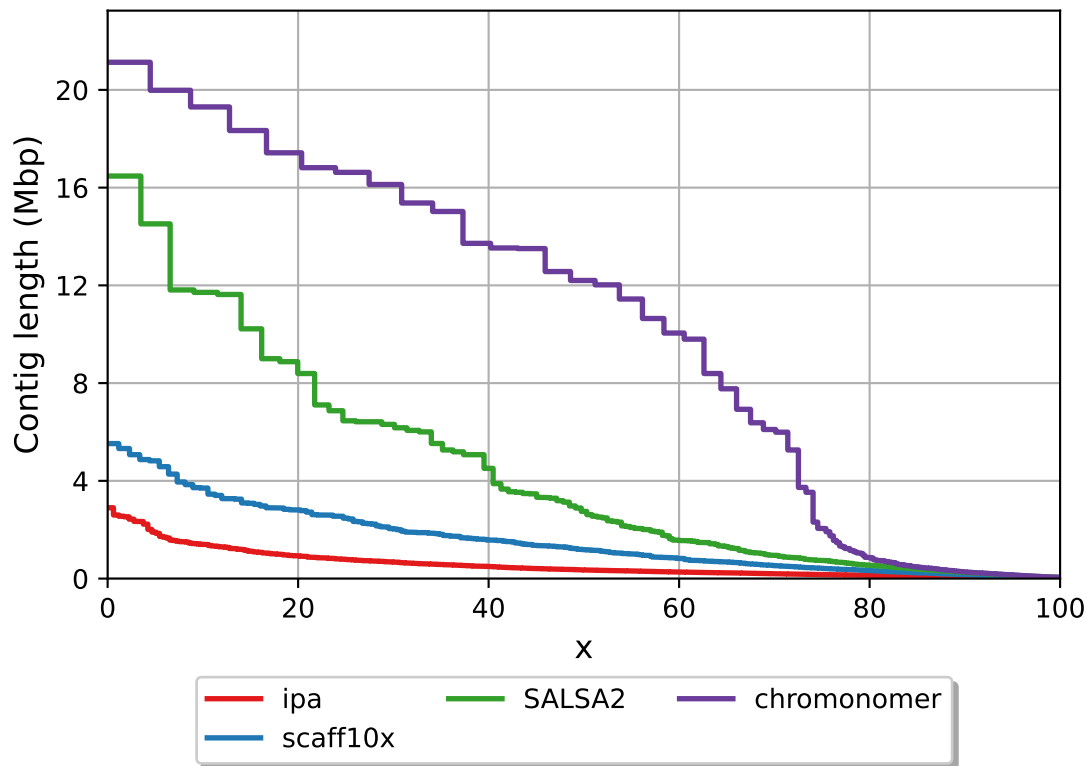


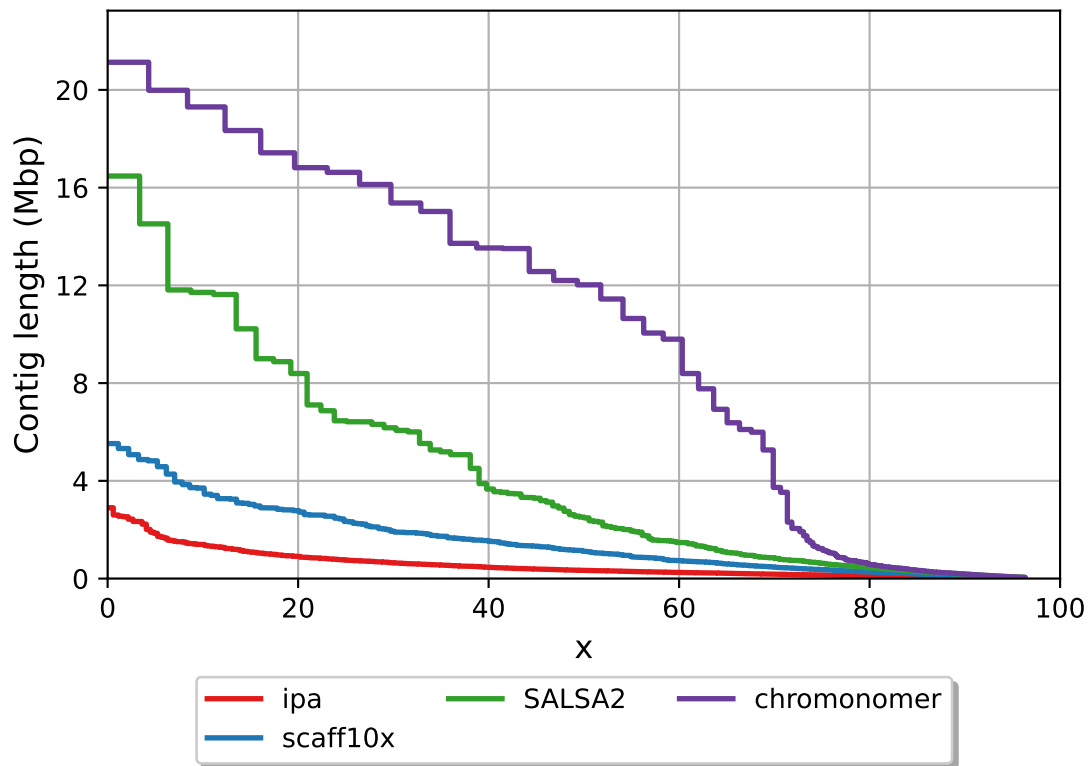
	ipa	scaff10x	SALSA2	chromonomer
Report				
# contigs (>= 0 bp)	2086	1106	705	549
# contigs (>= 1000 bp)	2086	1106	705	549
# contigs (>= 5000 bp)	2086	1106	705	549
# contigs (>= 10000 bp)	2086	1106	705	549
# contigs (>= 25000 bp)	2084	1104	705	549
# contigs (>= 50000 bp)	2057	1078	699	545
Total length (>= 0 bp)	471831811	471929811	472145811	472157411
Total length (>= 1000 bp)	471831811	471929811	472145811	472157411
Total length (>= 5000 bp)	471831811	471929811	472145811	472157411
Total length (>= 10000 bp)	471831811	471929811	472145811	472157411
Total length (>= 25000 bp)	471783108	471881108	472145811	472157411
Total length (>= 50000 bp)	470677046	470821567	471892474	471998837
# contigs	2086	1106	705	549
Largest contig	2899834	5525214	16473917	21130208
Total length	471831811	471929811	472145811	472157411
Reference length	-	-	-	-
Estimated reference length	490000000	490000000	490000000	490000000
GC (%)	44.71	44.71	44.71	44.71
Reference GC (%)	-	-	-	-
N50	353581	1188596	2749144	12200365
NG50	335796	1121656	2516285	12021477
N90	91777	162160	247754	276497
NG90	76626	115916	176999	185728
auN	581149.7	1582156.2	4514538.1	10600547.4
auNG	559601.9	1523809.6	4350041.3	10214544.9
L50	324	106	38	15
LG50	351	114	41	16
L90	1388	542	290	153
LG90	1583	661	366	224
# total reads	-	-	-	-
# left	-	-	-	-
# right	-	-	-	-
Mapped (%)	-	-	-	-
