

Report

	nextDenovo.asm	Canu.asm	Flye.asm	Shasta.asm	Wtdbg.asm
# contigs (>= 0 bp)	73	440	588	1555	632
# contigs (>= 1000 bp)	73	440	538	1186	614
# contigs (>= 5000 bp)	73	410	386	708	413
# contigs (>= 10000 bp)	73	376	307	545	297
# contigs (>= 25000 bp)	71	274	194	440	156
# contigs (>= 50000 bp)	68	175	123	360	95
Total length (>= 0 bp)	133330776	140572619	136061039	129969228	133160133
Total length (>= 1000 bp)	133330776	140572619	136026028	129822332	133147770
Total length (>= 5000 bp)	133330776	140485537	135576334	128592184	132543269
Total length (>= 10000 bp)	133330776	140220367	135002183	127481261	131693991
Total length (>= 25000 bp)	133291619	138476194	133224955	125857771	129510368
Total length (>= 50000 bp)	133166315	135006727	130706561	123007868	127392316
# contigs	73	424	461	872	510
Largest contig	25701192	14715425	12613153	1801407	23221757
Total length	133330776	140540470	135880693	129225244	132926651
Reference length	143726002	143726002	143726002	143726002	143726002
GC (%)	42.11	41.91	41.61	41.77	41.88
Reference GC (%)	42.01	42.01	42.01	42.01	42.01
N50	21195733	4298595	6016667	535885	12028162
NG50	18110856	4298595	6016667	440773	10631323
N75	13648743	777595	2182645	244480	3308195
NG75	3925274	714013	1367004	182722	1752322
L50	3	11	9	77	4
LG50	4	11	9	92	5
L75	5	33	17	167	9
LG75	7	36	20	218	13
# misassemblies	345	971	724	262	616
# misassembled contigs	48	226	217	78	191
Misassembled contigs length	96222572	64959149	73882780	8905149	110397929
# local misassemblies	137	433	670	123	185
# scaffold gap ext. mis.	0	0	0	0	0
# scaffold gap loc. mis.	0	0	0	0	0
# possible TEs	54	114	74	28	52
# unaligned mis. contigs	1	3	5	7	36
# unaligned contigs	1 + 36 part	8 + 122 part	11 + 118 part	191 + 76 part	89 + 291 part
Unaligned length	603053	769264	811595	1660668	2264882
Genome fraction (%)	92.109	93.614	91.799	88.085	91.504
Duplication ratio	1.011	1.047	1.032	1.016	1.002
# N's per 100 kbp	0.00	0.00	0.00	0.00	0.00
# mismatches per 100 kbp	90.86	183.12	220.48	609.69	179.86
# indels per 100 kbp	567.78	831.54	1334.52	1428.10	1081.15
Largest alignment	25696021	11699048	11981267	1799773	18844039
Total aligned length	132416893	139189216	134650393	127438699	130313270
NA50	6618721	3863099	5596752	527231	4309906
NGA50	6618721	3863099	5143715	434179	4174617
NA75	3269191	670044	1955654	230034	1573933
NGA75	2125978	611559	1267543	168924	928918
LA50	5	13	10	78	9
LGA50	5	13	11	94	10
LA75	11	38	20	172	20
LGA75	14	42	24	227	27

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	Flye.asm	Shasta.asm	Wtdbg.asm
# misassemblies	345	971	724	262	616
# contig misassemblies	345	971	724	262	616
# c. relocations	105	268	90	78	166
# c. translocations	234	702	632	182	449
# c. inversions	6	1	2	2	1
# scaffold misassemblies	0	0	0	0	0
# s. relocations	0	0	0	0	0
# s. translocations	0	0	0	0	0
# s. inversions	0	0	0	0	0
# misassembled contigs	48	226	217	78	191
Misassembled contigs length	96222572	64959149	73882780	8905149	110397929
# local misassemblies	137	433	670	123	185
# scaffold gap ext. mis.	0	0	0	0	0
# scaffold gap loc. mis.	0	0	0	0	0
# possible TEs	54	114	74	28	52
# unaligned mis. contigs	1	3	5	7	36
# mismatches	119317	244414	288562	765678	234645
# indels	745624	1109838	1746624	1793480	1410458
# indels (<= 5 bp)	740230	1095570	1688738	1751703	1404457
# indels (> 5 bp)	5394	14268	57886	41777	6001
Indels length	1325149	2065247	2975432	3366619	2082794

