

Report

	Homalodisca_vitripennis.A6A7A9_masurca_v1.sorted	Homalodisca_vitripennis.A6A7A9_masurca_v1.sorted.corrected	masurca.A6_A7_A9.flye.assembly	ragtag.scaffolds
# contigs (>= 0 bp)	34909	71987	34814	21155
# contigs (>= 1000 bp)	33215	66763	33120	19617
# contigs (>= 5000 bp)	27656	49622	27574	14867
# contigs (>= 10000 bp)	24406	33128	24333	12435
# contigs (>= 25000 bp)	18522	18509	18487	8722
# contigs (>= 50000 bp)	11507	9914	11496	5104
Total length (>= 0 bp)	1932147428	1932147428	1934422947	1935788847
Total length (>= 1000 bp)	1931011517	1929050025	1933287619	1934761508
Total length (>= 5000 bp)	1914636546	1881992522	1916950236	1920951169
Total length (>= 10000 bp)	1890480121	1764856414	1892867371	1903034666
Total length (>= 25000 bp)	1787010917	1529199244	1790011101	1838500144
Total length (>= 50000 bp)	1532140593	1223772004	1536001135	1708872862
# contigs	30304	56539	30215	17061
Largest contig	1810465	1810465	2021536	8558461
Total length	1925037438	1909063459	1927324502	1929531851
Reference length	1445215006	1445215006	1445215006	1445215006
GC (%)	32.87	32.86	32.87	32.87
Reference GC (%)	32.68	32.68	32.68	32.68
N50	119560	80021	120335	672405
NG50	170425	118610	171543	969695
N75	58472	32323	58624	174061
NG75	100051	64411	101128	529458
L50	4036	5636	4010	721
LG50	2345	3246	2322	423
L75	9876	15088	9828	2110
LG75	5143	7441	5098	920
# misassemblies	78359	66701	78455	86203
# misassembled contigs	13266	18408	13241	6223
Misassembled contigs length	1265267547	1124358278	1268888441	1432985218
# local misassemblies	167329	167724	167731	177584
# scaffold gap ext. mis.	7	4	8	192
# scaffold gap loc. mis.	25	25	25	2537
# possible TEs	31384	31168	31464	36218
# unaligned mis. contigs	11539	18570	11521	7489
# unaligned contigs	826 + 28386 part	4607 + 49329 part	822 + 28308 part	677 + 15591 part
Unaligned length	753221948	742932715	754073286	755161898
Genome fraction (%)	66.850	66.698	66.928	66.954
Duplication ratio	1.248	1.245	1.248	1.249
# N's per 100 kbp	0.48	0.45	0.48	71.23
# mismatches per 100 kbp	3175.90	3189.15	3177.85	3243.93
# indels per 100 kbp	157.23	156.71	157.26	157.91
Largest alignment	1149273	1149273	1159461	1159461
Total aligned length	1170514781	1164302779	1171940490	1171696864
NA50	2674	2884	2680	3111
NGA50	19735	20008	19890	23794
NGA75	1127	1086	1139	1248
LA50	48998	44883	48882	39563
LGA50	13198	13193	13121	10672
LGA75	120465	120382	119189	102026

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

	Homalodisca_vitripennis.A6A7A9_masurca_v1.sorted	Homalodisca_vitripennis.A6A7A9_masurca_v1.sorted.corrected	masurca.A6_A7_A9.flye.assembly	ragtag.scaffolds
# misassemblies	78359	66701	78455	86203
# contig misassemblies	78324	66685	78420	80226
# c. relocations	1263	1110	1266	1439
# c. translocations	76490	65200	76586	78202
# c. inversions	571	375	568	585
# scaffold misassemblies	35	16	35	5977
# s. relocations	5	4	5	1079
# s. translocations	30	12	30	4869
# s. inversions	0	0	0	29
# misassembled contigs	13266	18408	13241	6223
Misassembled contigs length	1265267547	1124358278	1268888441	1432985218
# local misassemblies	167329	167724	167731	177584
# scaffold gap ext. mis.	7	4	8	192
# scaffold gap loc. mis.	25	25	25	2537
# possible TEs	31384	31168	31464	36218
# unaligned mis. contigs	11539	18570	11521	7489
# mismatches	29811773	29867867	29864786	30497767
# indels	1475879	1467641	1477925	1484592
# indels (<= 5 bp)	1104639	1097842	1106155	1109892
# indels (> 5 bp)	371240	369799	371770	374700
Indels length	11938664	11913706	11954434	12011573

