

Report

	a5miseq	canu	falcon	flye	hifiasm	hinge	sga	spades
# contigs (>= 0 bp)	748300	5365	1961	1234	15377	1594	242031	1588
# contigs (>= 1000 bp)	5043	5365	1961	1178	15377	1583	116	72
# contigs (>= 5000 bp)	152	5353	1950	1103	15376	1475	7	2
# contigs (>= 10000 bp)	15	3699	1819	1019	15375	1340	1	1
# contigs (>= 25000 bp)	2	204	85	621	3254	164	1	0
# contigs (>= 50000 bp)	2	38	13	56	40	22	0	0
Total length (>= 0 bp)	314250807	73765313	28270938	30029756	334872860	24131172	32692313	346246
Total length (>= 1000 bp)	9031914	73765313	28270938	29993573	334872860	24123400	276512	158851
Total length (>= 5000 bp)	1196444	73715462	28227992	29777615	334870807	23795240	69866	22564
Total length (>= 10000 bp)	315767	57564687	26992996	29153080	334865164	22793308	30162	16600
Total length (>= 25000 bp)	131762	8050365	3204124	21371925	97402805	6318773	30162	0
Total length (>= 50000 bp)	131762	2846125	871770	4362960	2703643	1759454	0	0
# contigs	120438	5365	1961	1232	15377	1591	617	135
Largest contig	73731	155430	136597	246607	208224	159816	30162	16600
Total length	78542868	73765313	28270938	30028912	334872860	24130636	598035	201880
Reference length	3272089205	3272089205	3272089205	3272089205	3272089205	3272089205	3272089205	3272089205
GC (%)	40.62	38.62	39.72	40.39	39.59	39.54	47.12	50.94
Reference GC (%)	41.04	41.04	41.04	41.04	41.04	41.04	41.04	41.04
N50	602	13580	14011	28044	21918	14749	905	1882
N75	540	10057	11446	24323	19202	12349	618	1103
L50	47999	1908	715	381	6260	480	140	30
L75	82564	3476	1277	668	10342	936	346	65
# misassemblies	5369	4042	265	394	1886	2403	6	108
# misassembled contigs	5212	1780	193	221	513	728	5	67
Misassembled contigs length	3684062	24026697	4332023	7563271	13687771	12429163	3216	90121
# local misassemblies	273	5438	887	679	2236	2057	1	12
# scaffold gap ext. mis.	0	0	0	0	0	0	0	17
# scaffold gap loc. mis.	0	0	0	0	0	0	0	2
# unaligned mis. contigs	107	487	25	82	75	359	13	3
# unaligned contigs	1519 + 219 part	398 + 1402 part	1 + 148 part	42 + 251 part	20 + 409 part	147 + 1005 part	109 + 9 part	15 + 5 part
Unaligned length	1564582	12673230	765531	2278489	4108236	9953860	182724	25085
Genome fraction (%)	2.437	1.383	0.874	0.866	10.488	0.207	0.013	0.005
Duplication ratio	1.015	1.421	1.012	1.030	1.014	2.197	1.039	1.064
# N's per 100 kbp	887.83	0.00	0.00	0.33	0.00	0.00	0.00	985.24
# mismatches per 100 kbp	233.15	1695.62	1142.21	1272.70	166.09	4357.18	405.15	1356.09
# indels per 100 kbp	34.27	153.14	363.28	286.14	218.29	461.17	20.76	64.40
Largest alignment	18785	108455	64590	93090	74358	60176	7137	16600
Total aligned length	75924817	59774470	27427277	27601994	330374434	13733461	401793	166272
NA50	583	10241	12924	26154	21579	1386	596	827
NGA50	-	-	-	-	-	-	-	-
NA75	525	2443	10814	20358	18758	-	-	263
LA50	50458	2257	810	447	6407	2394	294	52
LA75	86057	5608	1409	762	10562	-	-	160

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

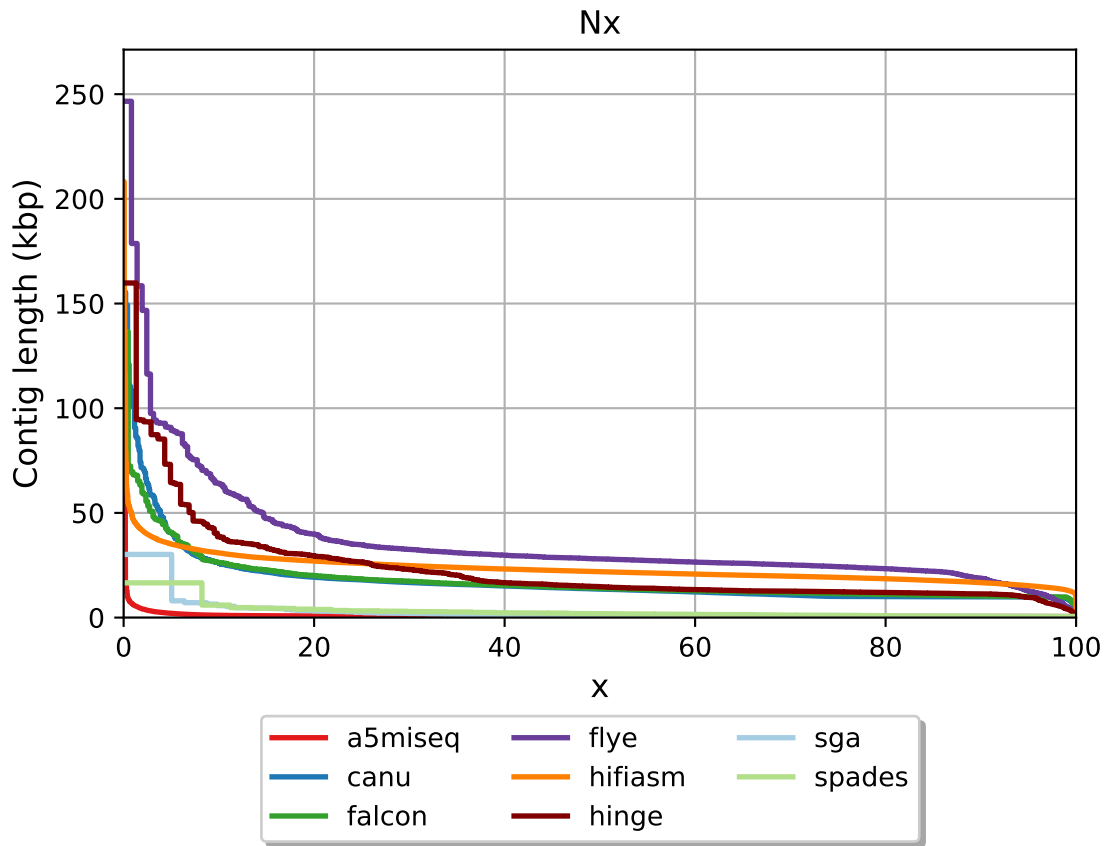
	a5miseq	canu	falcon	flye	hifiasm	hinge	sga	spades
# misassemblies	5369	4042	265	394	1886	2403	6	108
# contig misassemblies	5368	4042	265	394	1886	2403	6	43
# c. relocations	575	3610	52	204	1465	1875	2	18
# c. translocations	4751	432	213	190	415	393	4	24
# c. inversions	42	0	0	0	6	135	0	1
# scaffold misassemblies	1	0	0	0	0	0	0	65
# s. relocations	0	0	0	0	0	0	0	30
# s. translocations	1	0	0	0	0	0	0	35
# s. inversions	0	0	0	0	0	0	0	0
# misassembled contigs	5212	1780	193	221	513	728	5	67
Misassembled contigs length	3684062	24026697	4332023	7563271	13687771	12429163	3216	90121
# local misassemblies	273	5438	887	679	2236	2057	1	12
# scaffold gap ext. mis.	0	0	0	0	0	0	0	17
# scaffold gap loc. mis.	0	0	0	0	0	0	0	2
# unaligned mis. contigs	107	487	25	82	75	359	13	3
# mismatches	176747	729243	310378	342934	541861	281097	1620	2253
# indels	25981	65863	98715	77101	712152	29752	83	107
# indels (<= 5 bp)	23474	57353	95308	72927	688535	26653	66	88
# indels (> 5 bp)	2507	8510	3407	4174	23617	3099	17	19
Indels length	77055	265399	180032	168604	1205579	108171	438	508