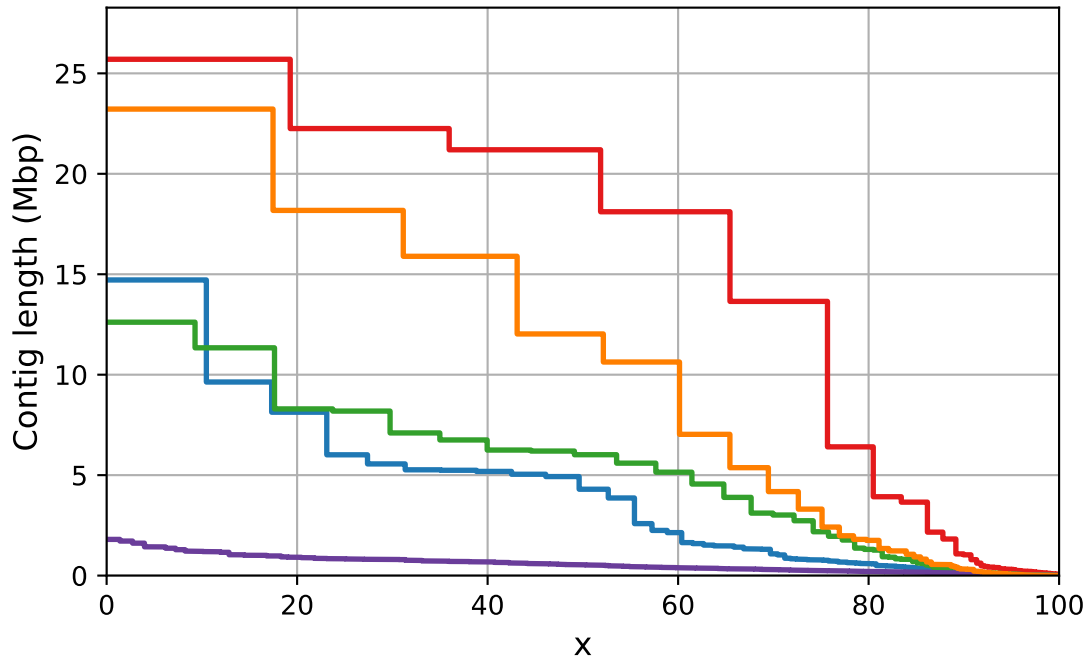
All statistics are based on contigs of size ≥ 3000 bp, unless otherwise noted (e.g., "# contigs (≥ 0 bp)" and "Total length (≥ 0 bp)" include all contigs).

Unaligned report

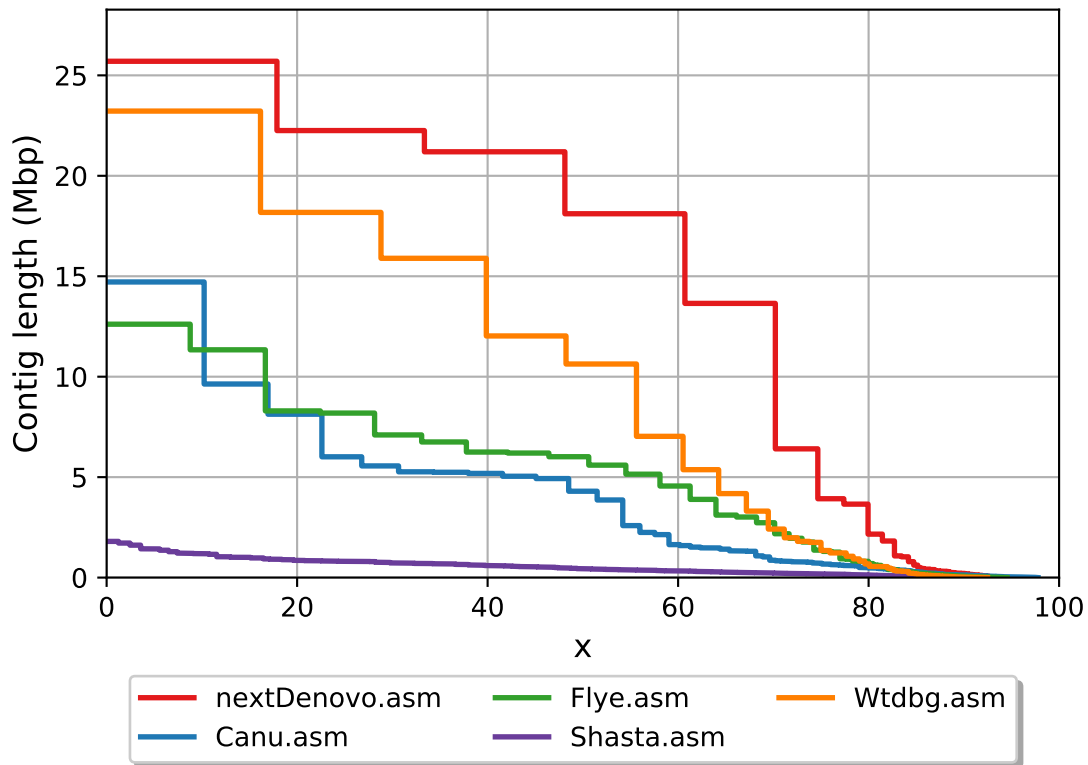
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# fully unaligned contigs	1	8	11	191	89
Fully unaligned length	18454	74442	135386	1126625	586727
# partially unaligned contigs	36	122	118	76	291
Partially unaligned length	584599	694822	676209	534043	1678155
# N's	0	0	0	0	0

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).

