

## Report

	nextDenovo.asm	Canu.asm	Falcon.asm	Flye.asm	Shasta.asm	Mecat.asm	Wtdbg.asm
# contigs (>= 0 bp)	88	2287	172	1348	1980	1243	756
# contigs (>= 1000 bp)	88	2287	171	1219	1581	1243	749
# contigs (>= 5000 bp)	88	2074	171	1023	1420	1243	627
# contigs (>= 10000 bp)	88	1981	171	817	1316	1243	422
# contigs (>= 25000 bp)	88	1838	155	670	890	1241	199
# contigs (>= 50000 bp)	87	1100	108	529	474	927	124
Total length (>= 0 bp)	126263508	229353659	140024976	131856505	143480908	202215921	132982734
Total length (>= 1000 bp)	126263508	229353659	140024465	131767988	143349001	202215921	132978236
Total length (>= 5000 bp)	126263508	228926528	140024465	131251488	142958226	202215921	132582179
Total length (>= 10000 bp)	126263508	228255080	140024465	129826462	142170312	202215921	131102740
Total length (>= 25000 bp)	126263508	225723008	139667800	127390413	134609583	202169766	127473488
Total length (>= 50000 bp)	126236942	196478528	138078710	122294258	119916278	188394579	124987927
# contigs	88	2107	171	1097	1468	1243	703
Largest contig	13144176	3980575	13319401	4836132	4378421	12631656	14128365
Total length	126263508	229056851	140024465	131553479	143148140	202215921	132890796
Reference length	119667750	119667750	119667750	119667750	119667750	119667750	119667750
GC (%)	36.72	37.12	36.67	36.09	37.18	35.95	38.16
Reference GC (%)	36.06	36.06	36.06	36.06	36.06	36.06	36.06
N50	8798661	231924	7960654	325940	357597	688687	5479602
NG50	8798661	873036	7979657	370306	560105	3525236	8707235
N75	2323231	69274	1507122	137772	93305	85155	1095469
NG75	3588034	460325	4810976	180227	185928	1096121	2182254
L50	6	161	7	88	77	34	7
LG50	6	40	6	71	50	8	6
L75	13	680	16	247	283	348	19
LG75	11	86	10	190	149	22	13
# misassemblies	1314	2314	1607	1570	1631	1783	1529
# misassembled contigs	63	383	89	362	357	250	156
Misassembled contigs length	121733667	93071570	118843437	60336085	48852060	128891514	118918494
# local misassemblies	1128	2571	1437	1189	1077	2196	1086
# scaffold gap ext. mis.	0	0	0	0	0	0	0
# scaffold gap loc. mis.	0	0	0	0	0	0	0
# possible TEs	398	764	464	422	432	698	568
# unaligned mis. contigs	0	8	0	39	79	0	25
# unaligned contigs	13 + 57 part	278 + 511 part	48 + 63 part	27 + 494 part	81 + 528 part	1 + 355 part	253 + 256 part
Unaligned length	5577991	13404835	6336453	4365056	11810280	5760459	12620722
Genome fraction (%)	96.006	99.528	96.938	96.517	97.774	98.166	93.695
Duplication ratio	1.052	1.813	1.154	1.103	1.124	1.675	1.074
# N's per 100 kbp	0.00	0.00	0.00	0.00	0.00	0.00	0.00
# mismatches per 100 kbp	668.46	1299.53	822.92	753.04	763.33	1052.95	722.82
# indels per 100 kbp	193.40	281.21	127.09	212.74	727.64	338.60	303.37
Largest alignment	5887963	3963652	10477942	4820655	3059195	5451806	7529822
Total aligned length	120235666	214635623	133317043	126764931	131090282	196116682	120017897
NA50	1136416	115341	1459104	280334	255952	202014	756810
NGA50	1504454	539509	1909294	328298	384761	901832	945708
NA75	354228	48301	270481	93990	41634	62905	192079
NGA75	472949	246039	676191	128725	118594	339389	316618
LA50	24	288	22	102	96	123	35
LGA50	21	60	15	82	60	27	27
LA75	73	1116	81	310	463	649	122
LGA75	61	140	41	230	202	80	82

All statistics are based on contigs of size >= 3000 bp, unless otherwise noted (e.g., "# contigs (>= 0 bp)" and "Total length (>= 0 bp)" include all contigs).

## Misassemblies report

	nextDenovo.asm	Canu.asm	Falcon.asm	Flye.asm	Shasta.asm	Mecat.asm	Wtdbg.asm
# misassemblies	1314	2314	1607	1570	1631	1783	1529
# contig misassemblies	1314	2314	1607	1570	1631	1783	1529
# c. relocations	455	894	599	487	504	665	503
# c. translocations	841	1387	991	1067	1109	1096	996
# c. inversions	18	33	17	16	18	22	30
# scaffold misassemblies	0	0	0	0	0	0	0
# s. relocations	0	0	0	0	0	0	0
# s. translocations	0	0	0	0	0	0	0
# s. inversions	0	0	0	0	0	0	0
# misassembled contigs	63	383	89	362	357	250	156
Misassembled contigs length	121733667	93071570	118843437	60336085	48852060	128891514	118918494
# local misassemblies	1128	2571	1437	1189	1077	2196	1086
# scaffold gap ext. mis.	0	0	0	0	0	0	0
# scaffold gap loc. mis.	0	0	0	0	0	0	0
# possible TEs	398	764	464	422	432	698	568
# unaligned mis. contigs	0	8	0	39	79	0	25
# mismatches	766783	1545365	953135	868404	891733	1235015	809191
# indels	221849	334413	147194	245331	850040	397142	339617
# indels (<= 5 bp)	193600	282821	116926	209979	774051	348909	312065
# indels (> 5 bp)	28249	51592	30268	35352	75989	48233	27552
Indels length	3212953	5807670	3336031	3271840	4773675	5585981	3419592