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).

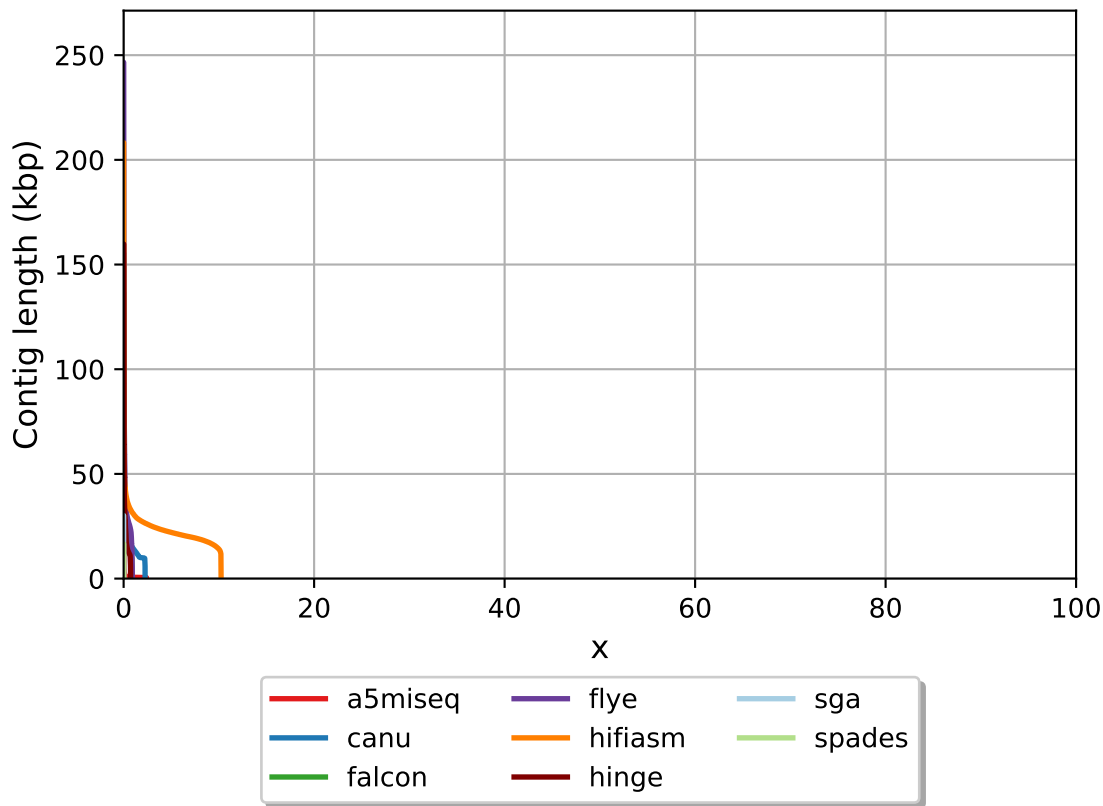
Unaligned report

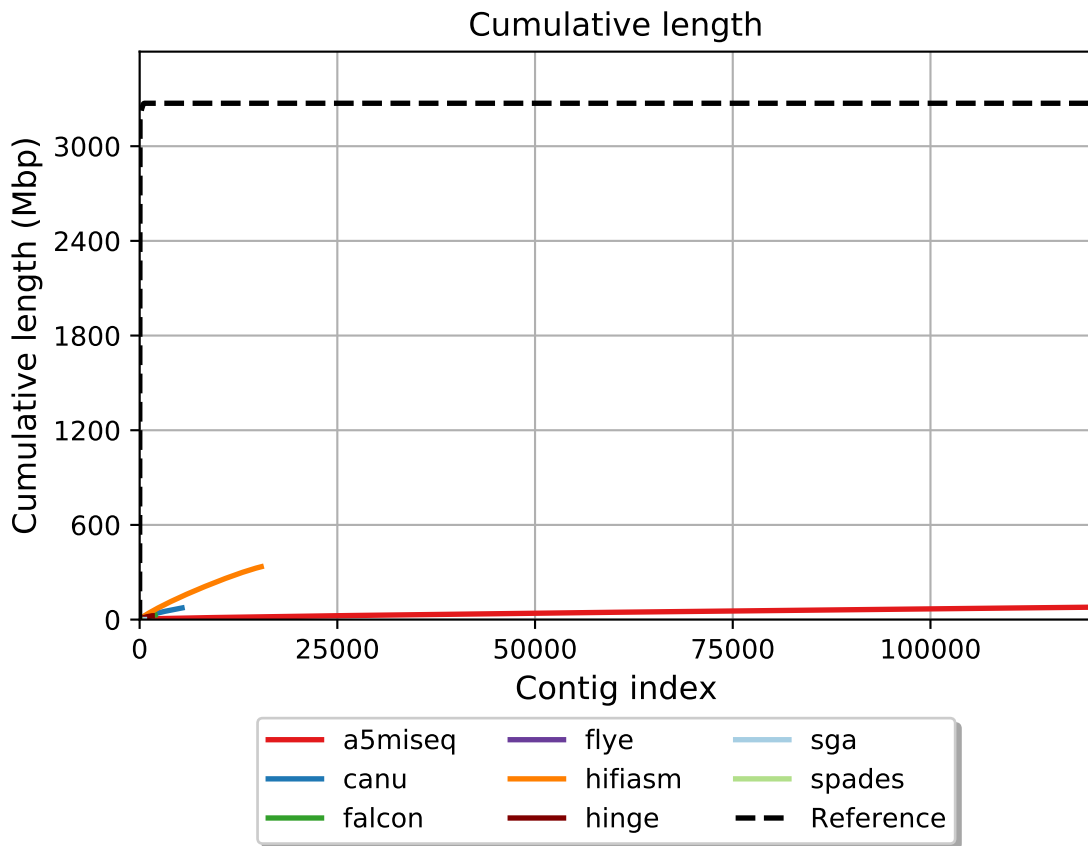
	a5miseq	canu	falcon	flye	hifiasm	hinge	sga	spades
# fully unaligned contigs	1519	398	1	42	20	147	109	15
Fully unaligned length	1327725	4419980	136597	383749	587213	2007596	175934	20781
# partially unaligned contigs	219	1402	148	251	409	1005	9	5
Partially unaligned length	236857	8253250	628934	1894740	3521023	7946264	6790	4304
# N's	697329	0	0	100	0	0	0	1989