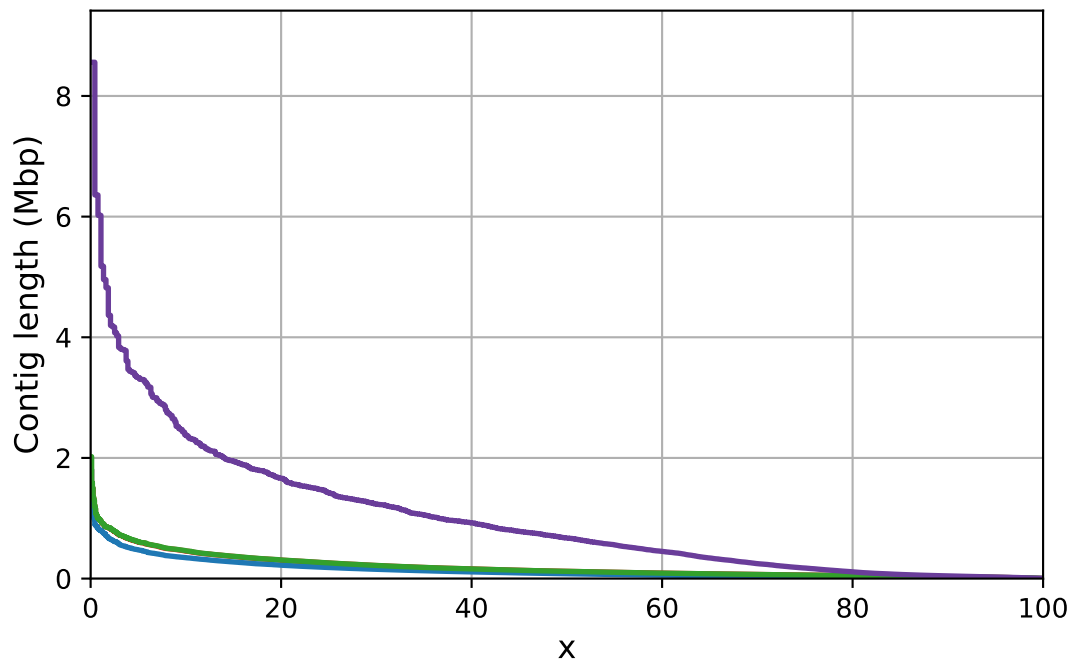
All statistics are based on contigs of size ≥ 3000 bp, unless otherwise noted (e.g., "# contigs (≥ 0 bp)" and "Total length (≥ 0 bp)" include all contigs).

Unaligned report

	Homalodisca_vitripennis.A6A7A9_masurca_v1.sorted	Homalodisca_vitripennis.A6A7A9_masurca_v1.sorted.corrected	masurca.A6_A7_A9.flye.assembly	ragtag.scaffolds
# fully unaligned contigs	826	4607	822	677
Fully unaligned length	6645752	32150999	6592795	5370513
# partially unaligned contigs	28386	49329	28308	15591
Partially unaligned length	746576196	710781716	747480491	749791385
# N's	9200	8600	9300	1374400