Reference mapped (%)	-	-	-	-
Properly paired (%)	-	-	-	-
Reference properly paired (%)	-	-	-	-
Avg. coverage depth	-	-	-	-
Reference avg. coverage depth	-	-	-	-
Coverage >= 1x (%)	-	-	-	-
Reference coverage >= 1x (%)	-	-	-	-
# large blocks misassemblies	-	-	-	-
# misassemblies	-	-	-	-
# misassembled contigs	-	-	-	-
Misassembled contigs length	-	-	-	-
# local misassemblies	-	-	-	-
# scaffold gap ext. mis.	-	-	-	-
# scaffold gap loc. mis.	-	-	-	-
# structural variations	-	-	-	-
# possible TEs	-	-	-	-
# unaligned mis. contigs	-	-	-	-
# unaligned contigs	-	-	-	-
Unaligned length	-	-	-	-
Genome fraction (%)	-	-	-	-
Duplication ratio	-	-	-	-
Avg contig read support	-	-	-	-
# N's per 100 kbp	0.01	20.78	66.51	68.97
# mismatches per 100 kbp	-	-	-	-
# indels per 100 kbp	-	-	-	-
# genomic features	-	-	-	-
# operons	-	-	-	-
Complete BUSCO (%)	-	-	-	-
Partial BUSCO (%)	-	-	-	-
# predicted genes (unique)	-	-	-	-
# predicted genes (>= 0 bp)	-	-	-	-
# predicted genes (>= 300 bp)	-	-	-	-
# predicted genes (>= 1500 bp)	-	-	-	-
# predicted genes (>= 3000 bp)	-	-	-	-
# predicted rRNA genes	-	-	-	-
Largest alignment	-	-	-	-
Total aligned length	-	-	-	-
NA50	-	-	-	-
NGA50	-	-	-	-
NA90	-	-	-	-
NGA90	-	-	-	-
auNA	-	-	-	-
auNGA	-	-	-	-
LA50	-	-	-	-
LGA50	-	-	-	-
LA90	-	-	-	-
LGA90	-	-	-	-
K-mer-based compl. (%)	-	-	-	-
K-mer-based cor. length (%)	-	-	-	-
K-mer-based mis. length (%)	-	-	-	-

