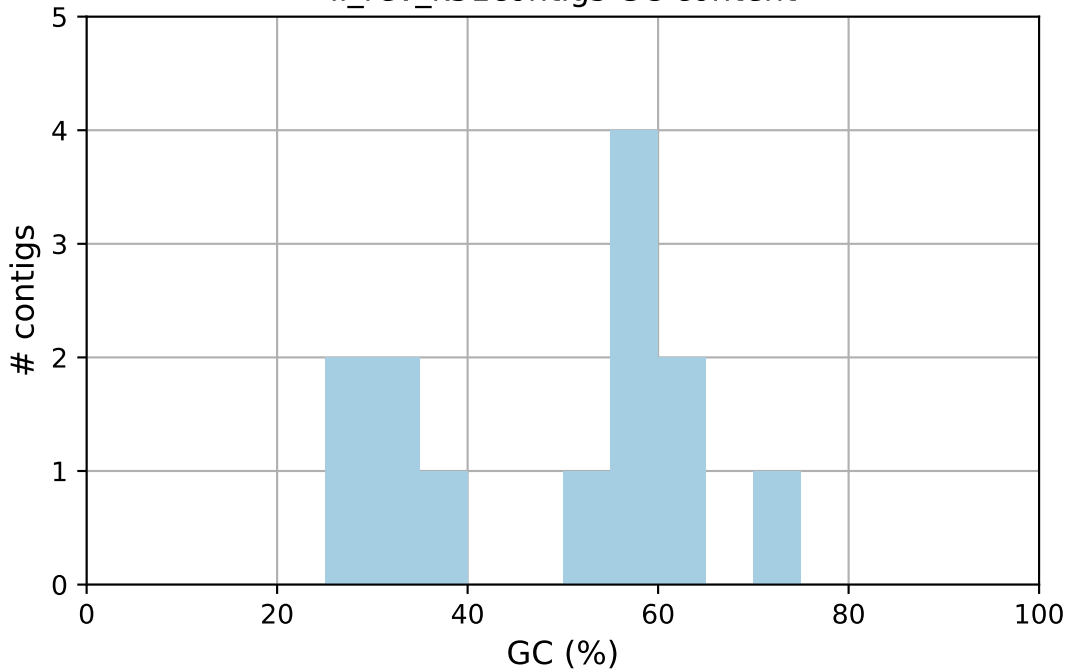
il_for_k51_contigs

il_rev_contigs GC content



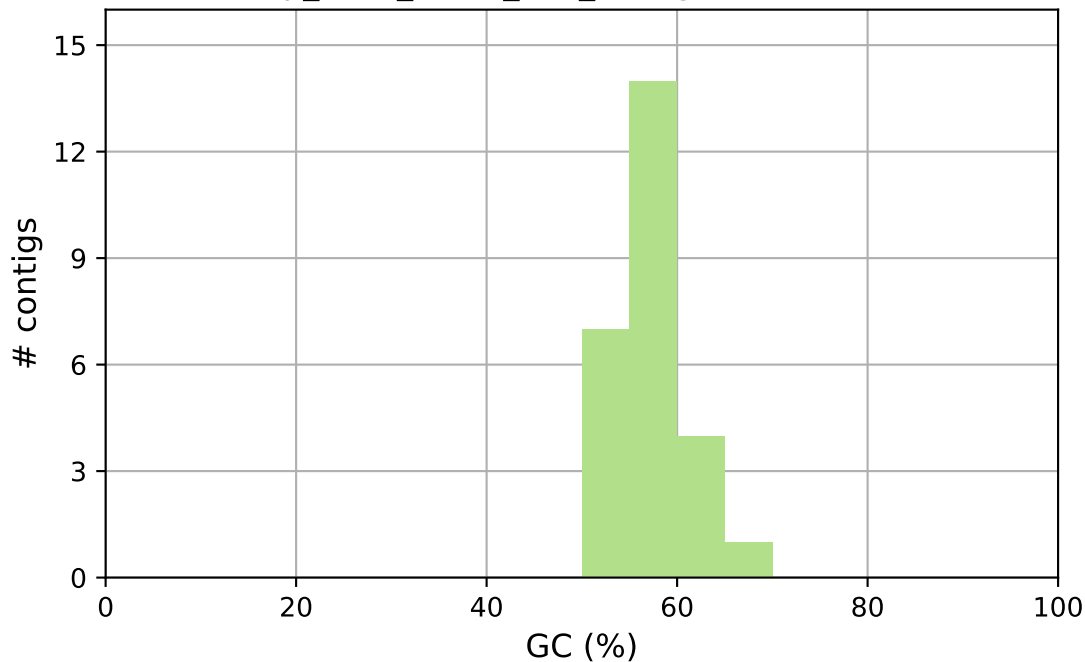
il_rev_contigs

il_rev_k51contigs GC content