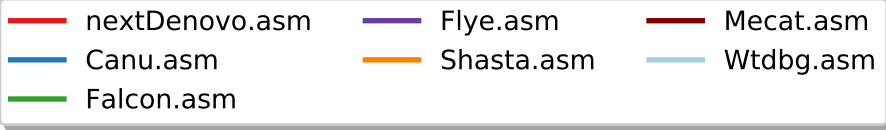
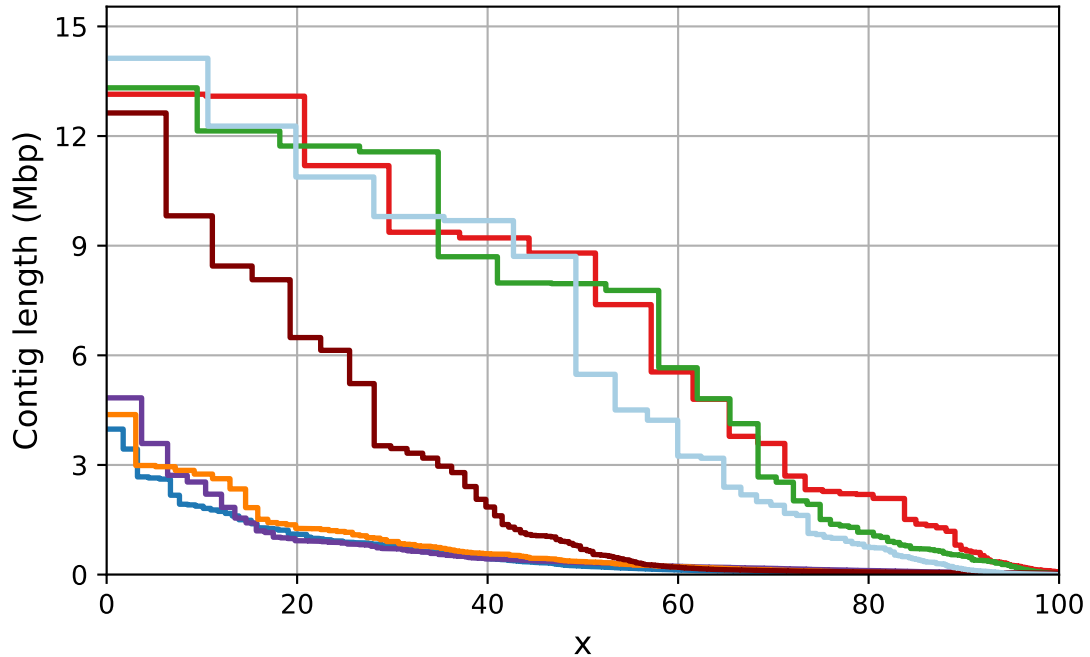
All statistics are based on contigs of size  $\geq 3000$  bp, unless otherwise noted (e.g., "# contigs ( $\geq 0$  bp)" and "Total length ( $\geq 0$  bp)" include all contigs).

## Unaligned report

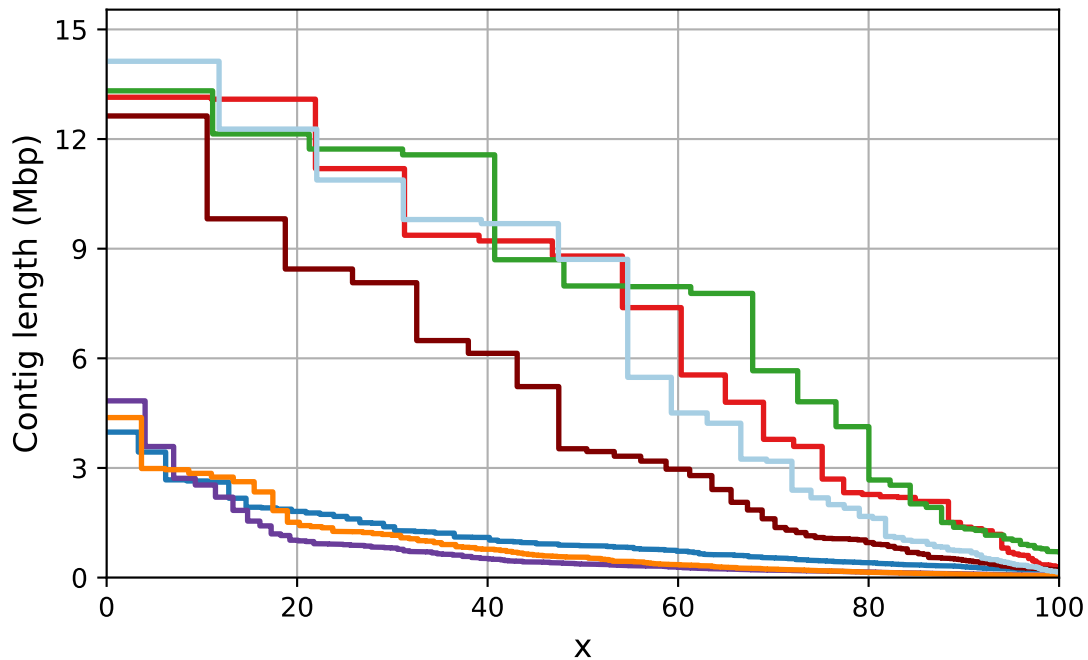
	nextDenovo.asm	Canu.asm	Falcon.asm	Flye.asm	Shasta.asm	Mecat.asm	Wtdbg.asm
# fully unaligned contigs	13	278	48	27	81	1	253
Fully unaligned length	2032112	6905284	2210296	243365	5732184	37796	8224468
# partially unaligned contigs	57	511	63	494	528	355	256
Partially unaligned length	3545879	6499551	4126157	4121691	6078096	5722663	4396254
# N's	0	0	0	0	0	0	0

All statistics are based on contigs of size  $\geq 3000$  bp, unless otherwise noted (e.g., "# contigs ( $\geq 0$  bp)" and "Total length ( $\geq 0$  bp)" include all contigs).