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

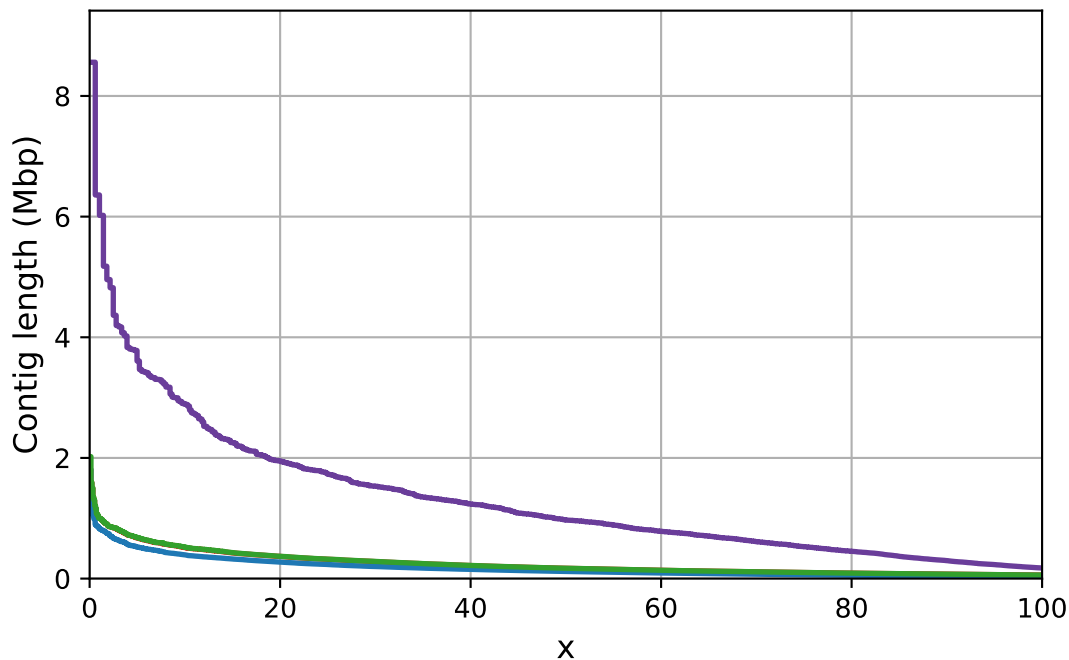


ripennisi.A6A7A9_masurca_v1.sorted

ripennisi.A6A7A9_masurca_v1.sorted.corrected

masurca.A6_A7_A9.flye.assembly

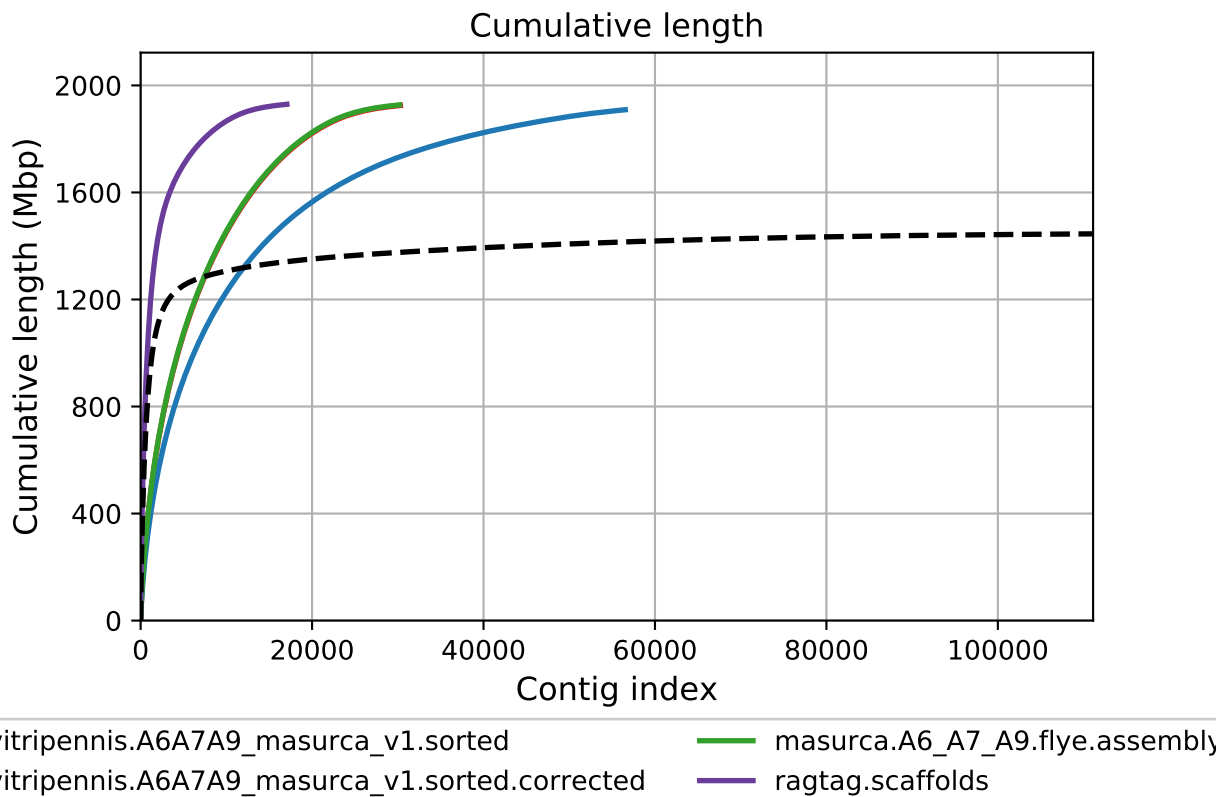