il_rev_k51contigs

np_canu_1000l_80x_contigs GC content



np_canu_1000l_80x_contigs

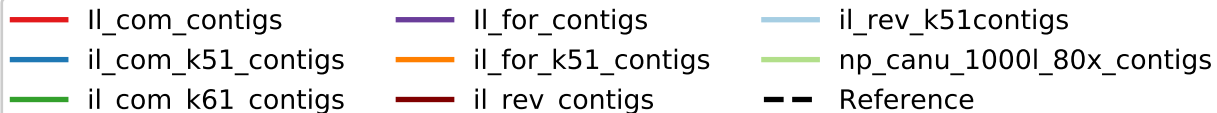
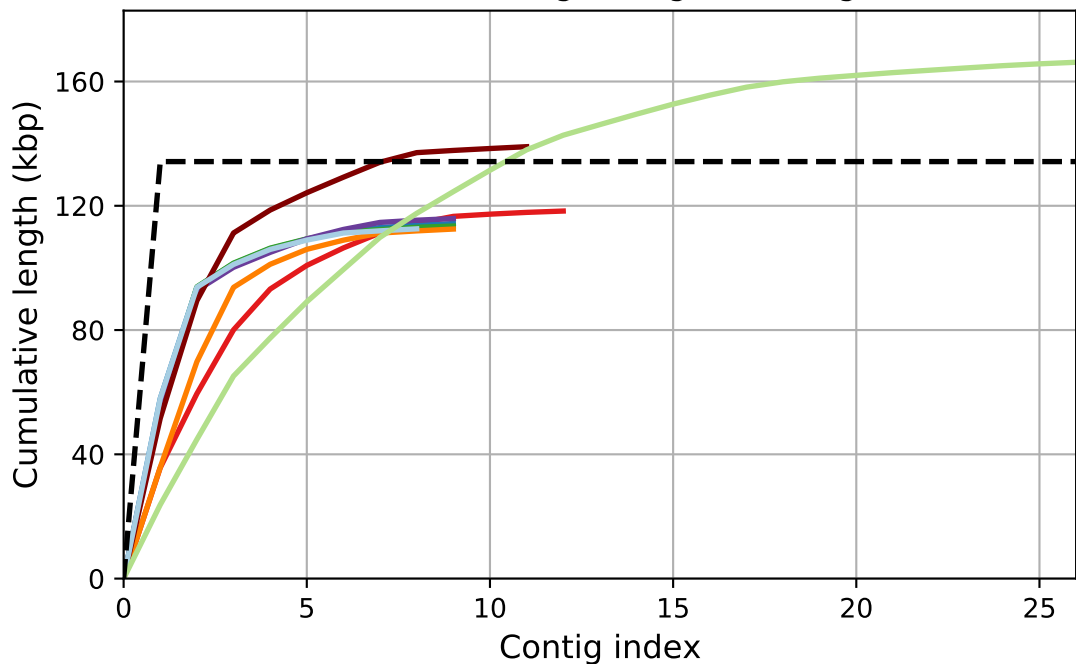
FRCurve (misassemblies)