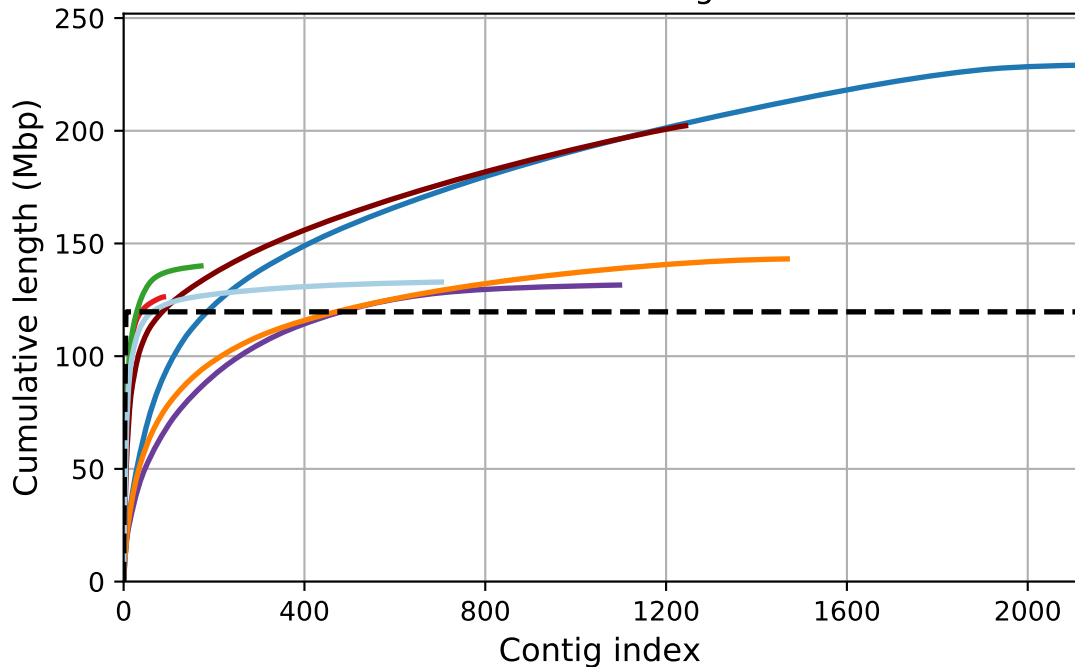
Nx



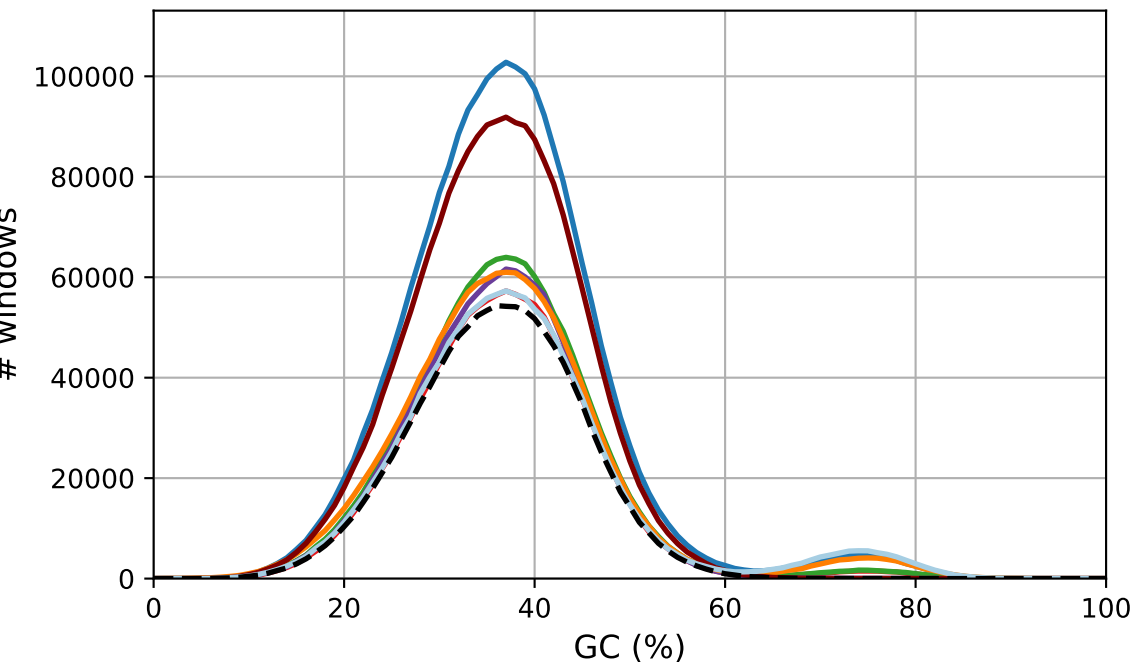
# NGx



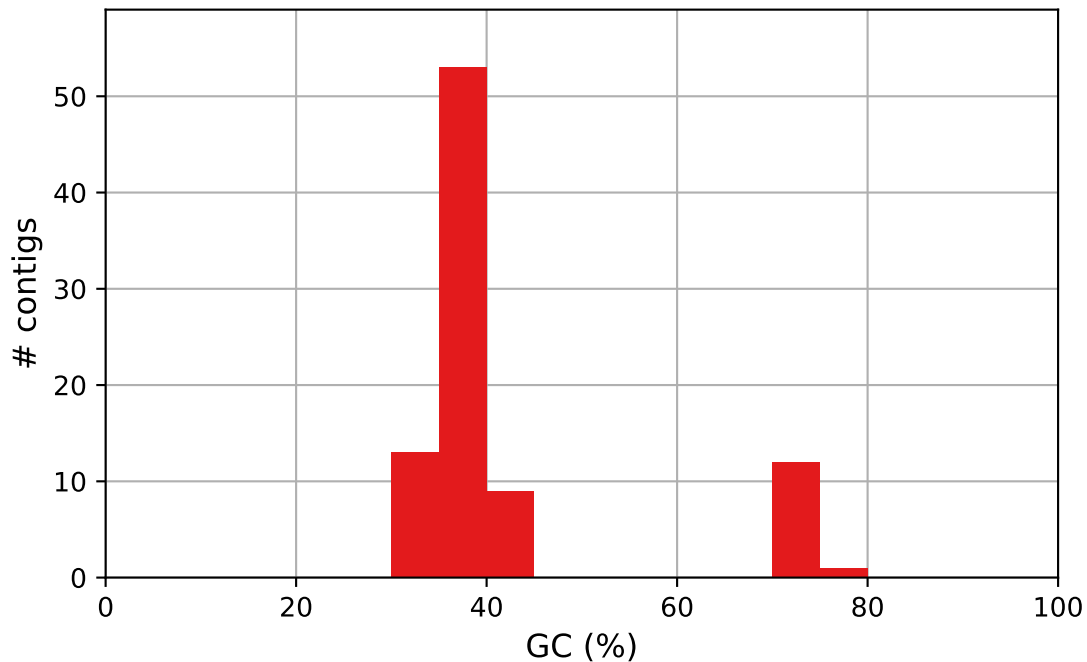