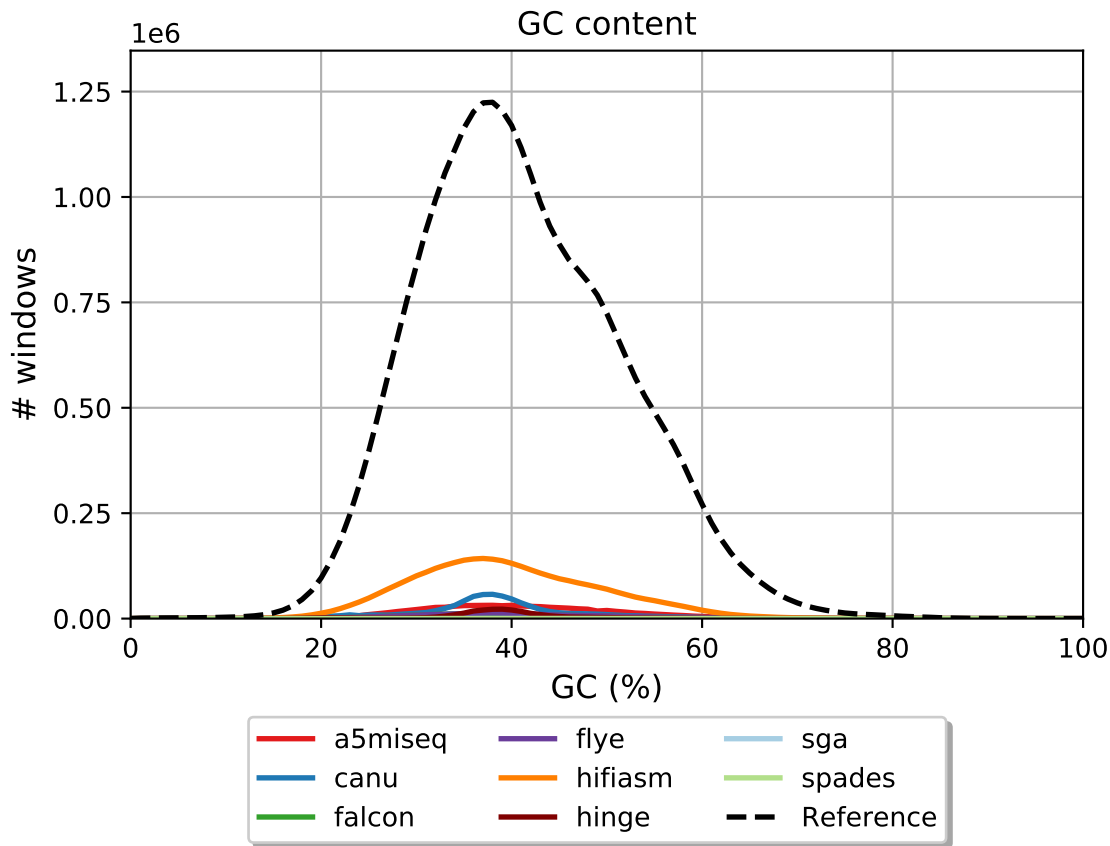
All statistics are based on contigs of size ≥ 500 bp, unless otherwise noted (e.g., "# contigs (≥ 0 bp)" and "Total length (≥ 0 bp)" include all contigs).