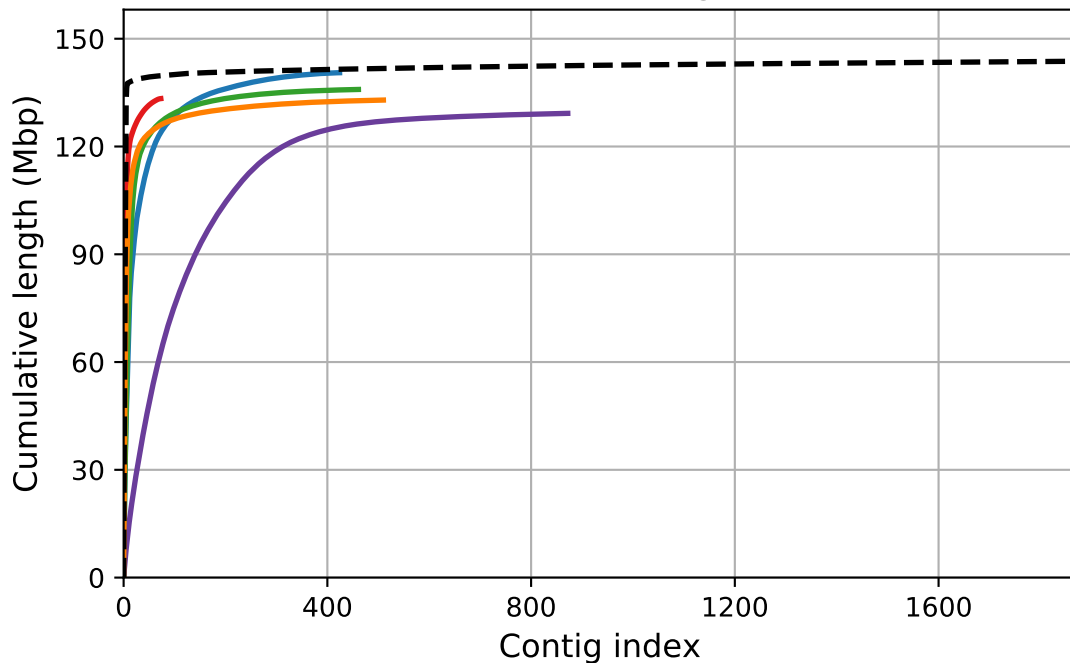
Nx



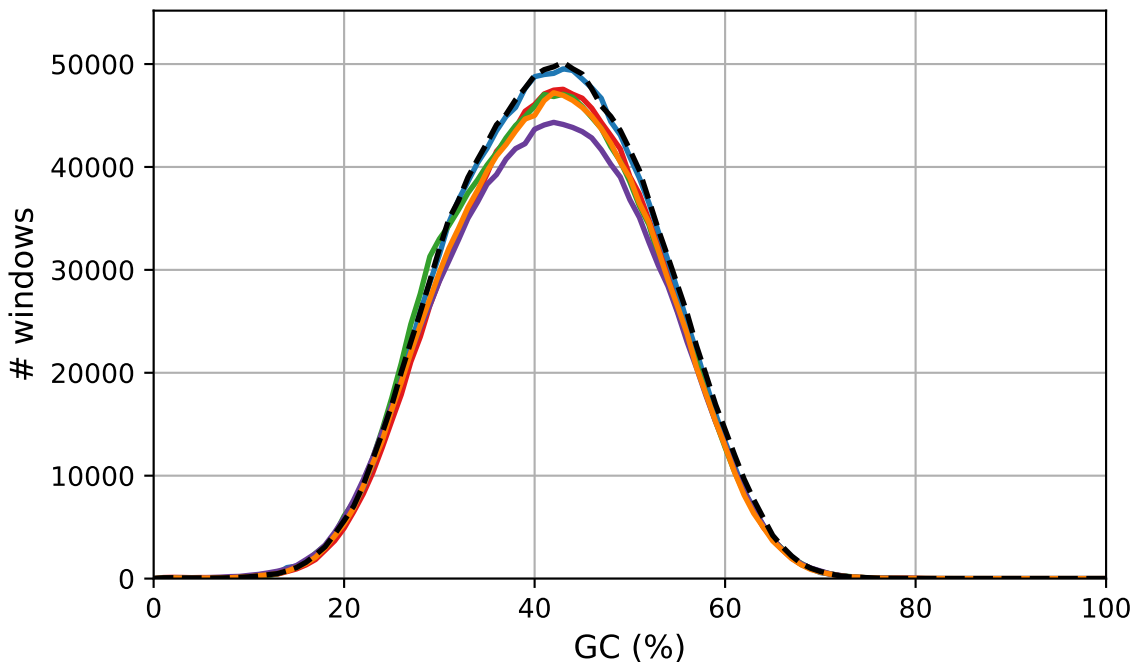
NGx



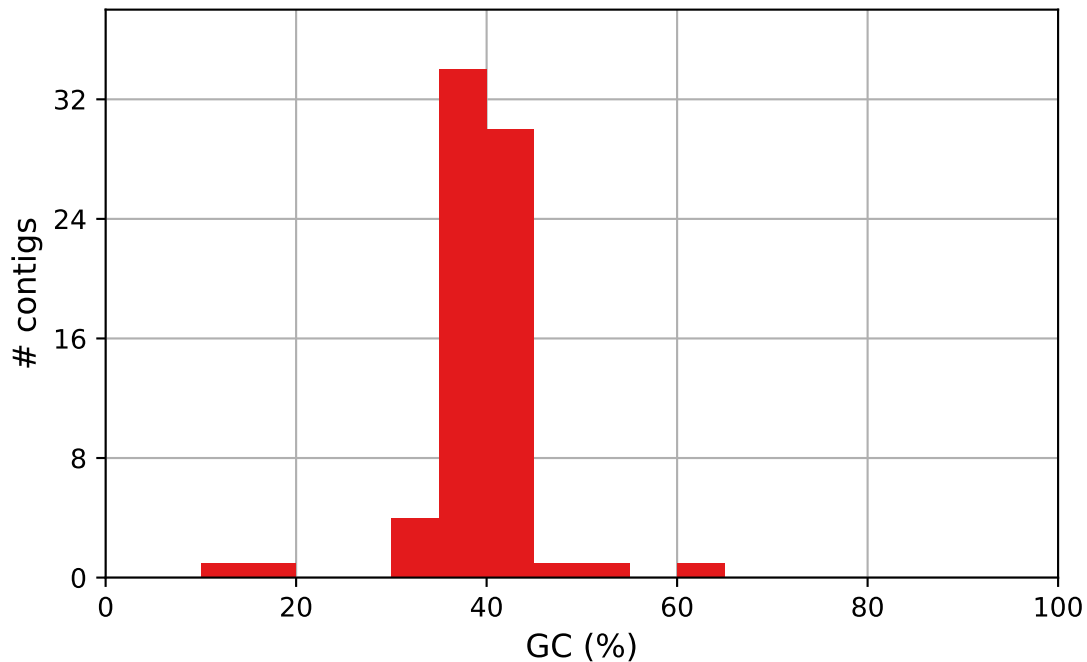