### Cumulative length



# GC content



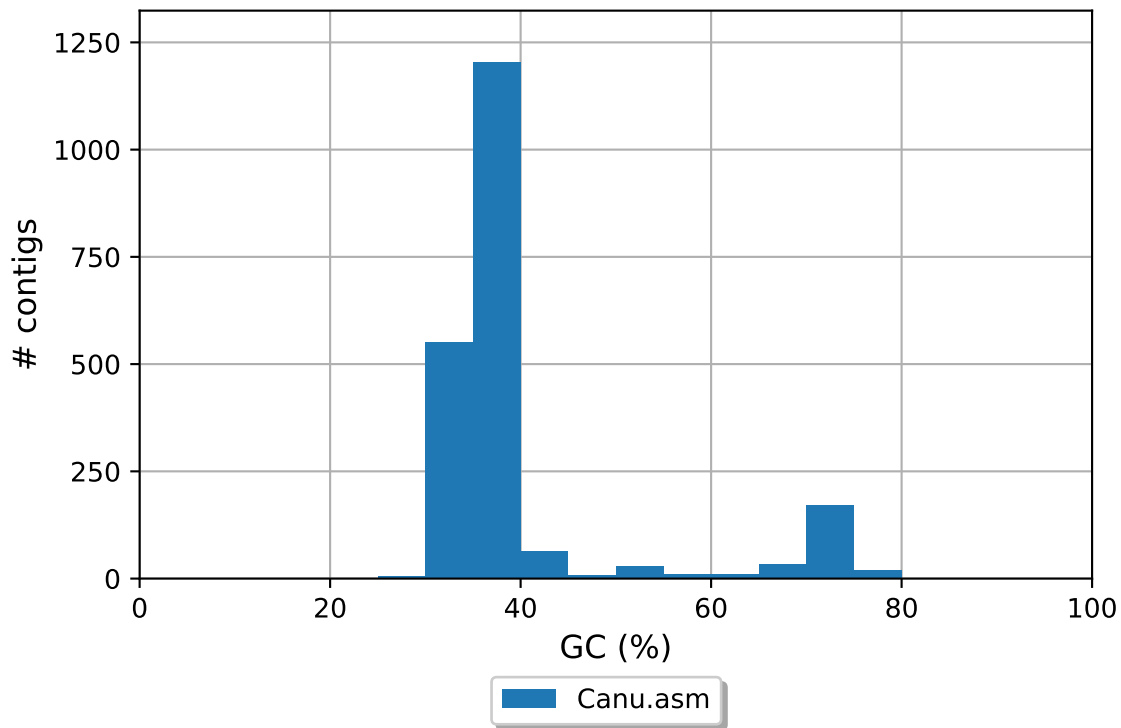
nextDenovo.asm GC content



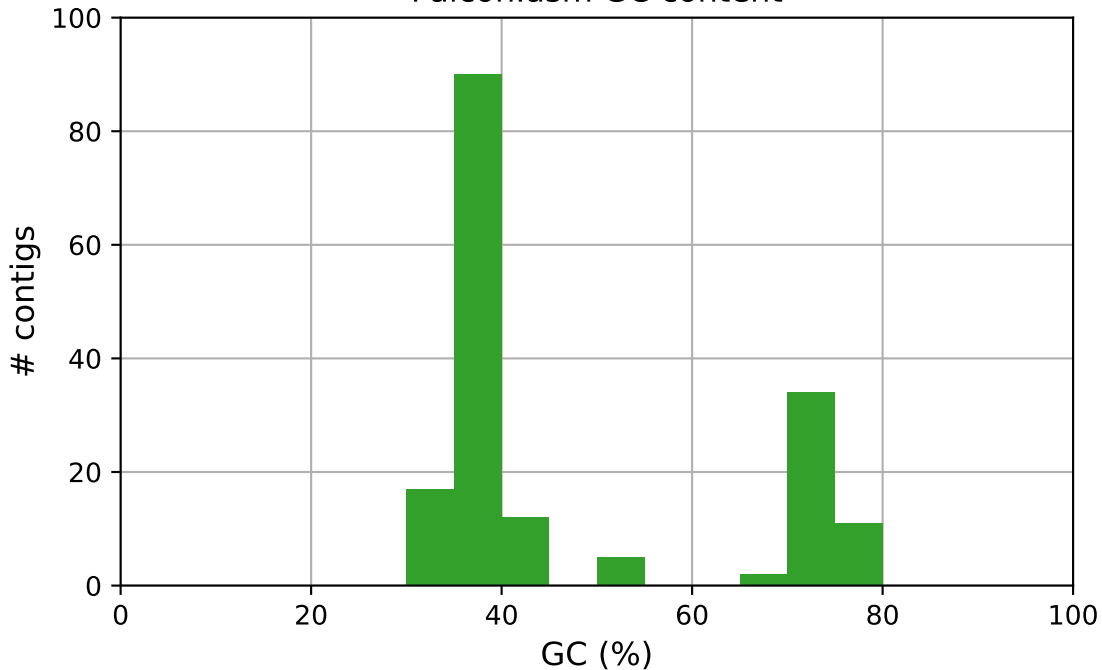
nextDenovo.asm