NGx



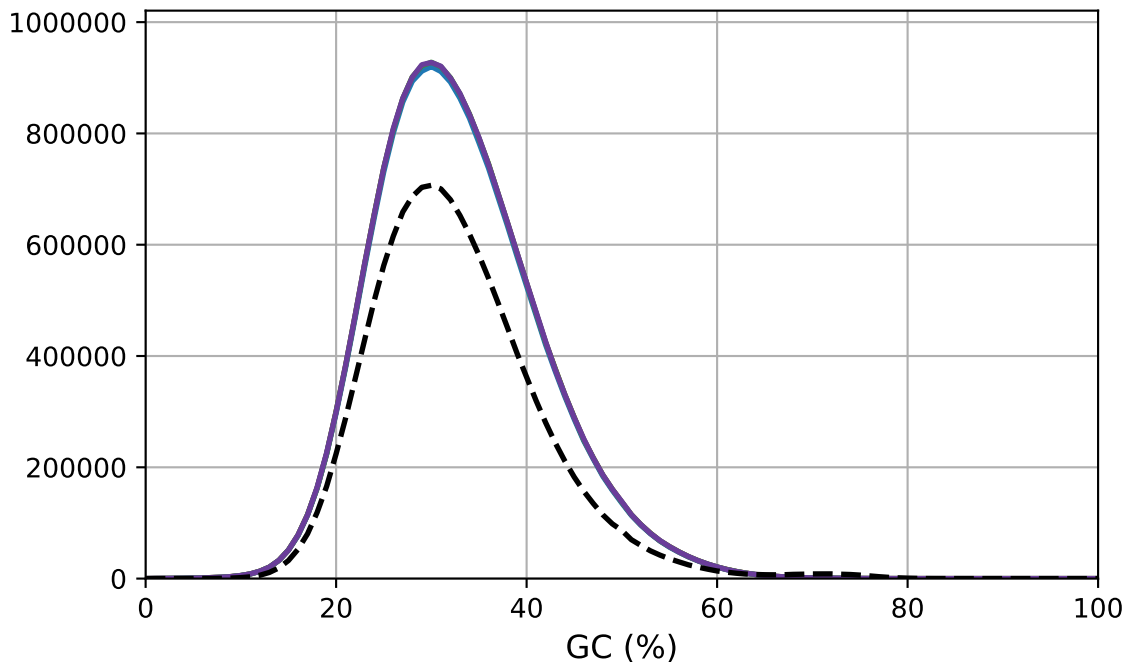
ripennis.A6A7A9_masurca_v1.sorted

masurca.A6_A7_A9.flye.assembly

ripennis.A6A7A9_masurca_v1.sorted.corrected



GC content



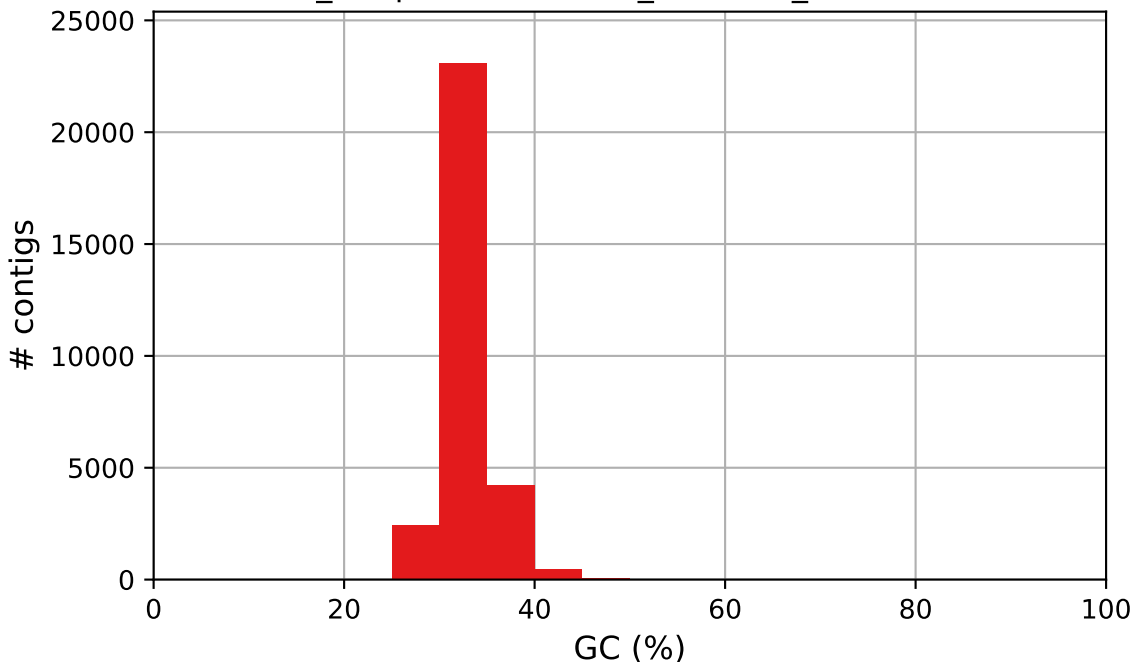