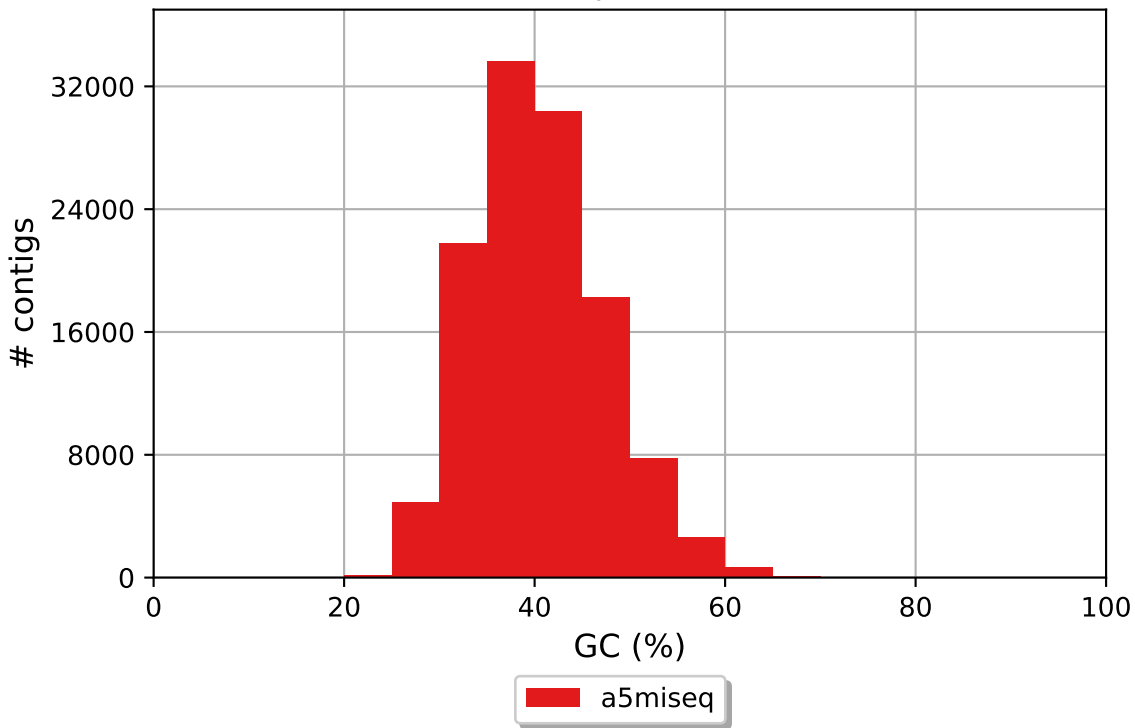
NGx



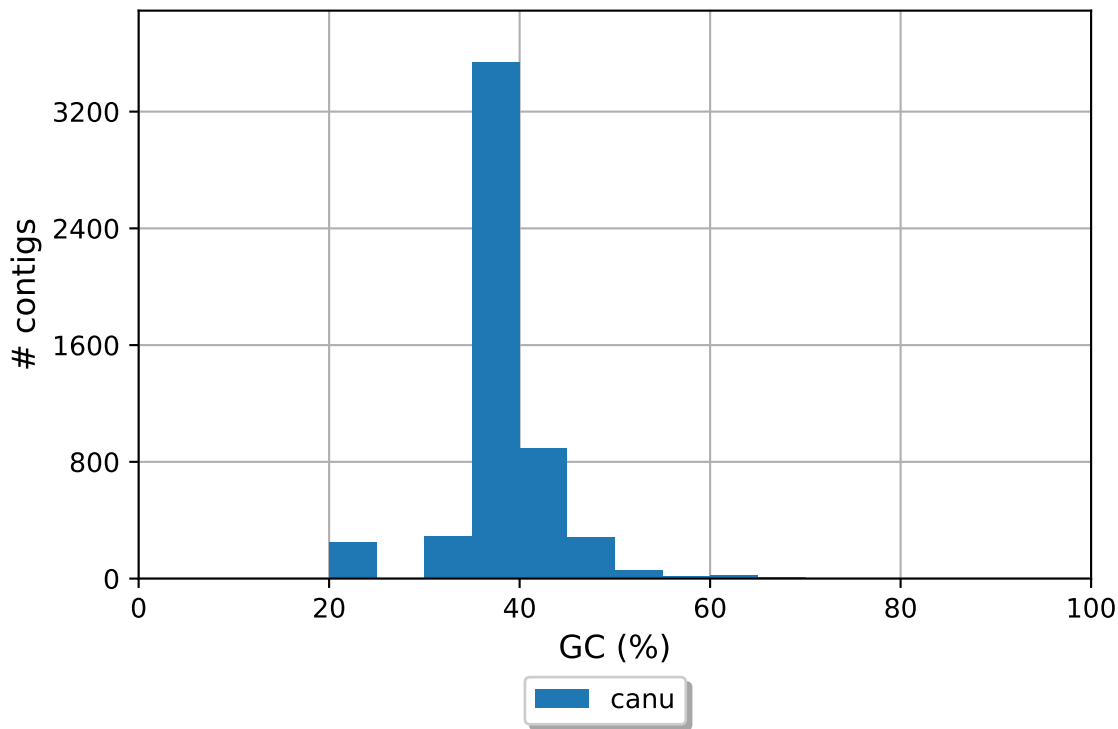




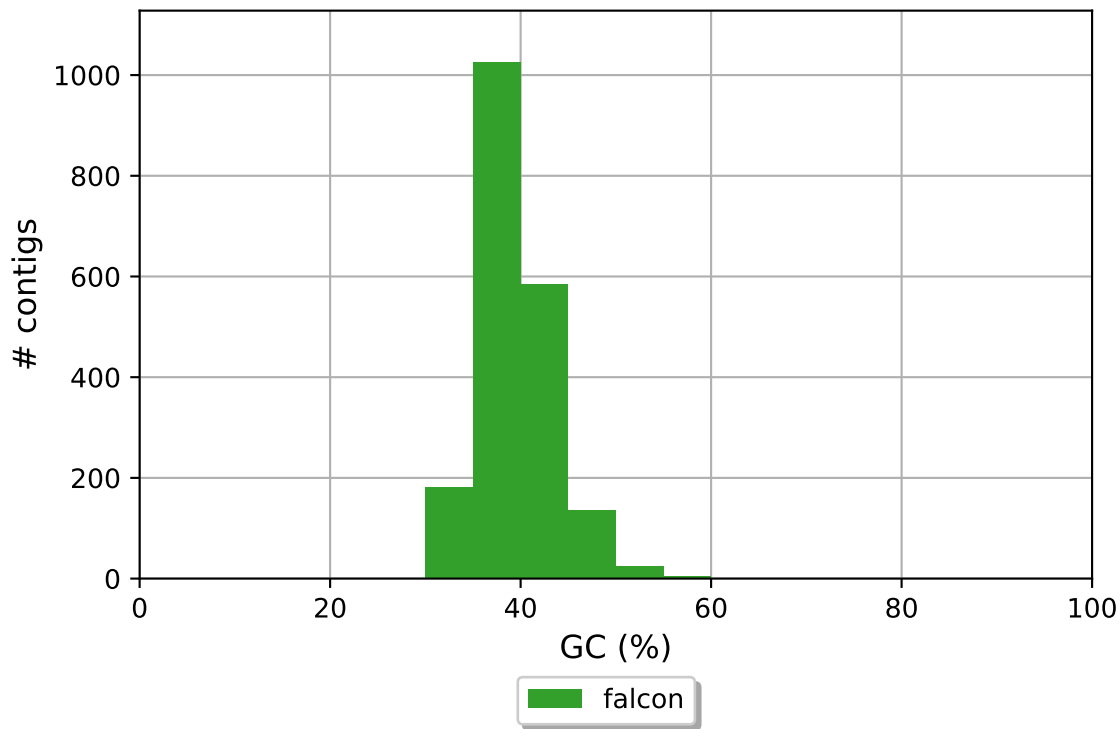
a5miseq GC content