Cumulative length



GC content

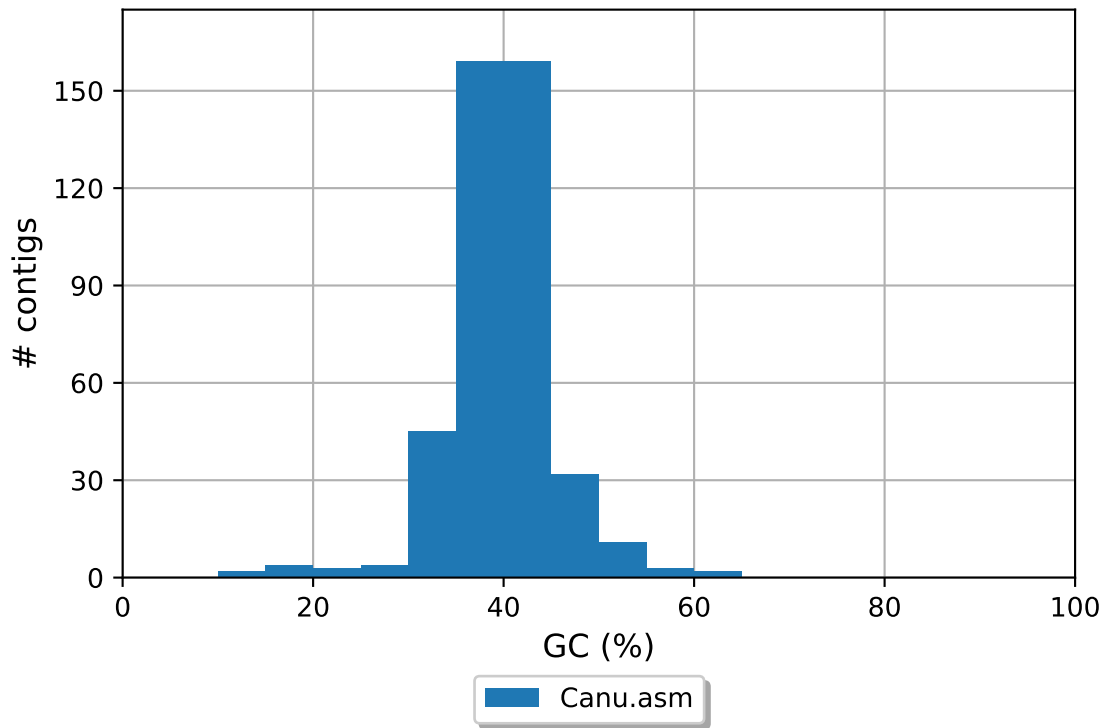


nextDenovo.asm GC content

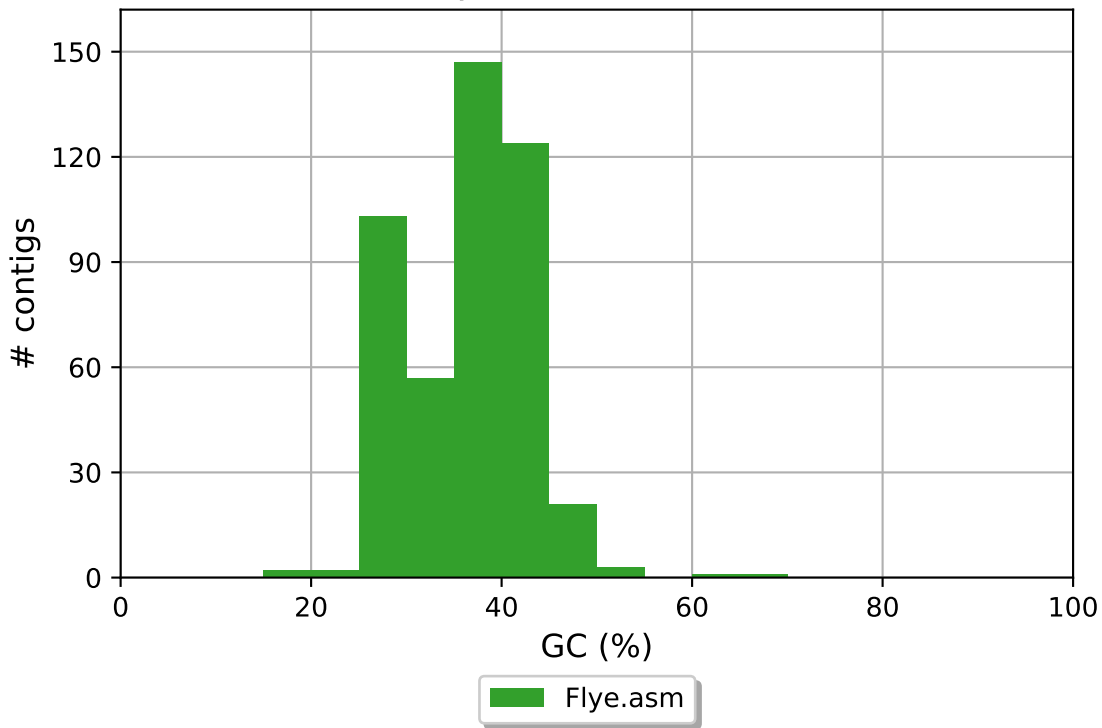