vitripennis.A6A7A9_masurca_v1.sorted

vitripennis.A6A7A9_masurca_v1.sorted.corrected

masurca.A6_A7_A9.flye.assembly

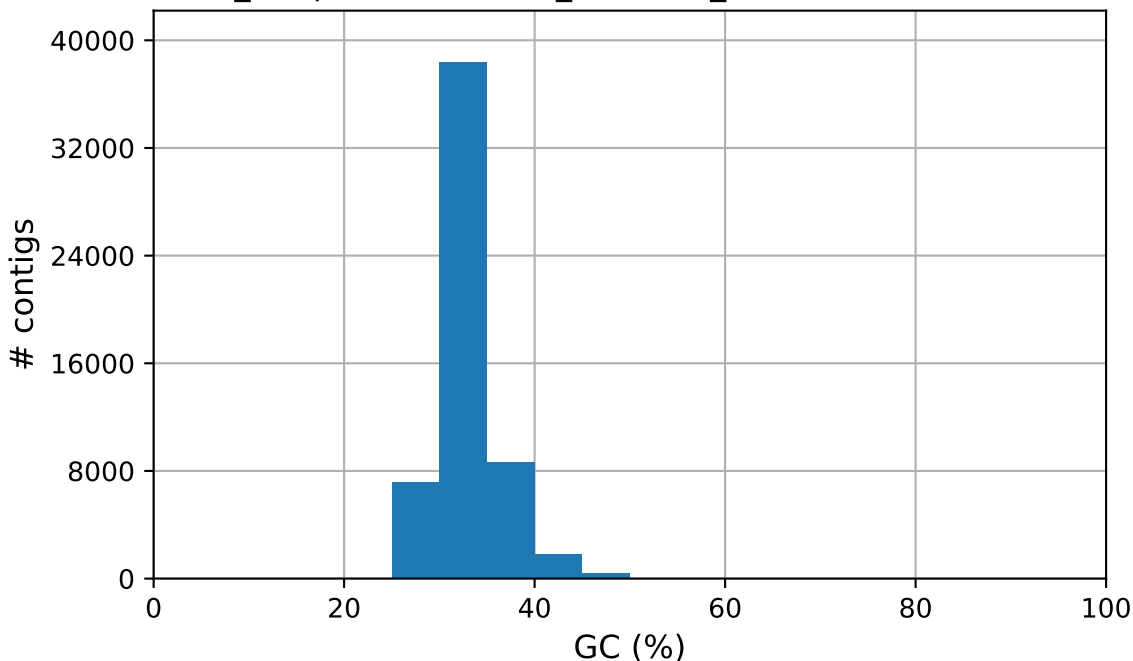
ragtag.scaffolds

Homalodisca_vitripennis.A6A7A9_masurca_v1.sorted GC content



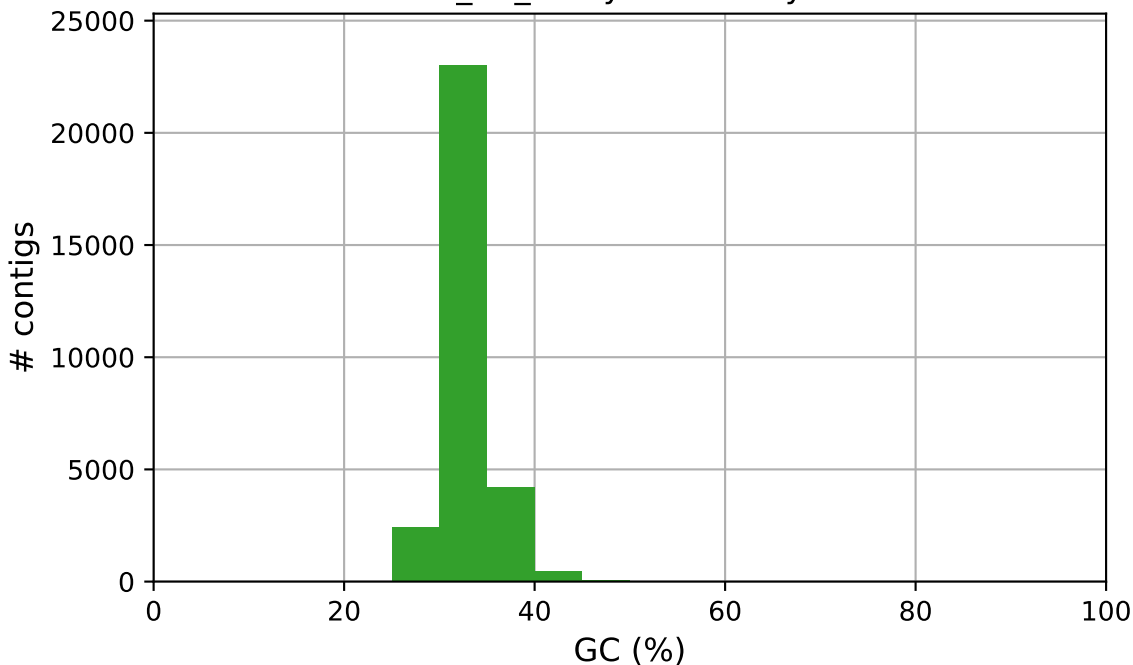