Canu.asm GC content

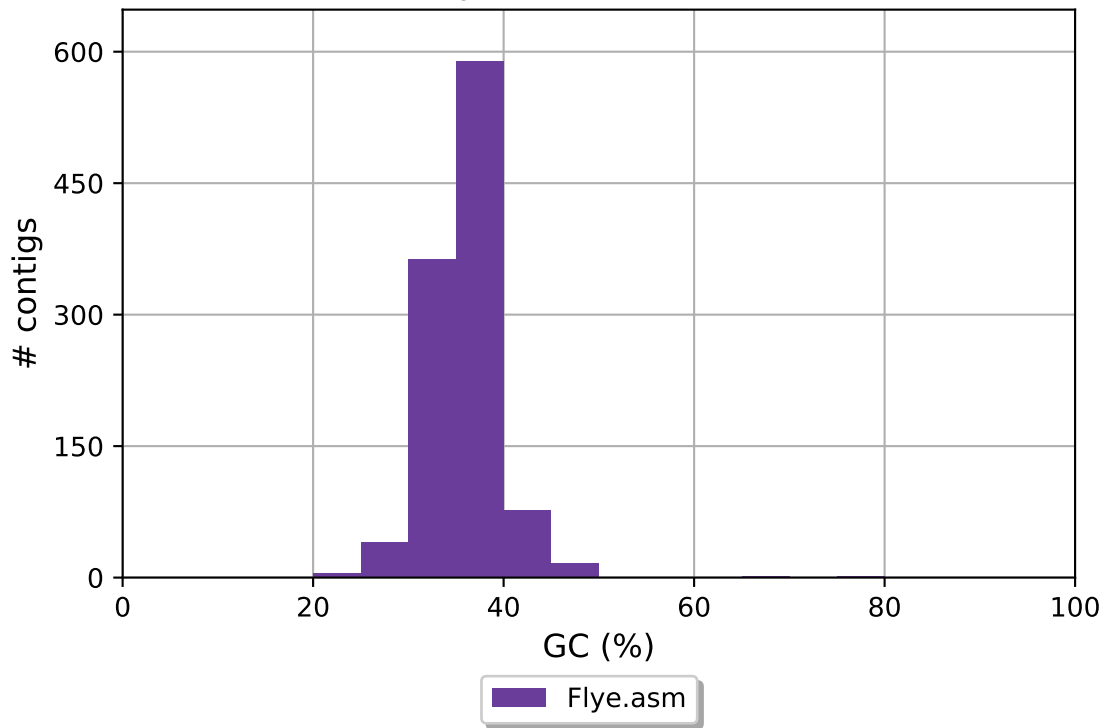


Falcon.asm GC content

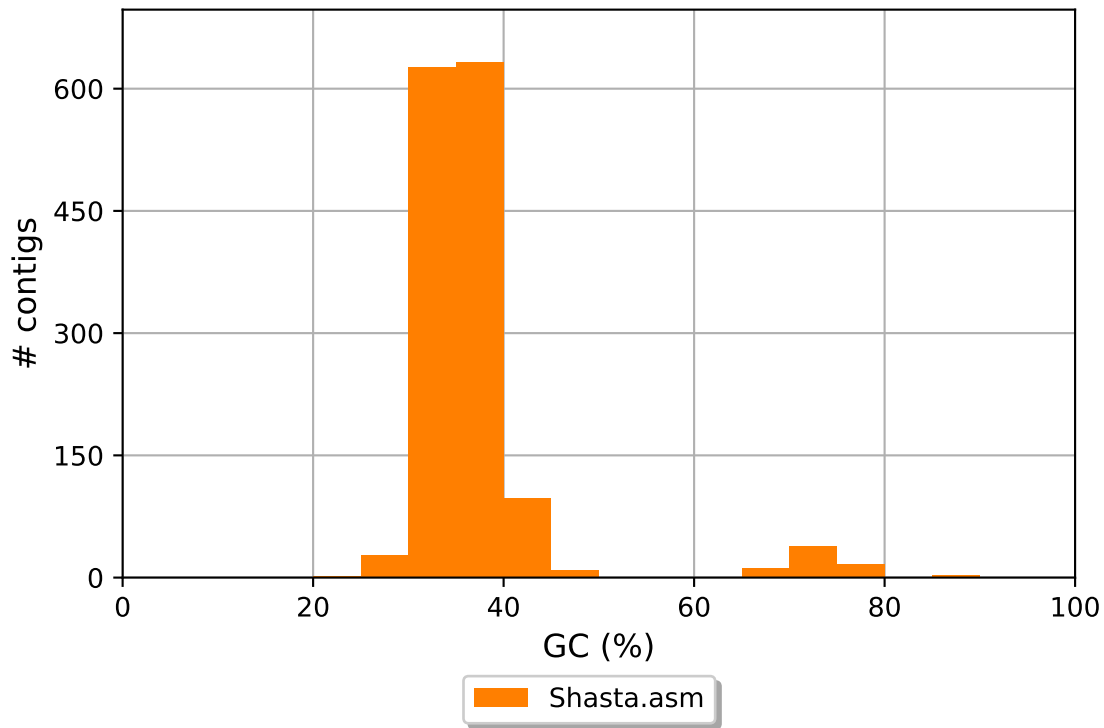


Falcon.asm

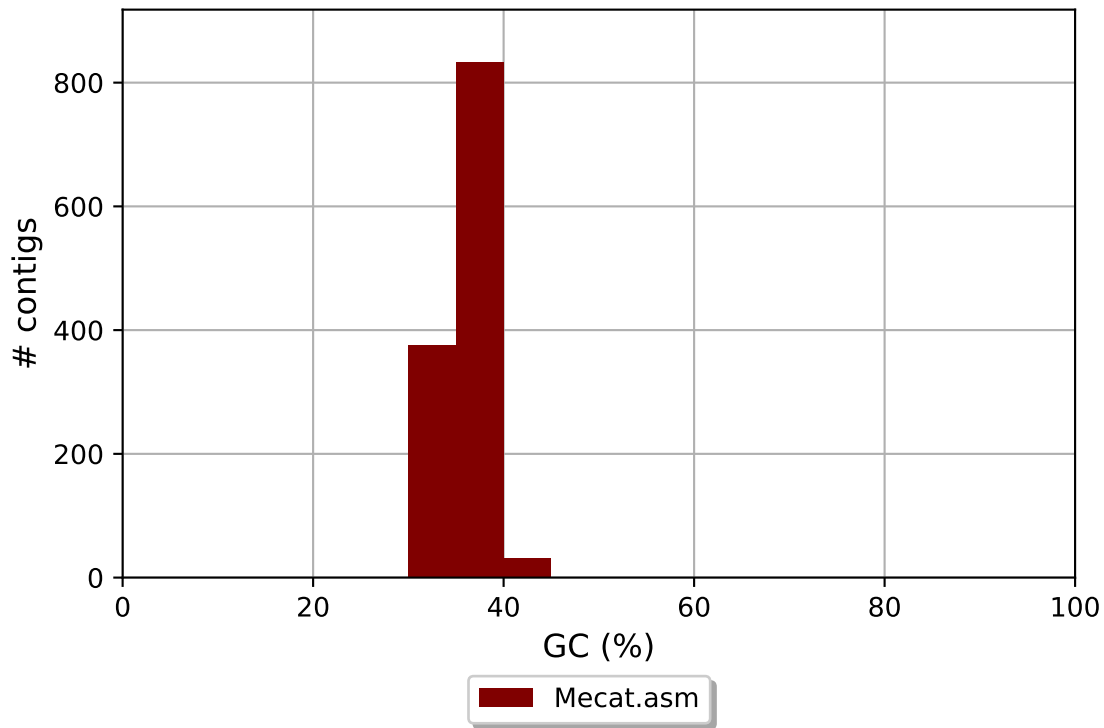