nextDenovo.asm

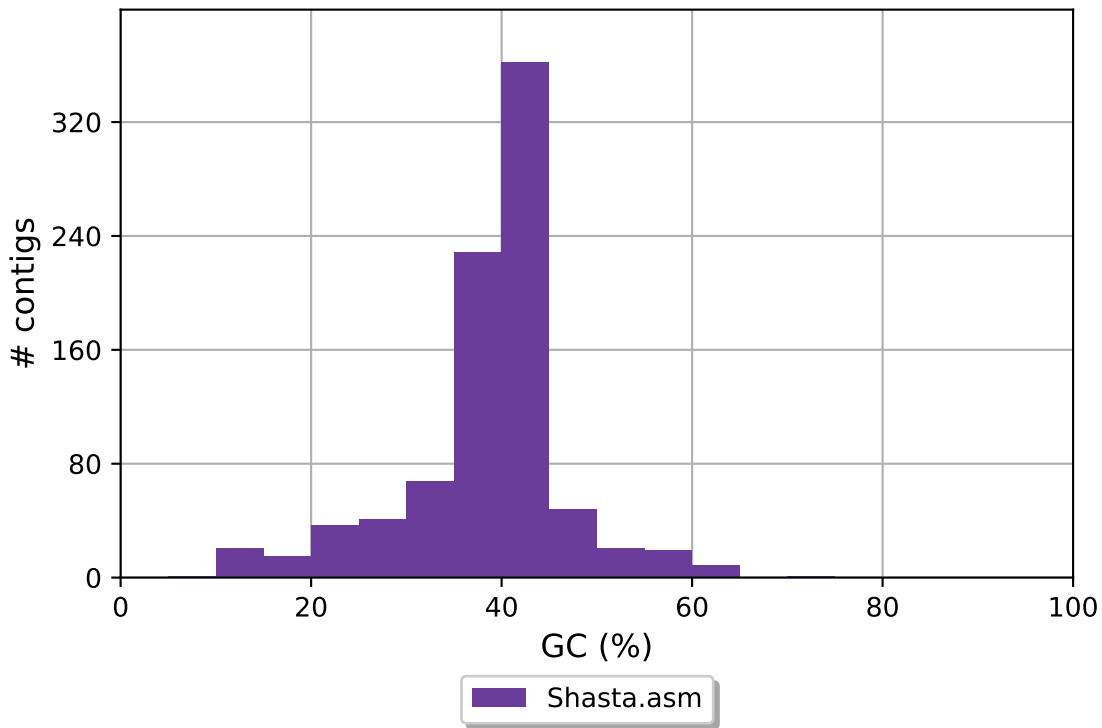
Canu.asm GC content



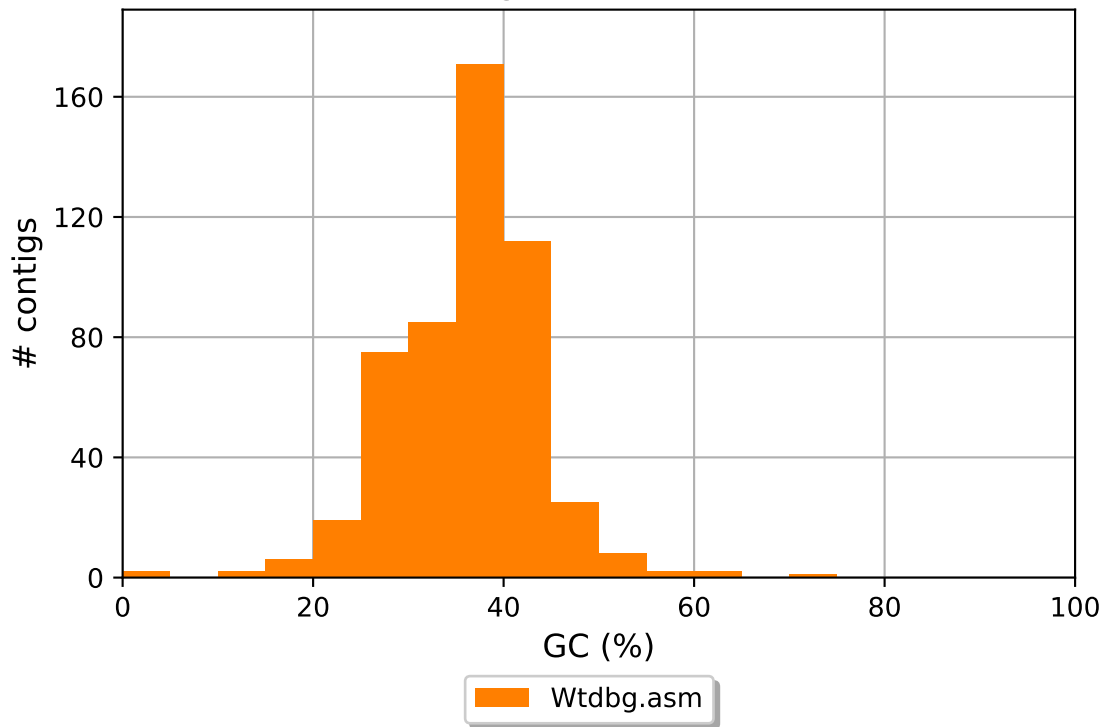