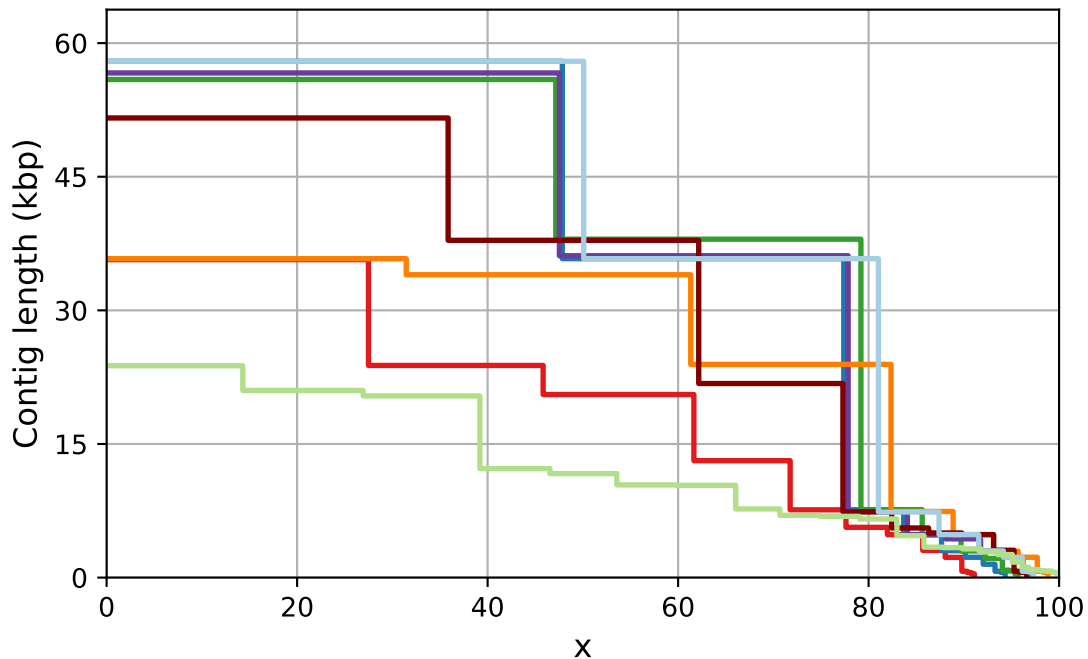
Legend:

- il_com_contigs
- il_for_contigs
- il_rev_k51contigs
- il_com_k51_contigs
- il_for_k51_contigs
- np_canu_1000l_80x_contigs
- il_com_k61_contigs
- il_rev_contigs

Cumulative length (aligned contigs)