Homalodisca_vitripennis.A6A7A9_masurca_v1.sorted

Homalodisca_vitripennis.A6A7A9_masurca_v1.sorted.corrected GC content



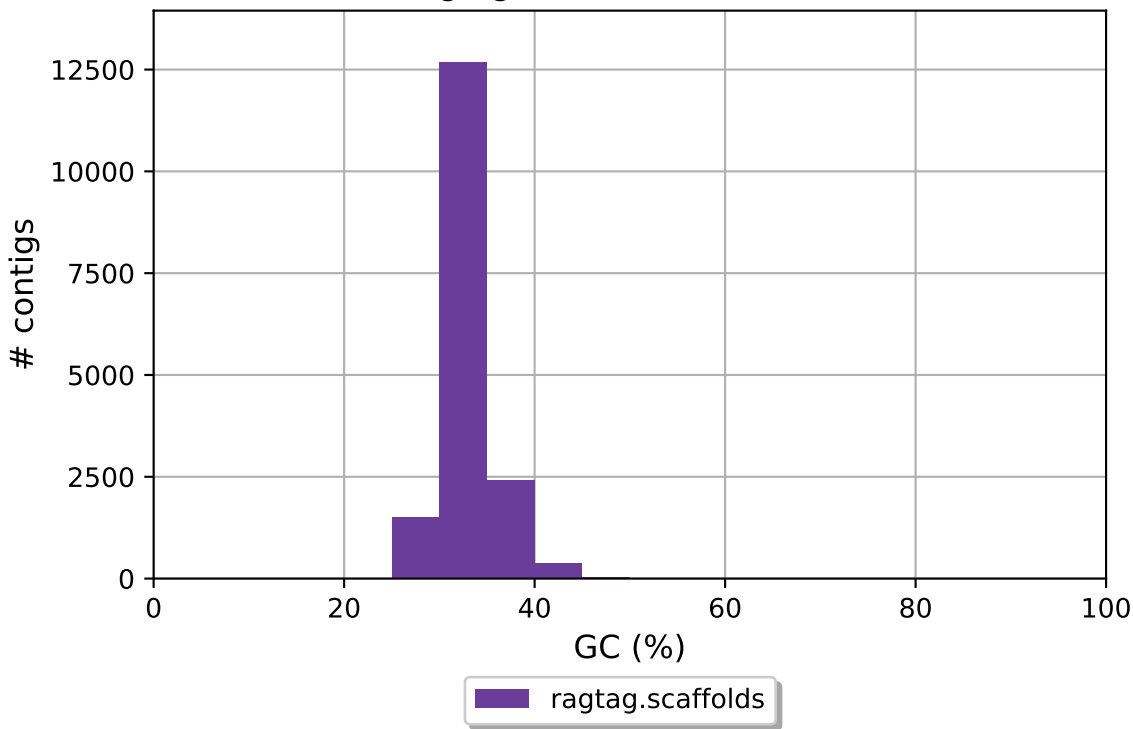
Homalodisca_vitripennis.A6A7A9_masurca_v1.sorted.corrected