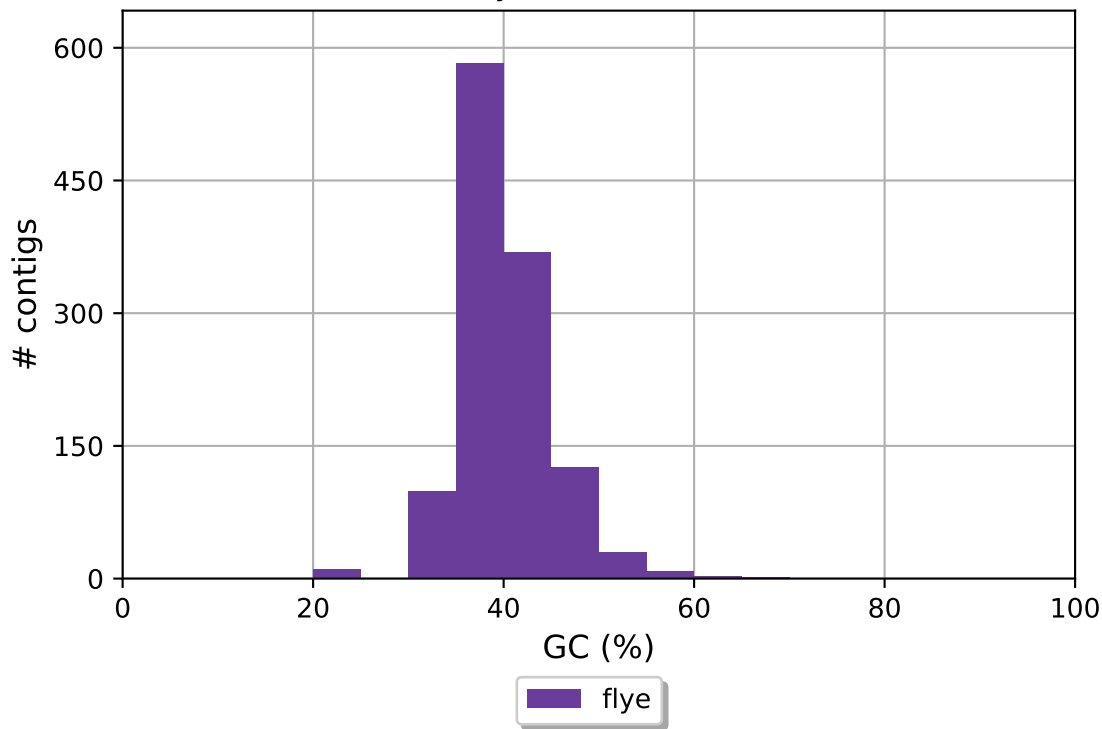
canu GC content



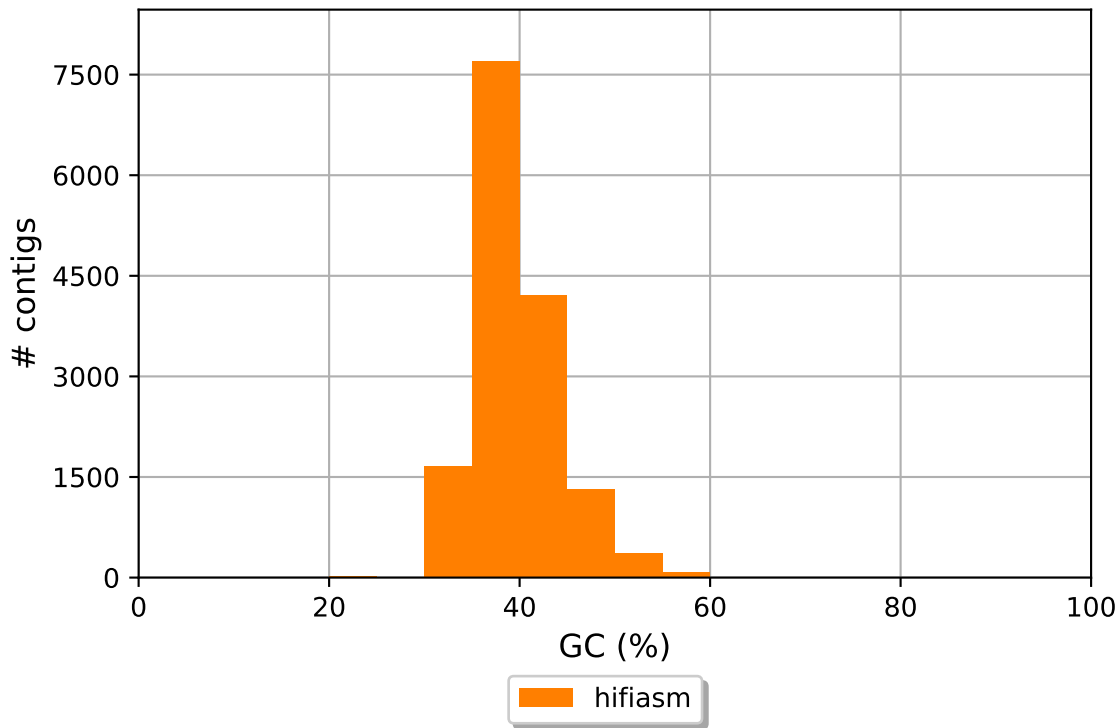
falcon GC content



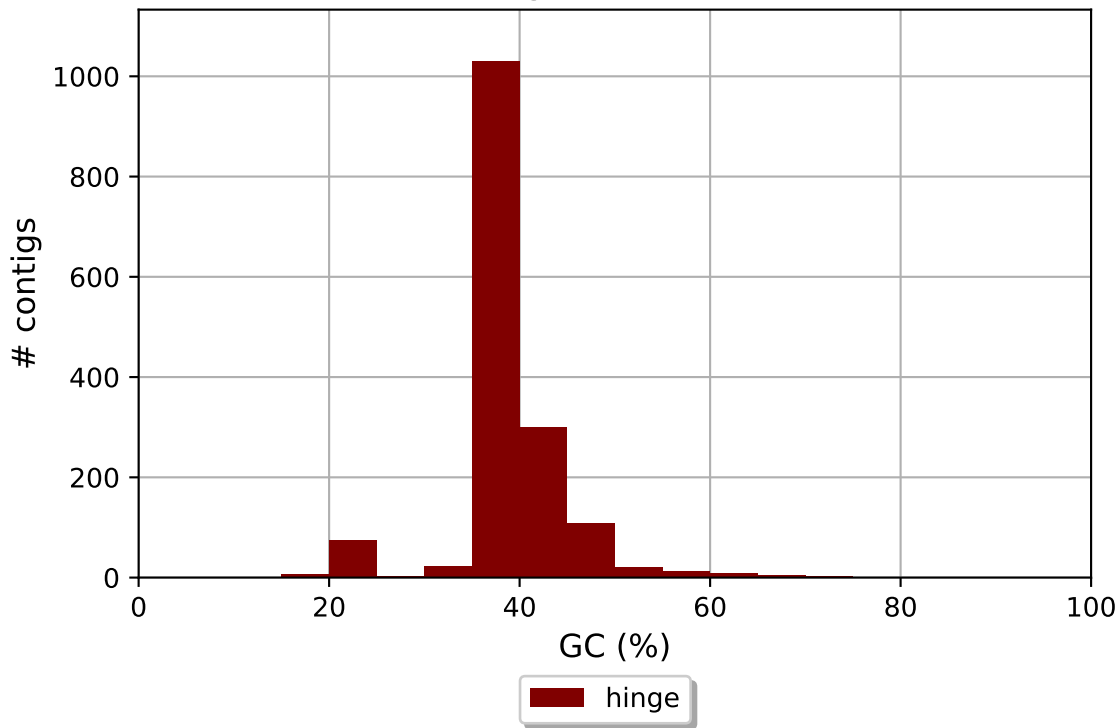
flye GC content