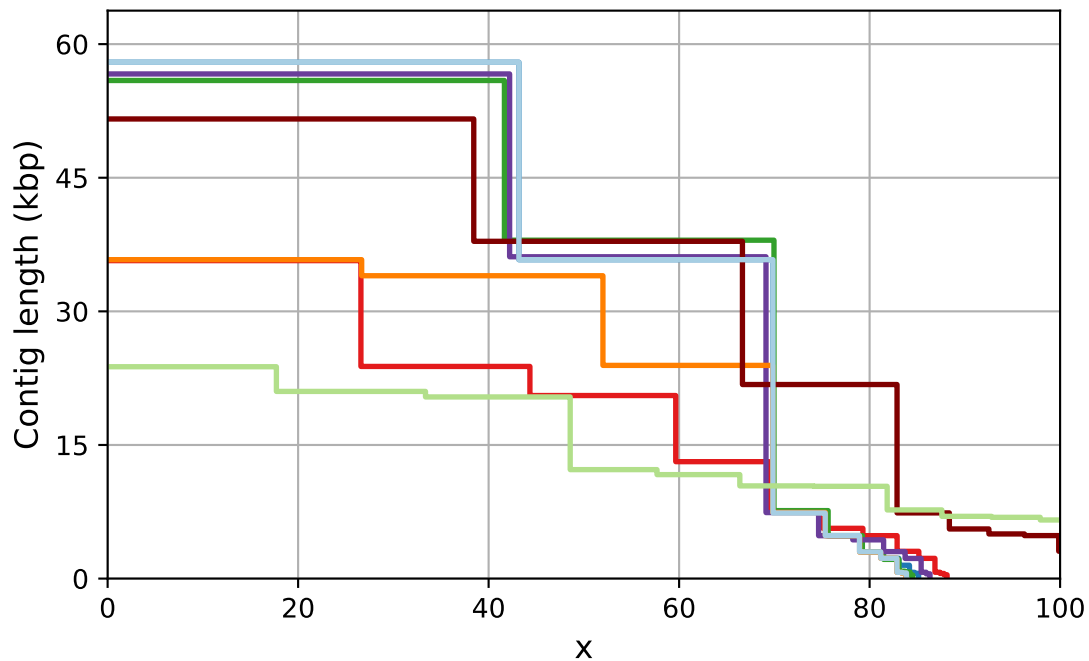


NAx



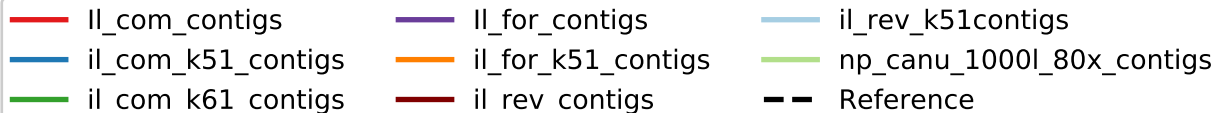
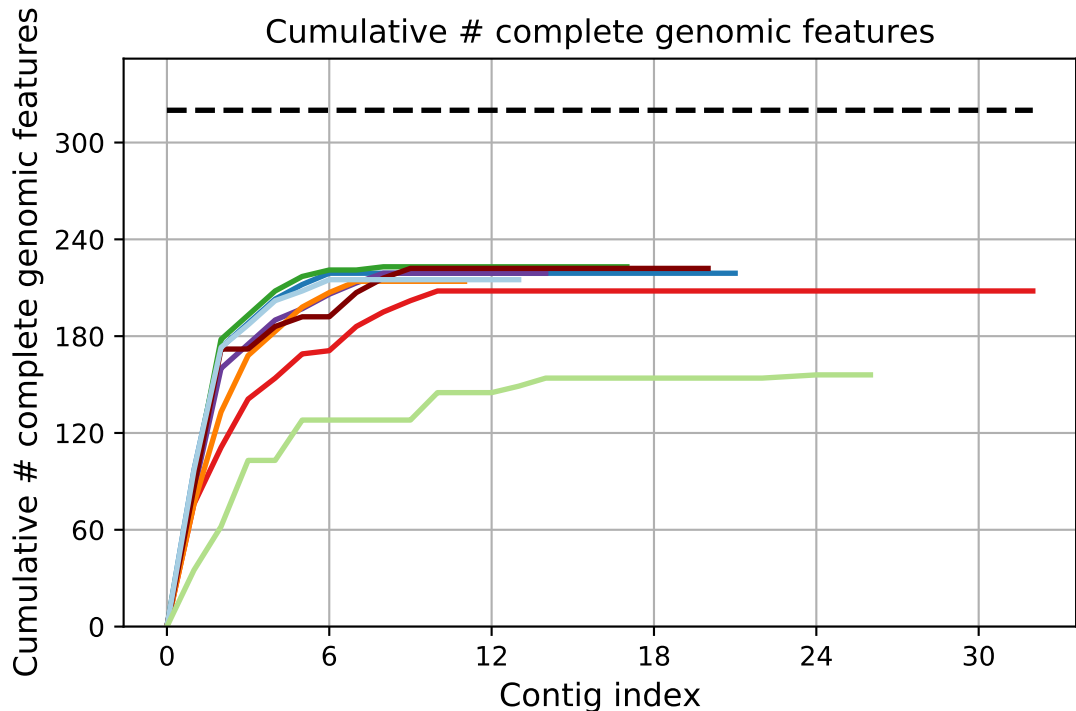
- il_com_contigs
 — il_for_contigs
— il_rev_k51contigs
- il_com_k51_contigs
 — il_for_k51_contigs
— np_canu_1000l_80x_contigs
- il_com_k61_contigs
 — il_rev_contigs