# Flye.asm GC content



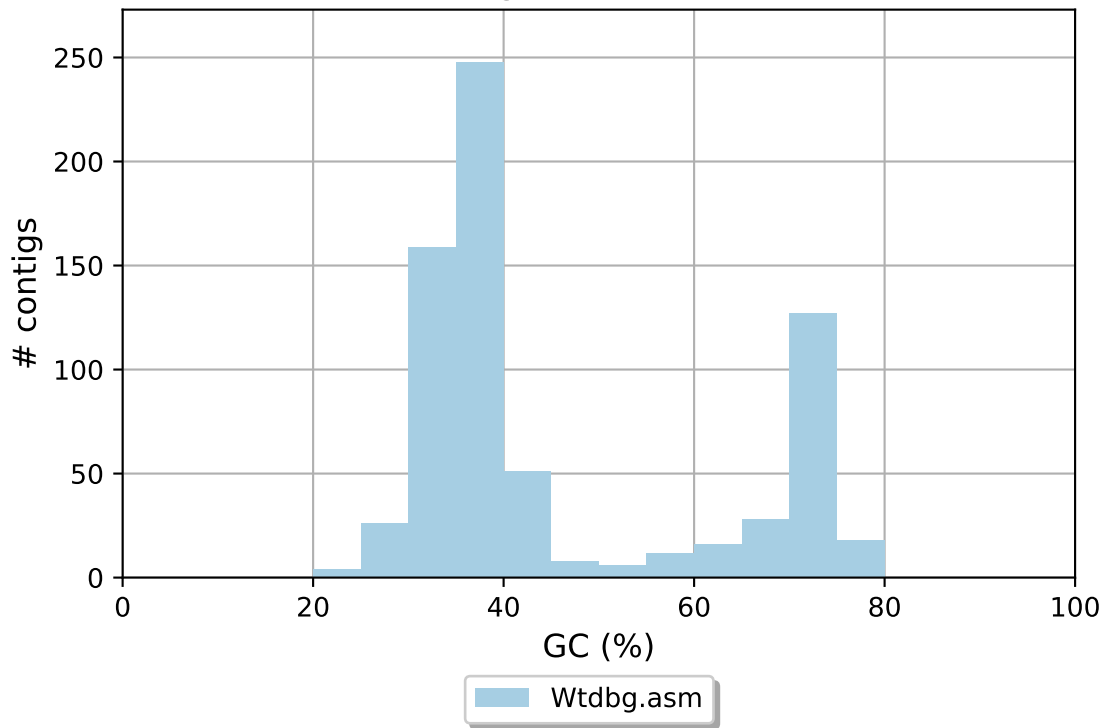
Shasta.asm GC content



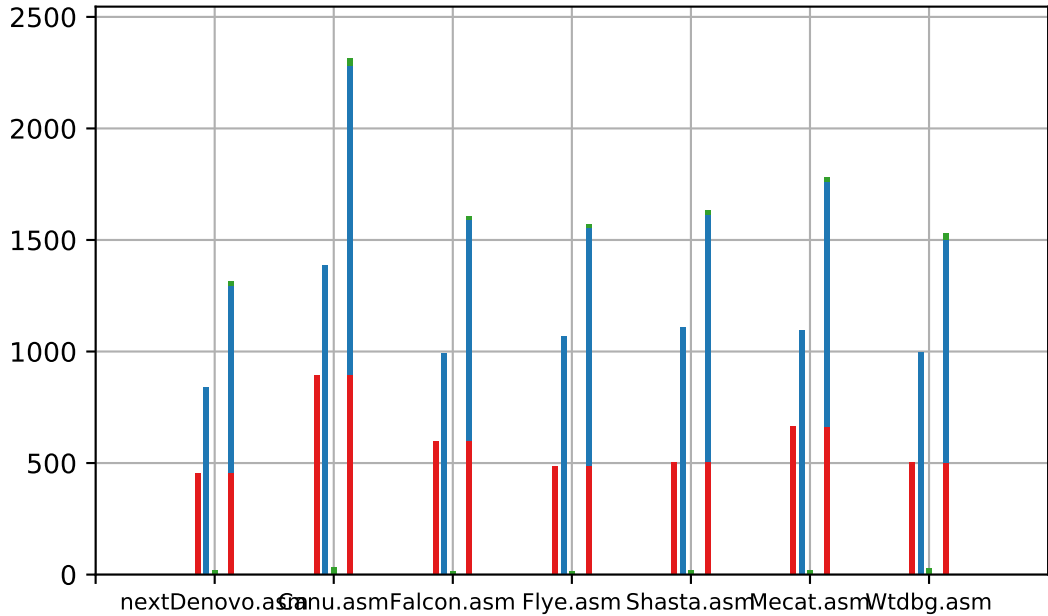