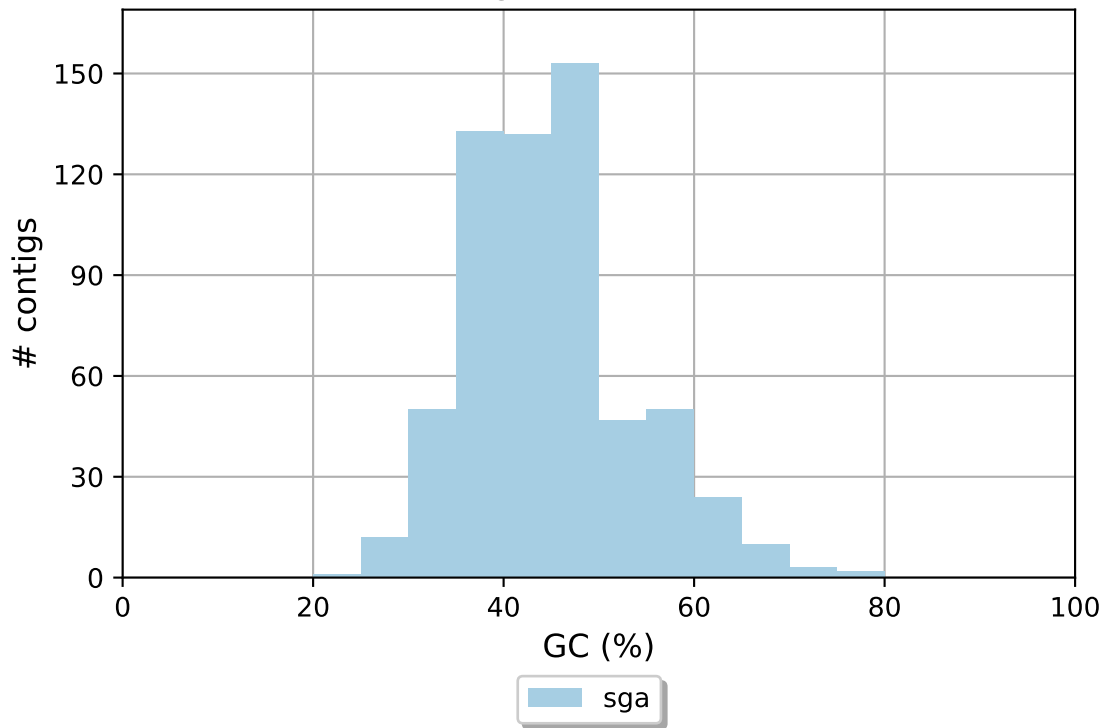
hifiasm GC content



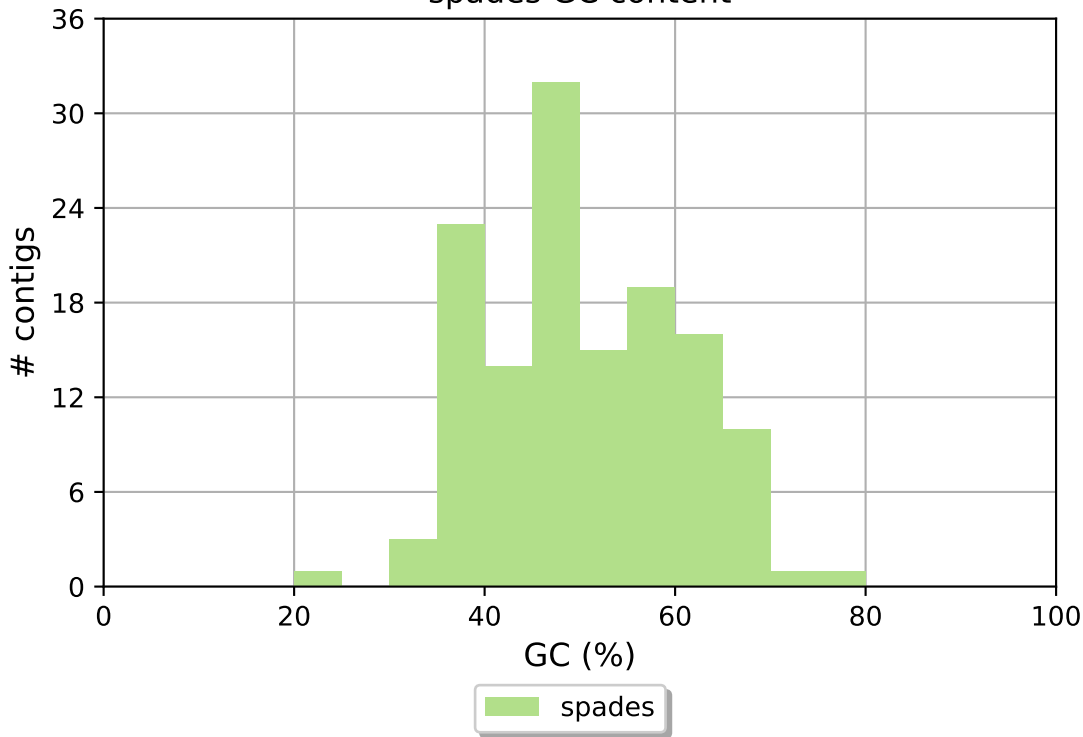
hinge GC content



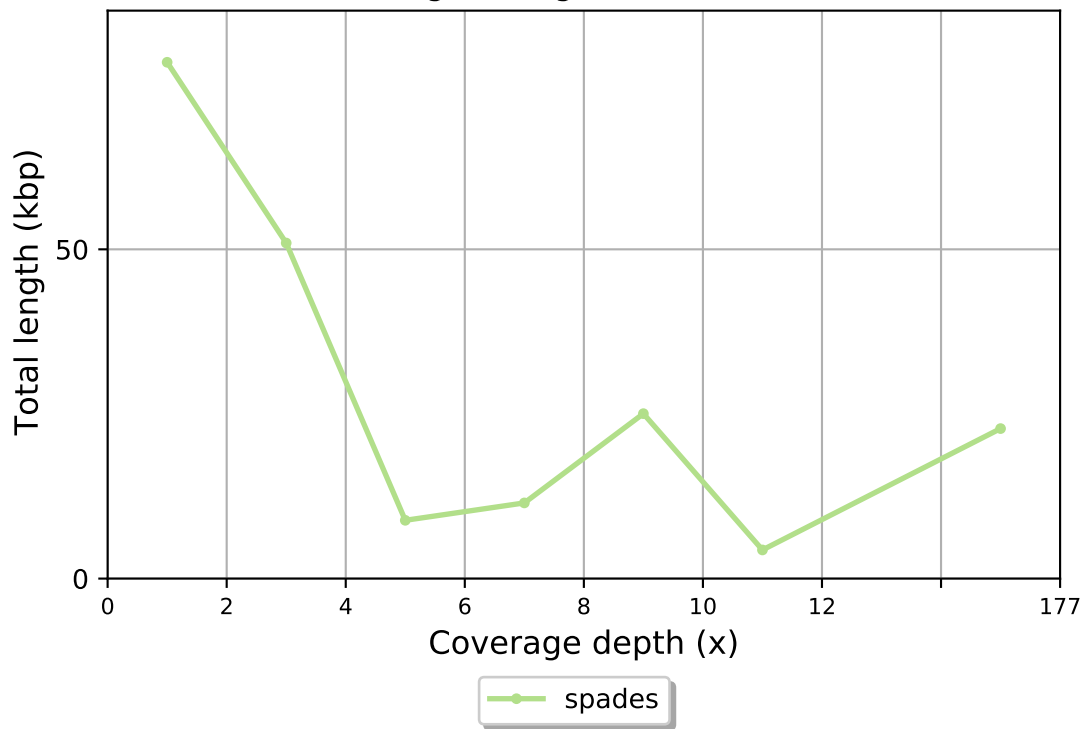
sga GC content