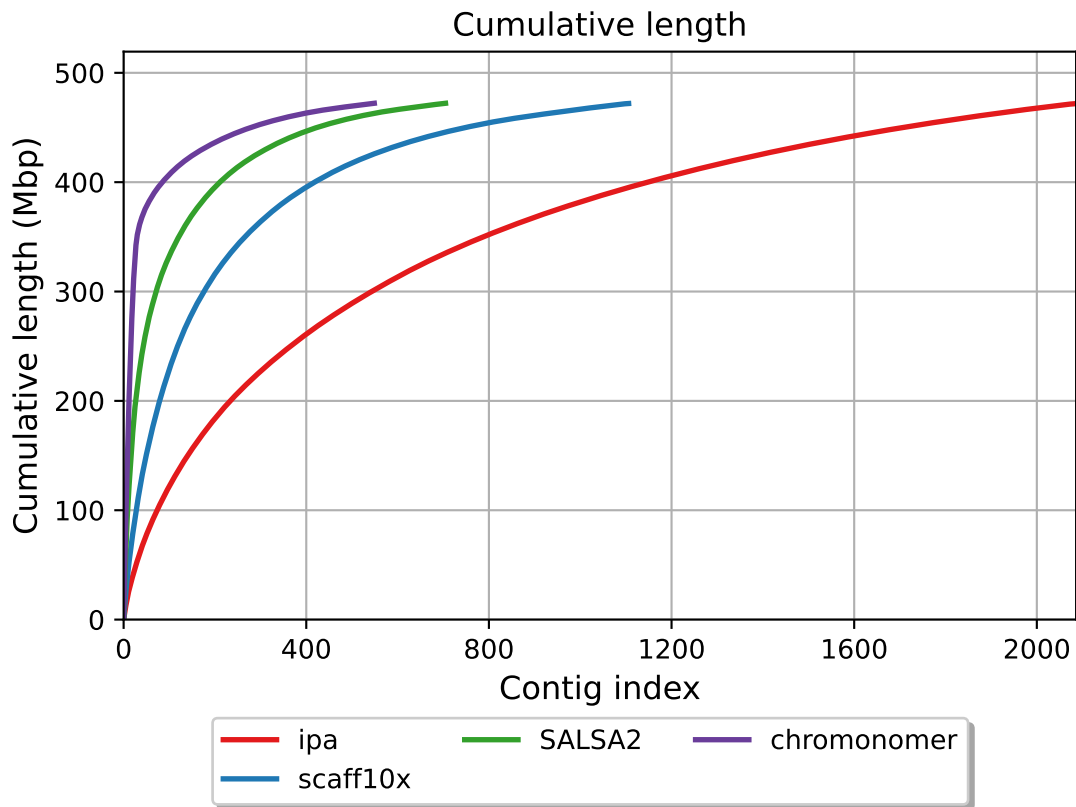
All statistics are based on contigs of size >= 3000 bp, unless otherwise noted (e.g., "# contigs (>= 0 bp)" and "Total length (>= 0 bp)" include all contigs).