NGAx

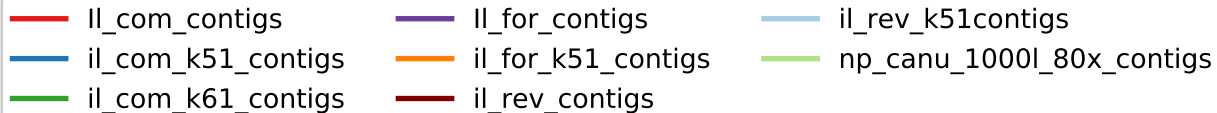
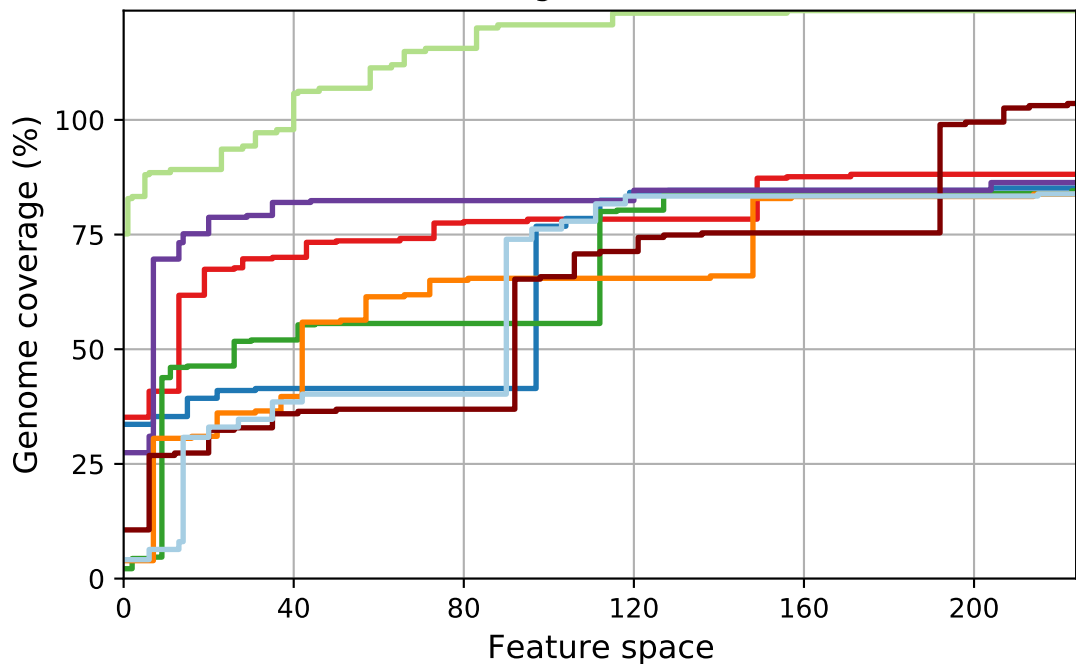


- il_com_contigs
 — il_for_contigs
— il_rev_k51contigs
- il_com_k51_contigs
 — il_for_k51_contigs
— np_canu_1000l_80x_contigs
- il_com_k61_contigs
 — il_rev_contigs