Mecat.asm GC content



Wtdbg.asm GC content



# Misassemblies



# relocations

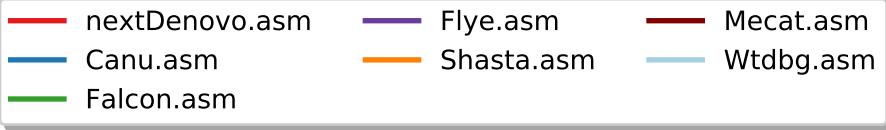
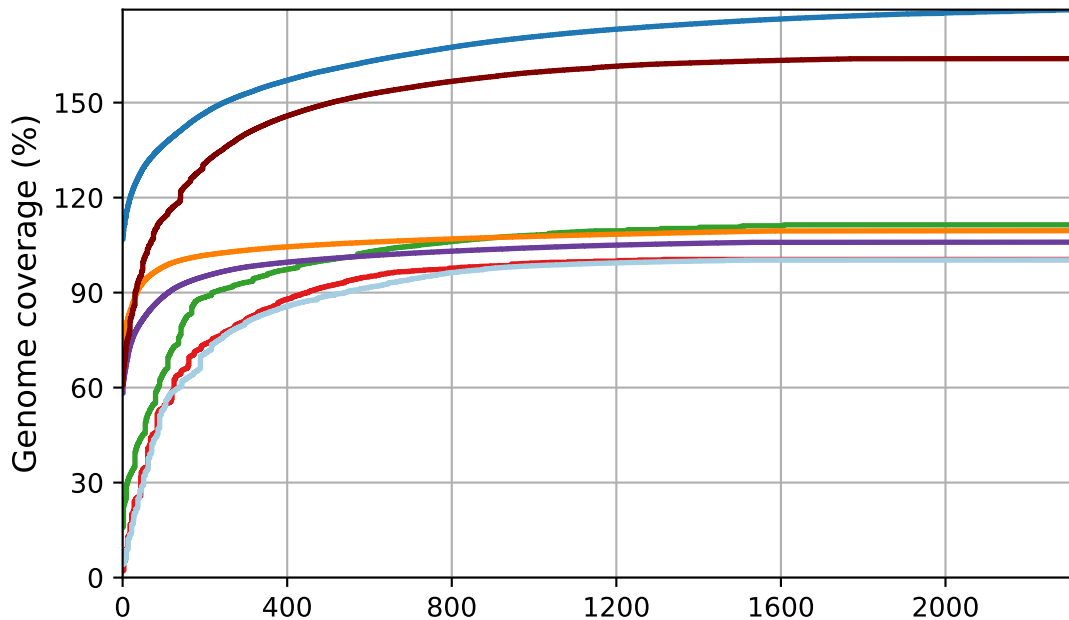