Nx



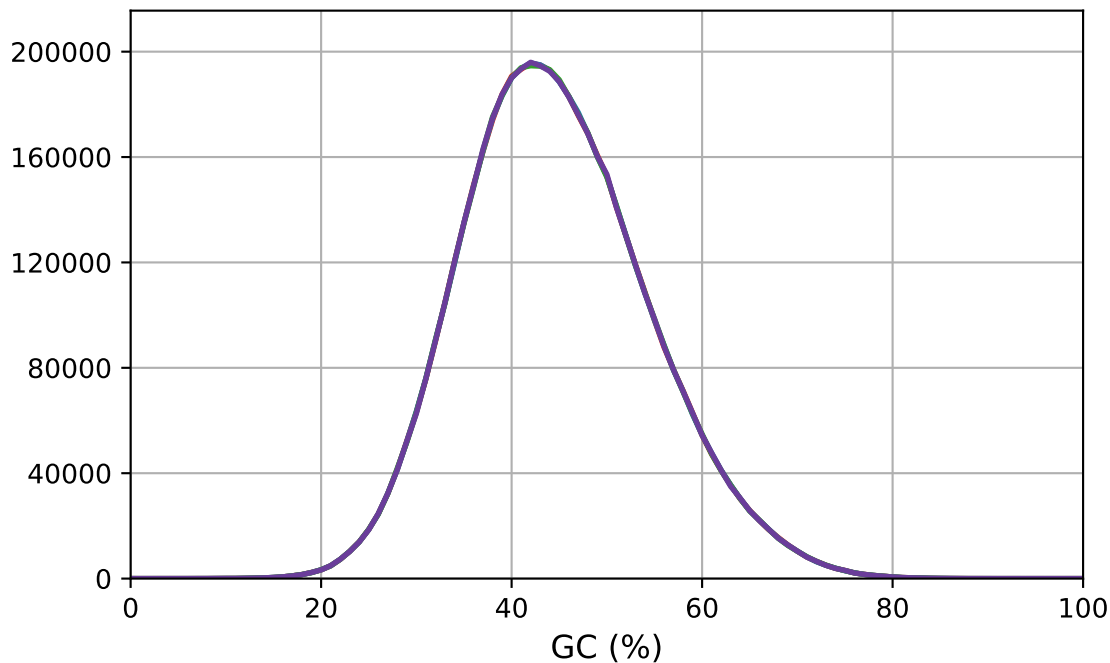
# NGx





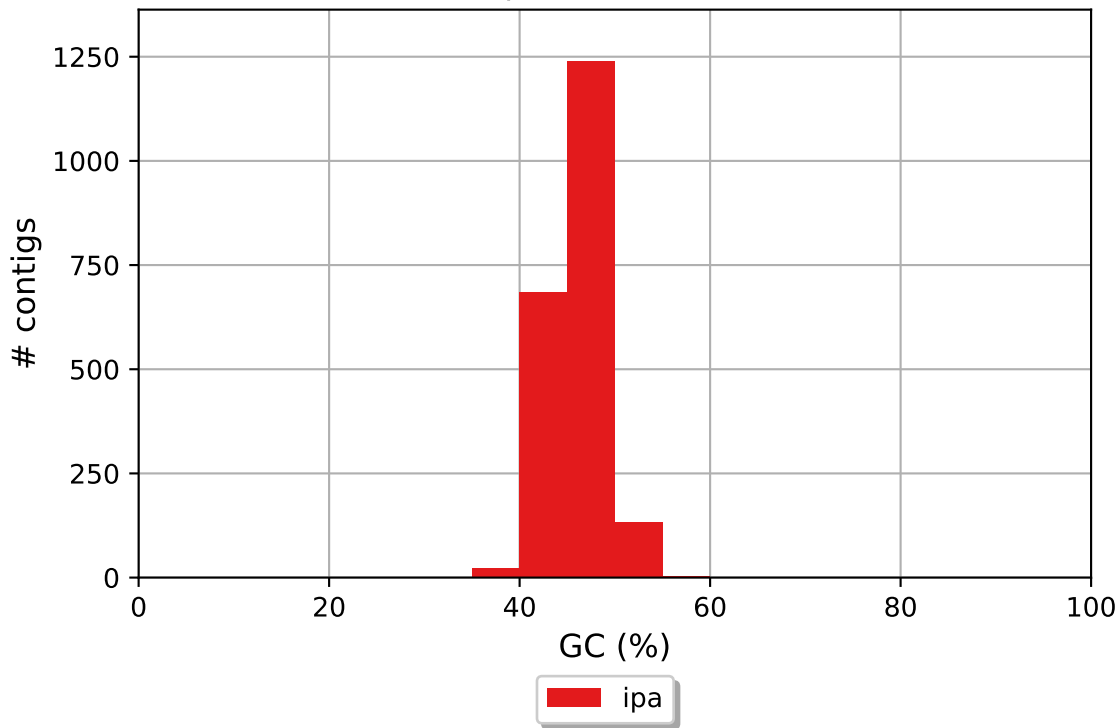