Flye.asm GC content



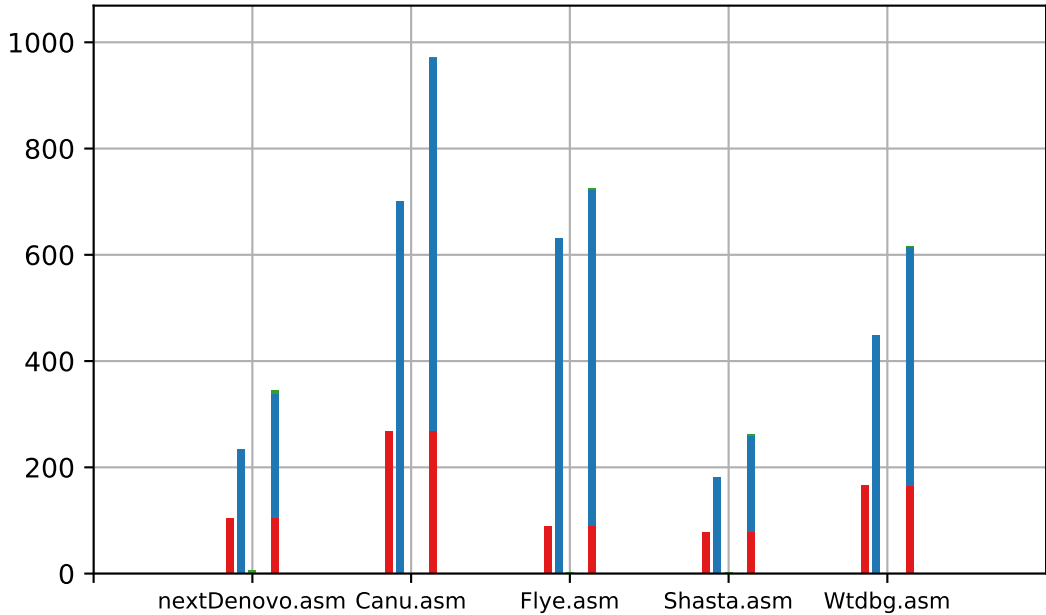
Shasta.asm GC content



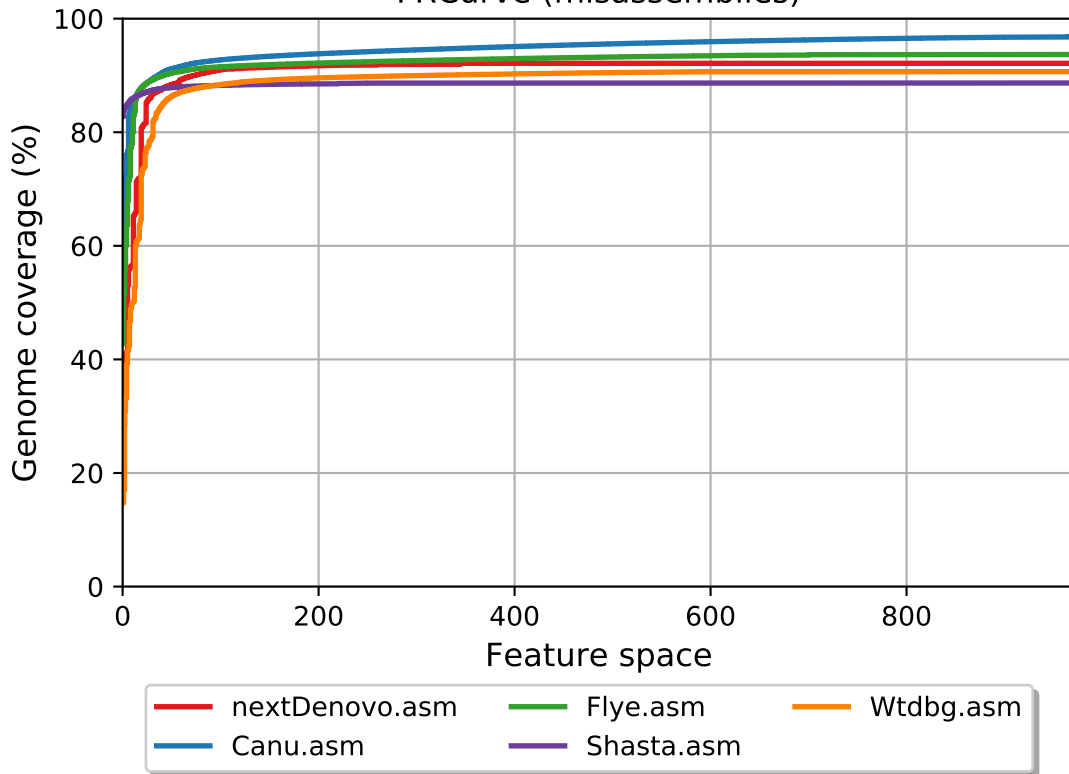
Wtdbg.asm GC content