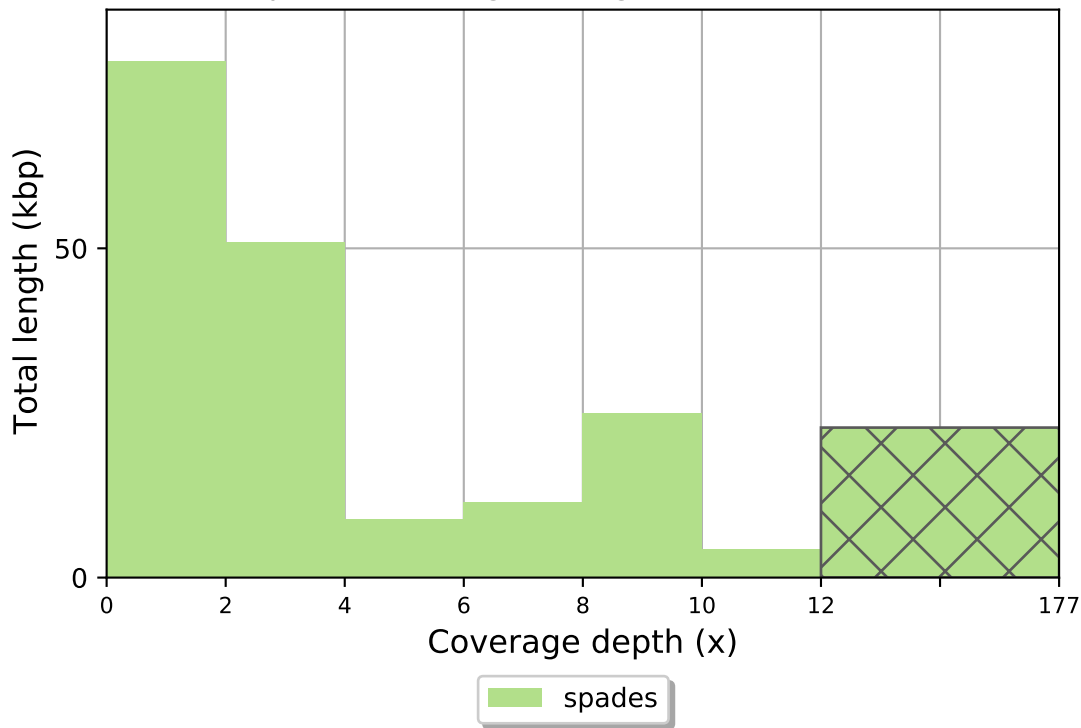
spades GC content



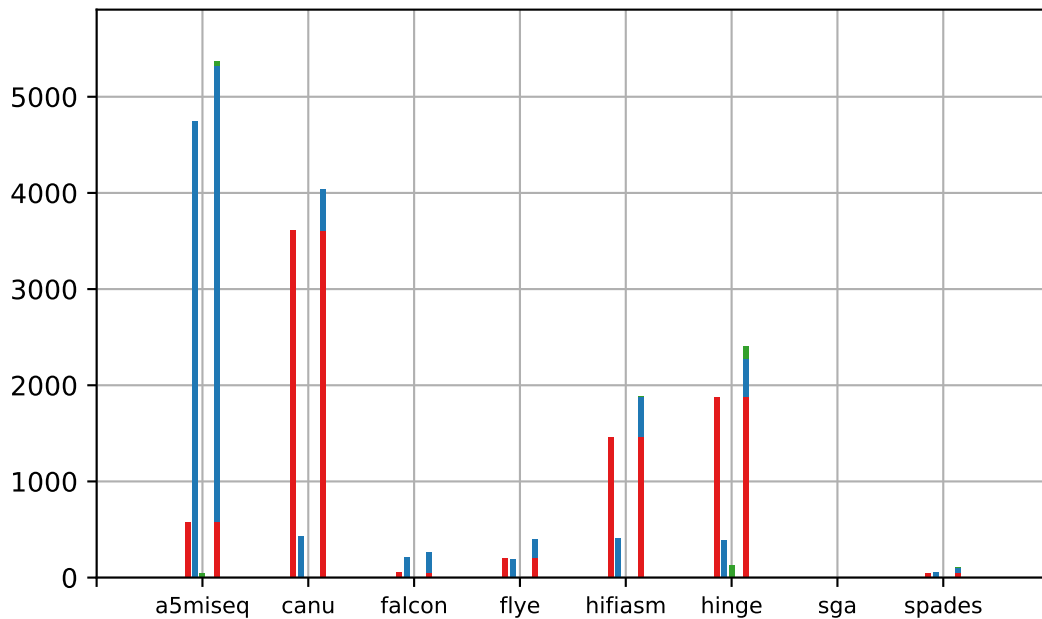
Coverage histogram (bin size: 2x)



spades coverage histogram (bin size: 2x)