# windows

# GC content

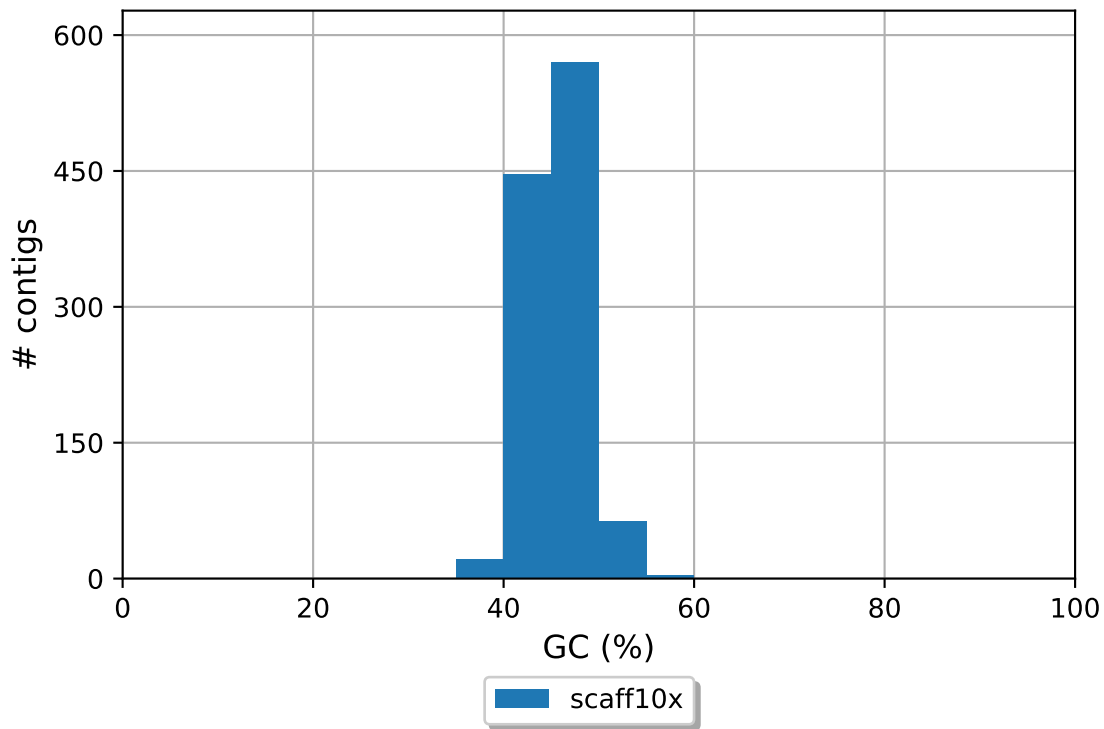


ipa SALSA2 chromonomer  
scaff10x