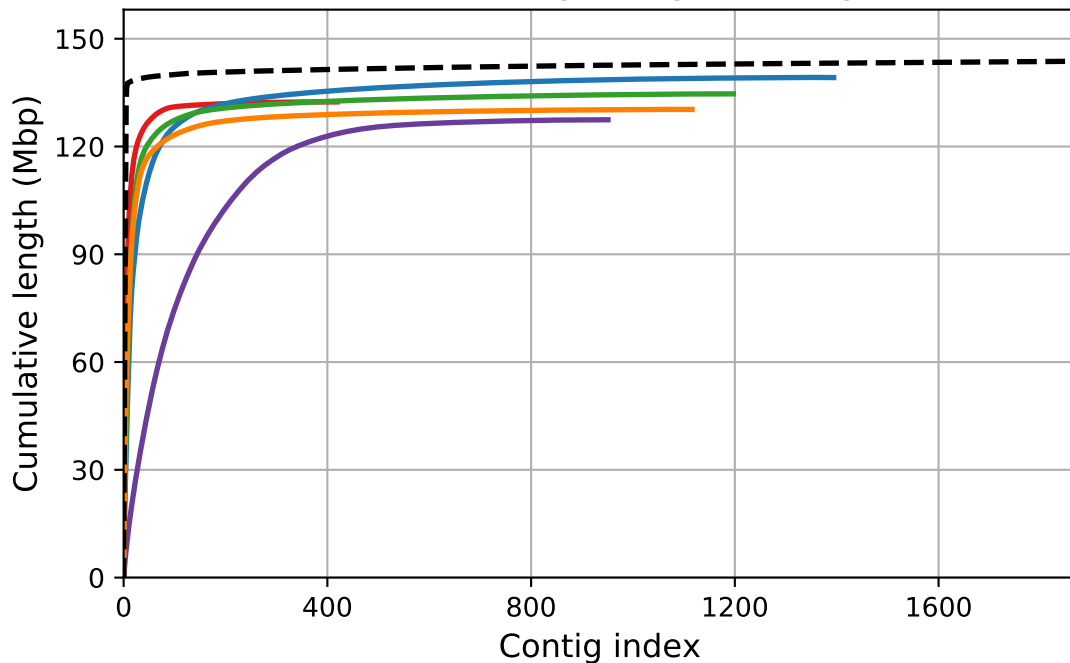
Misassemblies



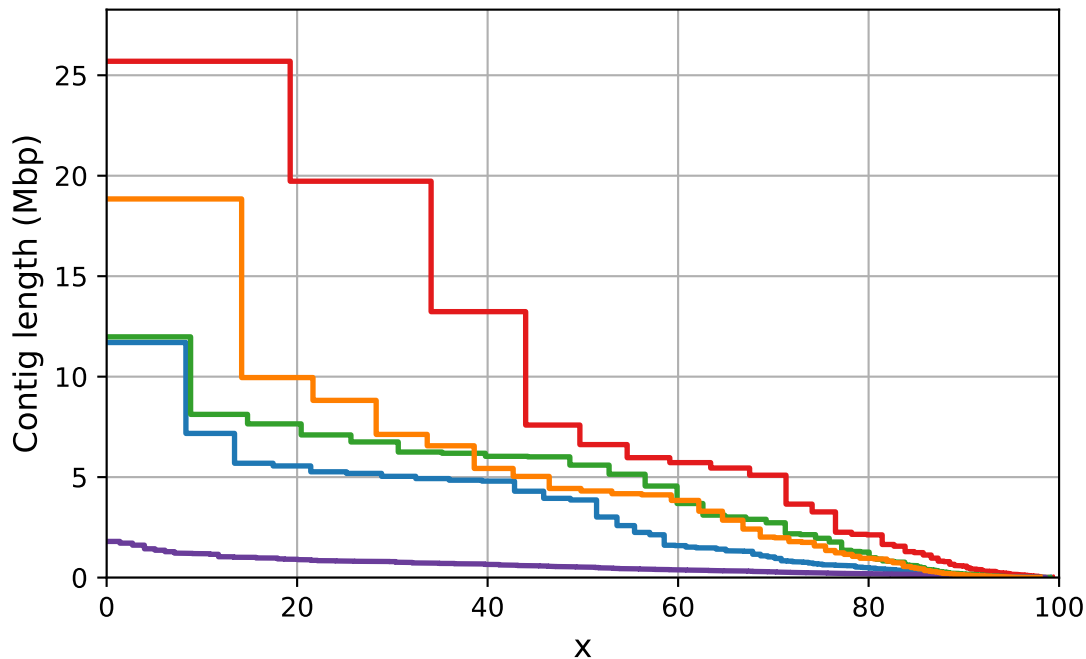
FRCurve (misassemblies)