masurca.A6_A7_A9.flye.assembly GC content

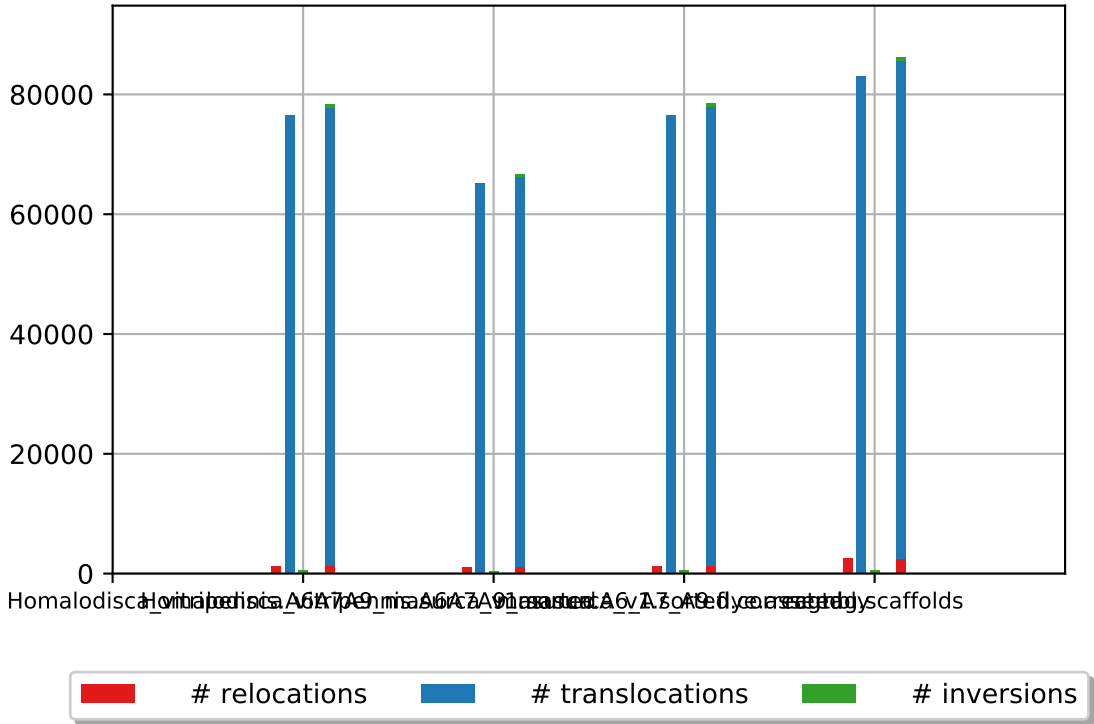


masurca.A6_A7_A9.flye.assembly

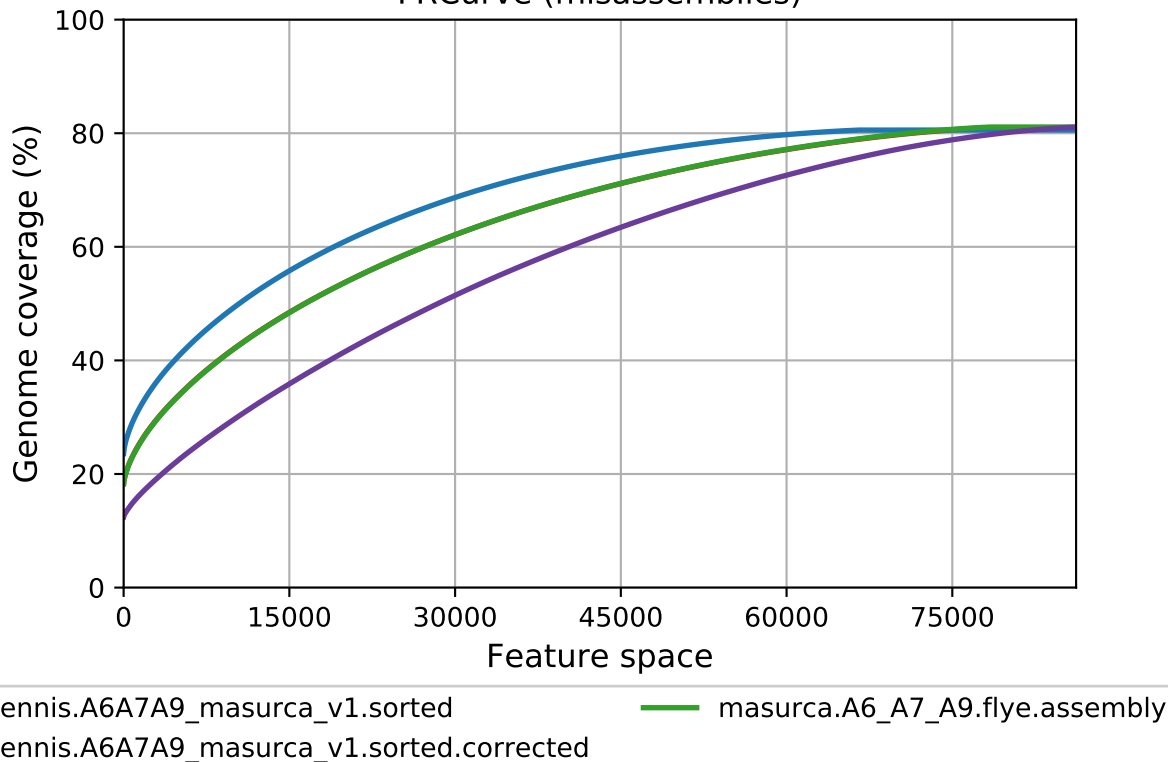
ragtag.scaffolds GC content



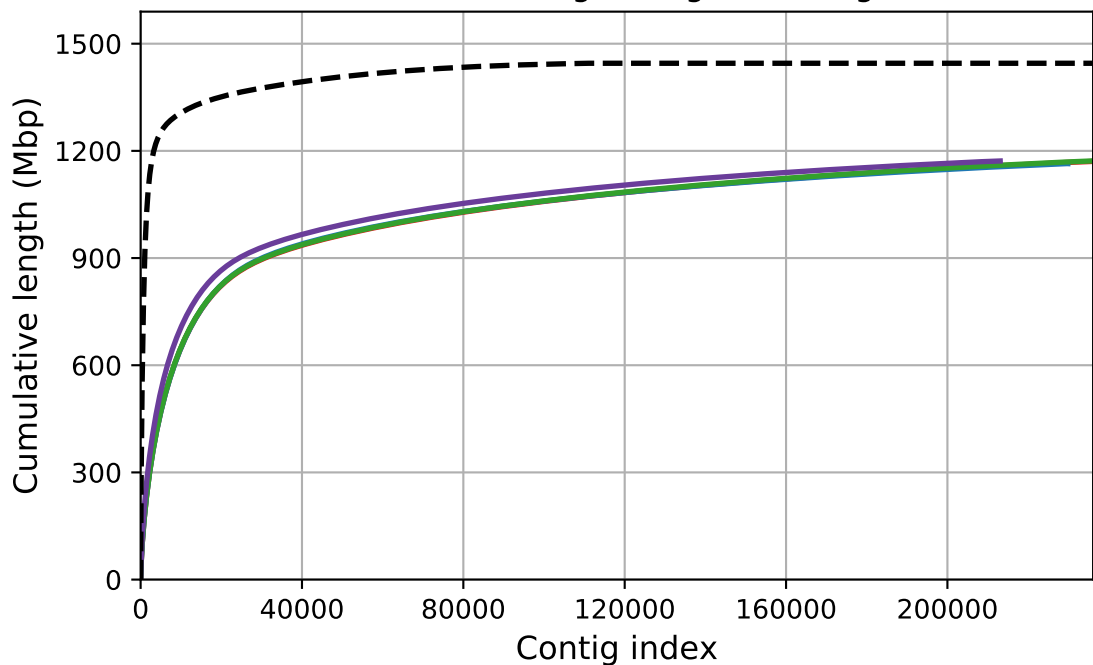
Misassemblies



FRCurve (misassemblies)



Cumulative length (aligned contigs)