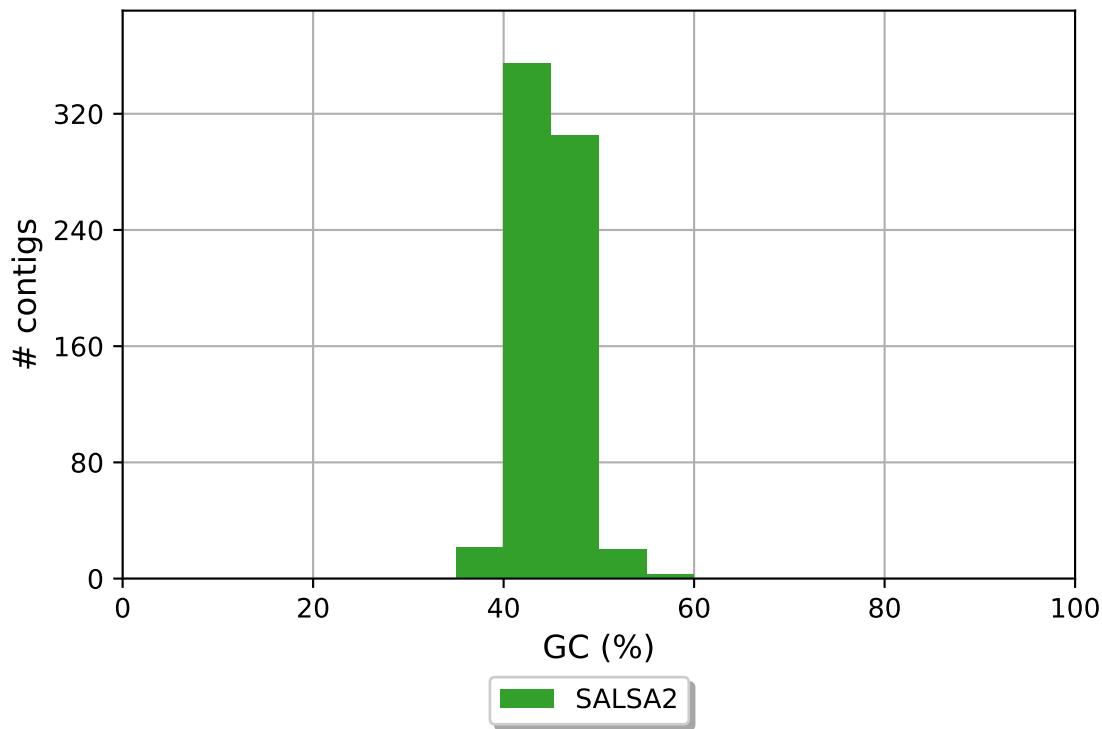
ipa GC content



scaff10x GC content



SALSA2 GC content





chromonomer GC content