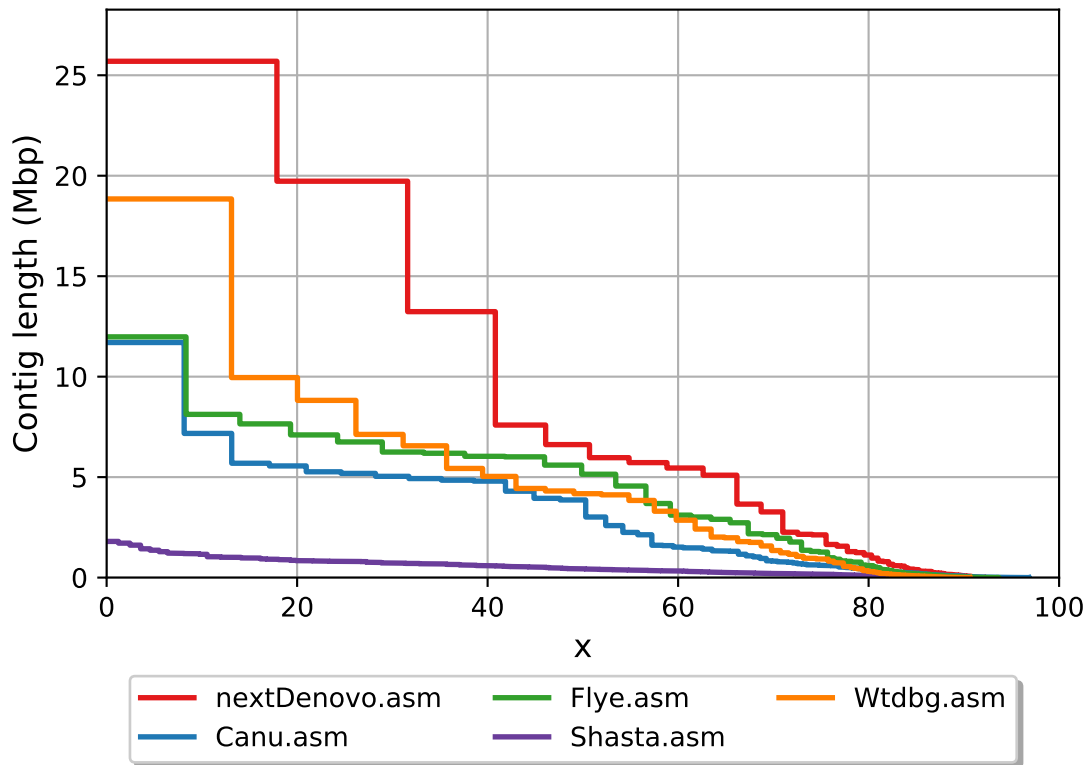
Cumulative length (aligned contigs)



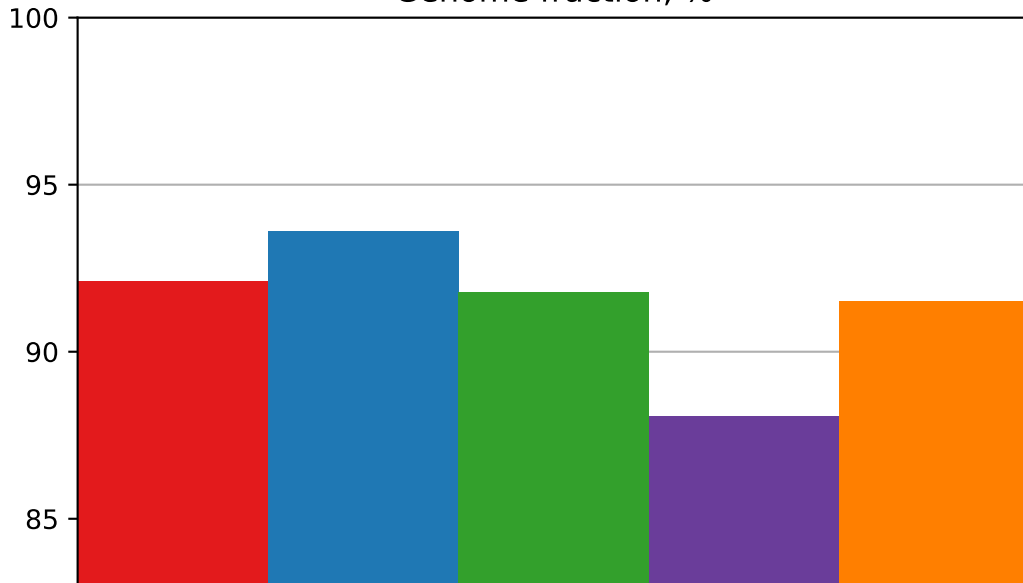
NAX



NGAx



Genome fraction, %



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