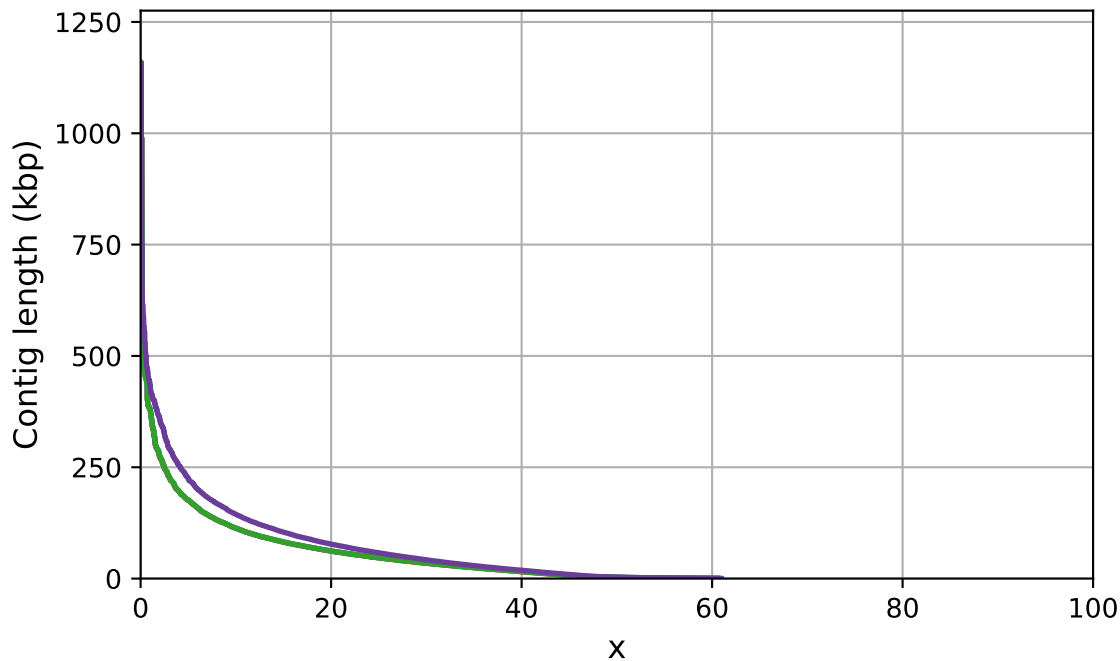
vitripennis.A6A7A9_masurca_v1.sorted

masurca.A6_A7_A9.flye.assembly

vitripennis.A6A7A9_masurca_v1.sorted.corrected

ragtag.scaffolds

NAx

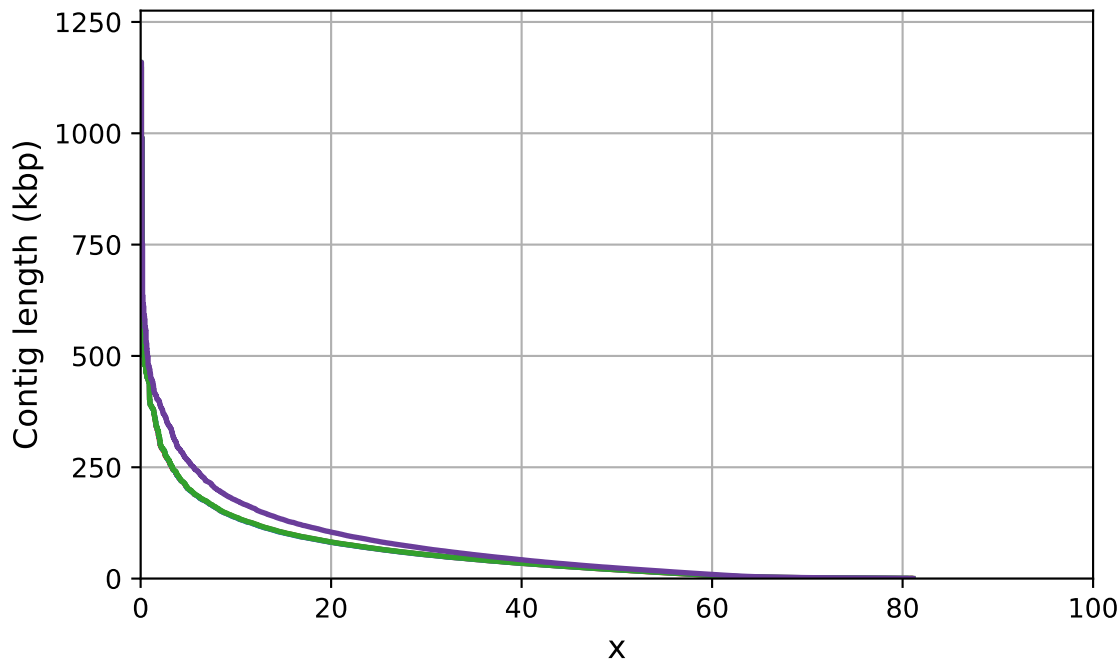


ripennis.A6A7A9_masurca_v1.sorted

masurca.A6_A7_A9.flye.assembly

ripennis.A6A7A9_masurca_v1.sorted.corrected

NGAx

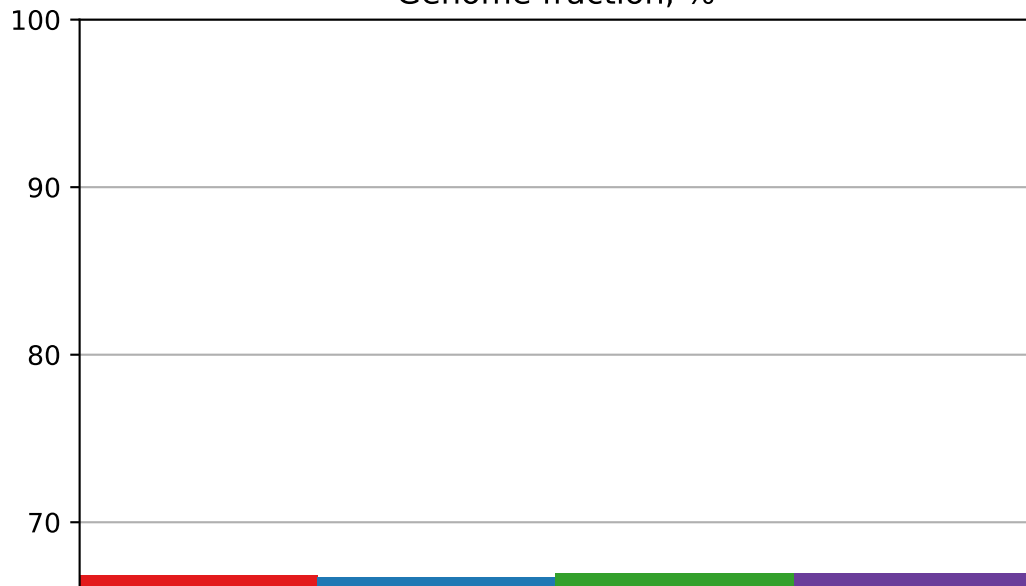


ripennisi.A6A7A9_masurca_v1.sorted

masurca.A6_A7_A9.flye.assembly

ripennisi.A6A7A9_masurca_v1.sorted.corrected

Genome fraction, %



ripennisi.A6A7A9_masurca_v1.sorted

masurca.A6_A7_A9.flye.assembly

ripennisi.A6A7A9_masurca_v1.sorted.corrected