# translocations



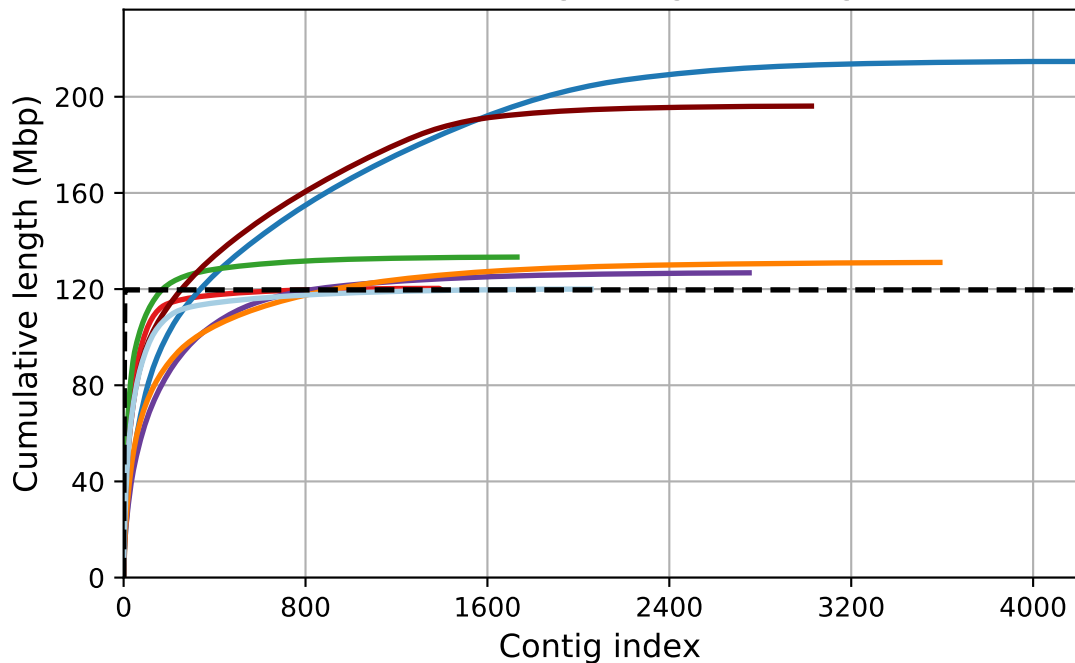
# inversions

FRCurve (misassemblies)

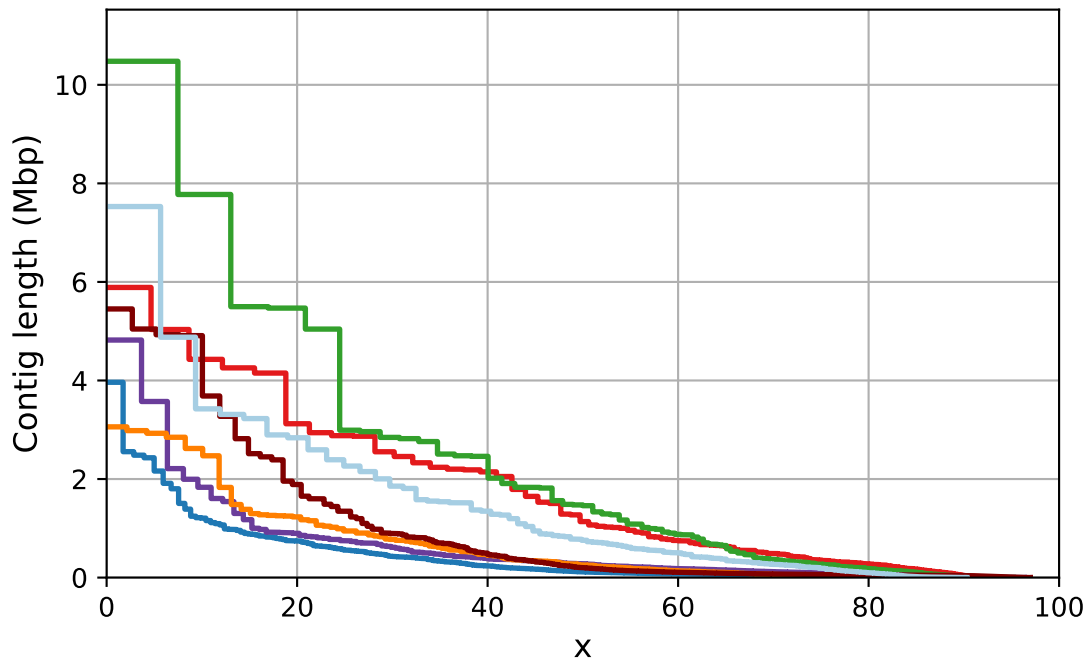




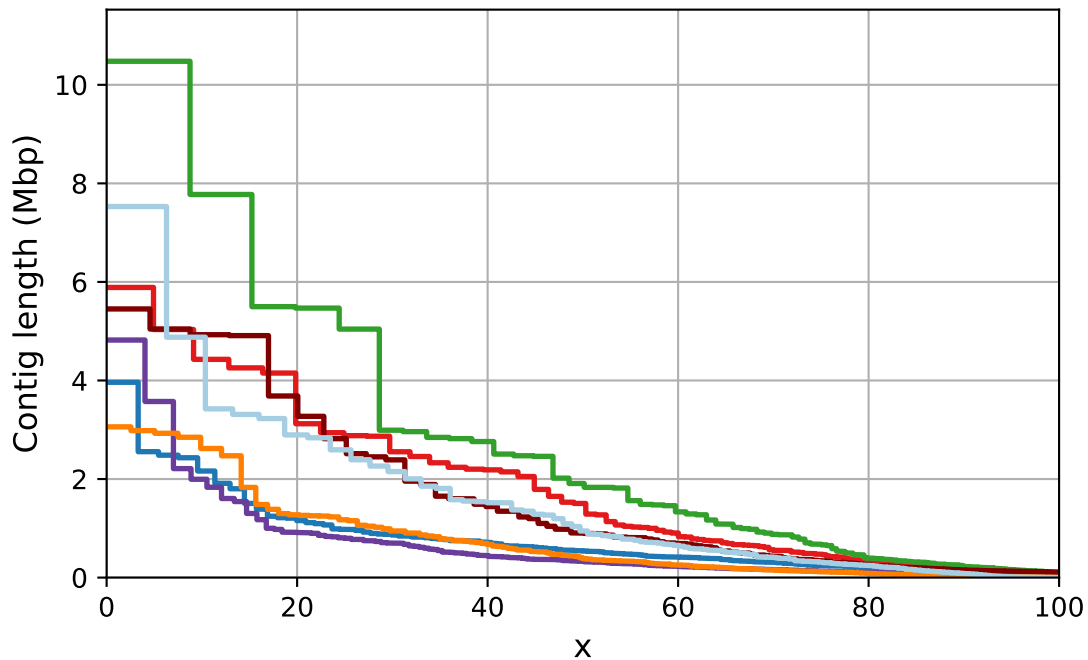
Cumulative length (aligned contigs)



# NAX



# NGAx



Genome fraction, %