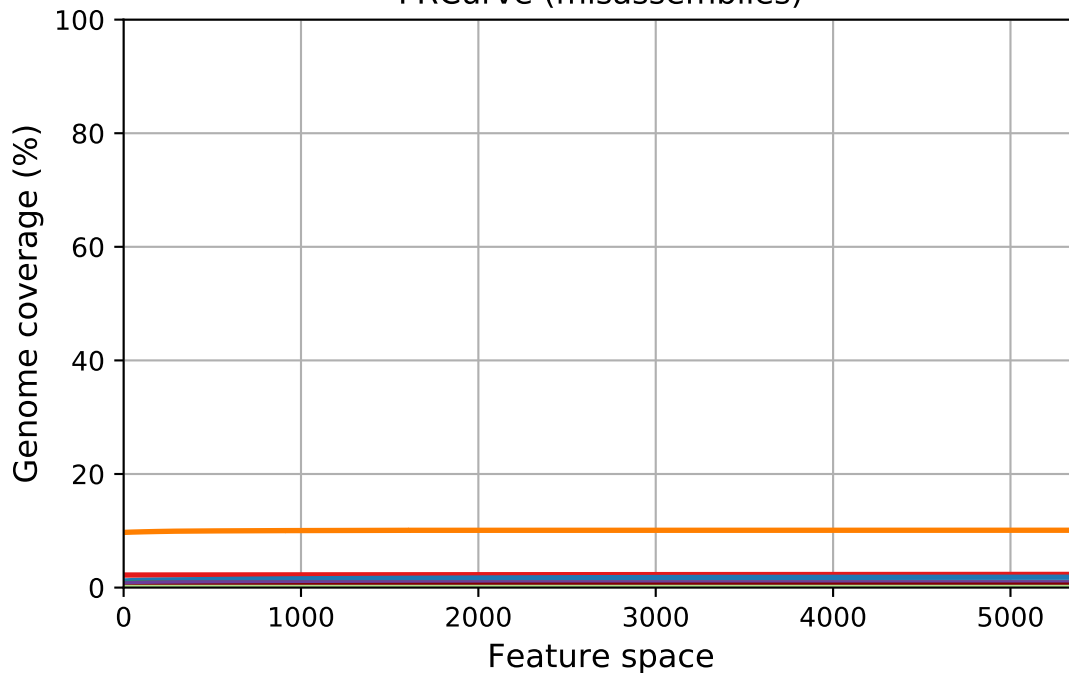


Misassemblies

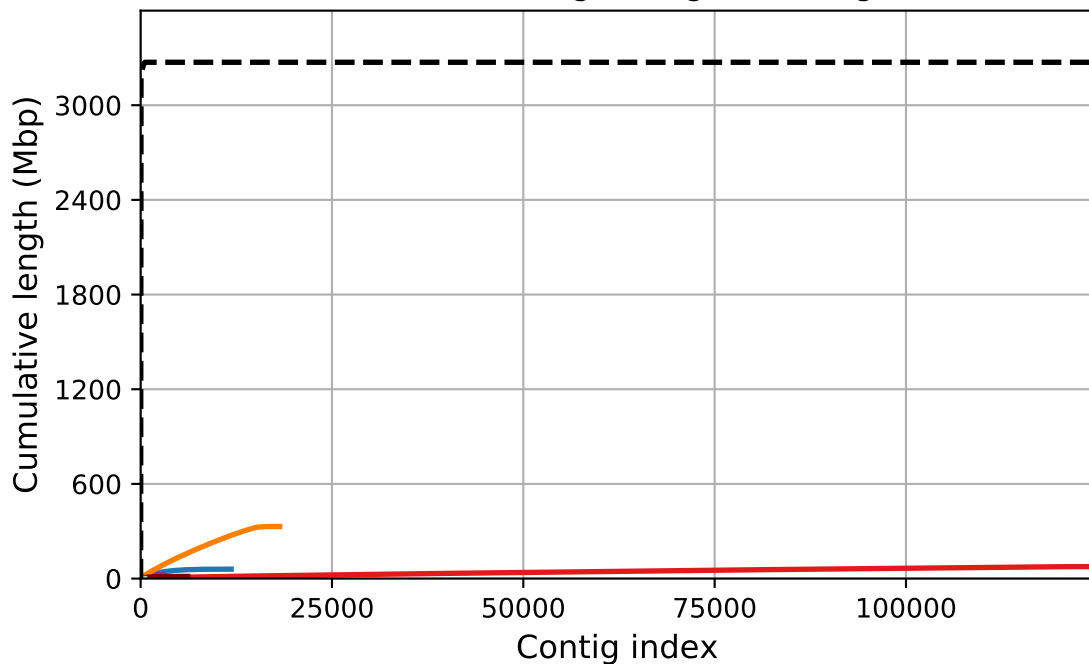


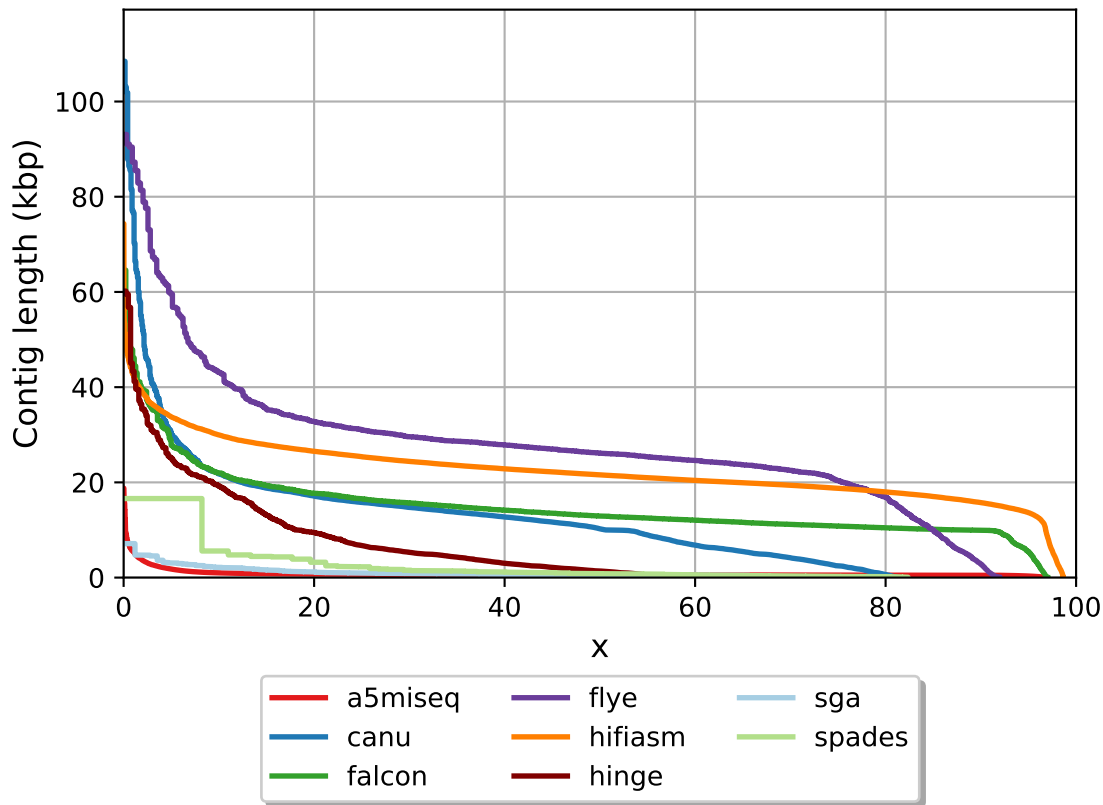
■ # relocations ■ # translocations ■ # inversions

FRCurve (misassemblies)

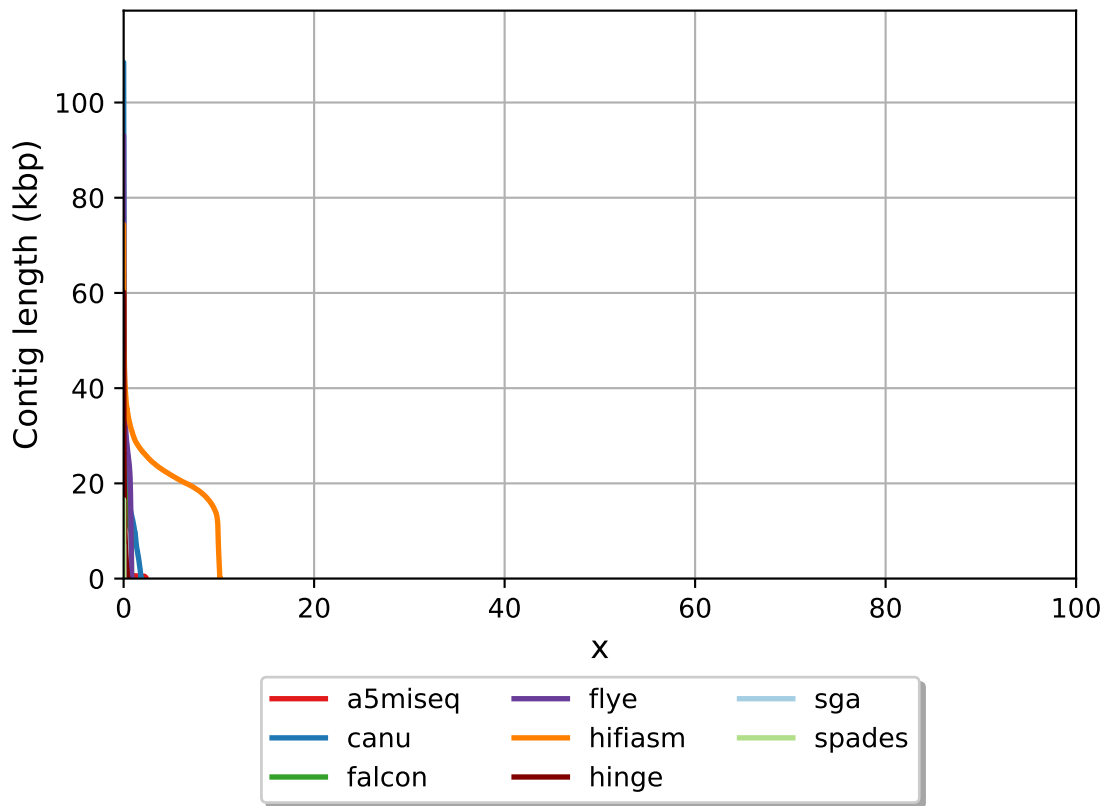


Cumulative length (aligned contigs)



Na^x 

NGAx



Genome fraction, %