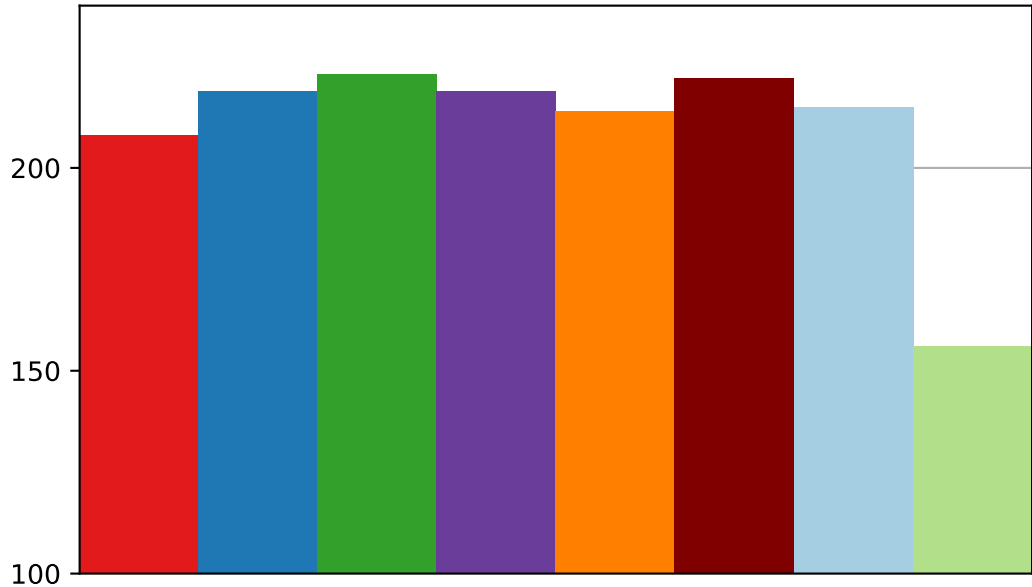
Cumulative # complete genomic features



FRCurve (genomic features)

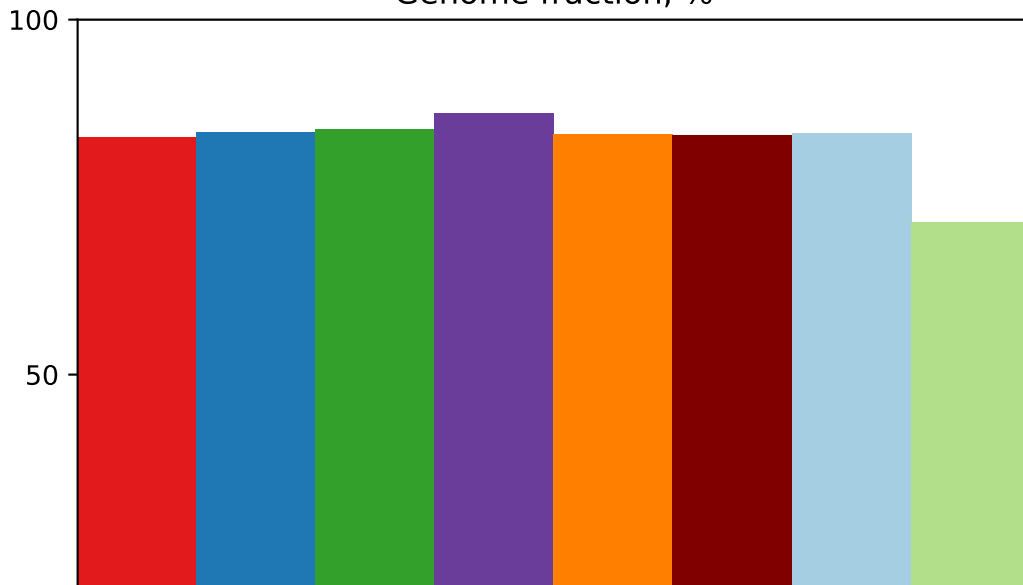










complete genomic features



il_com_contigs	il_for_contigs	il_rev_k51contigs
il_com_k51_contigs	il_for_k51_contigs	np_canu_1000l_80x_contigs
il_com_k61_contigs	il_rev_contigs	

Genome fraction, %



 il_com_contigs	 il_for_contigs	 il_rev_k51contigs
 il_com_k51_contigs	 il_for_k51_contigs	 np_canu_1000l_80x_contigs
 il_com_k61_contigs	 il_rev_contigs	