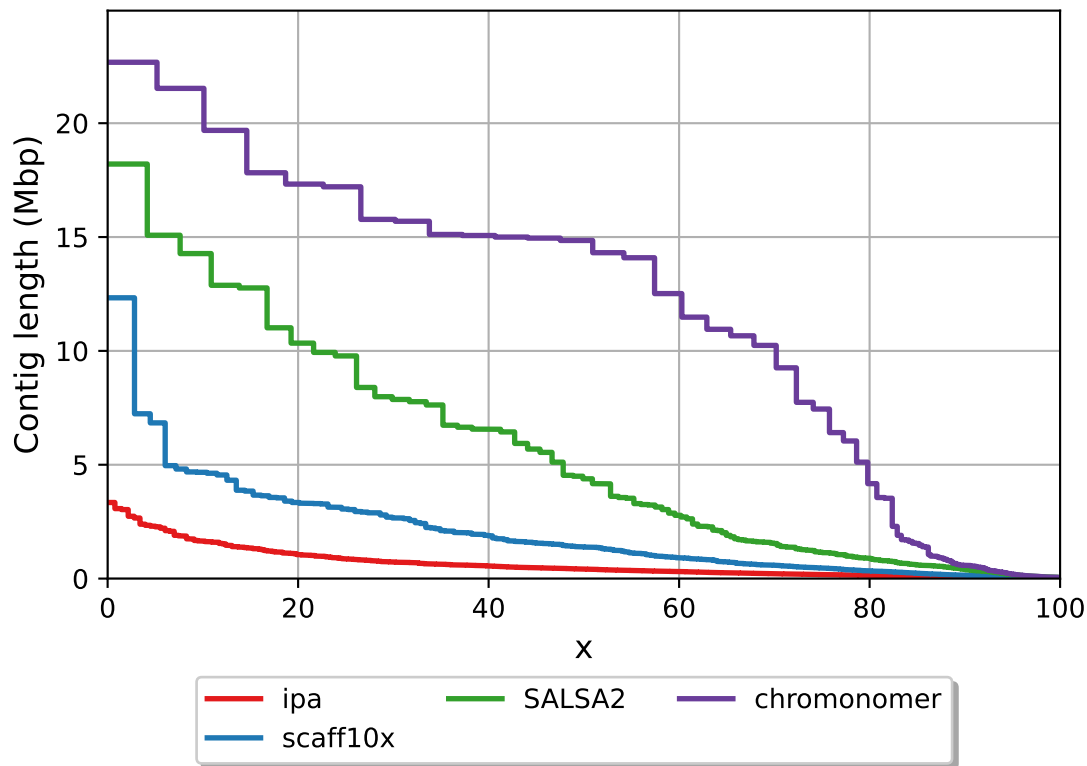


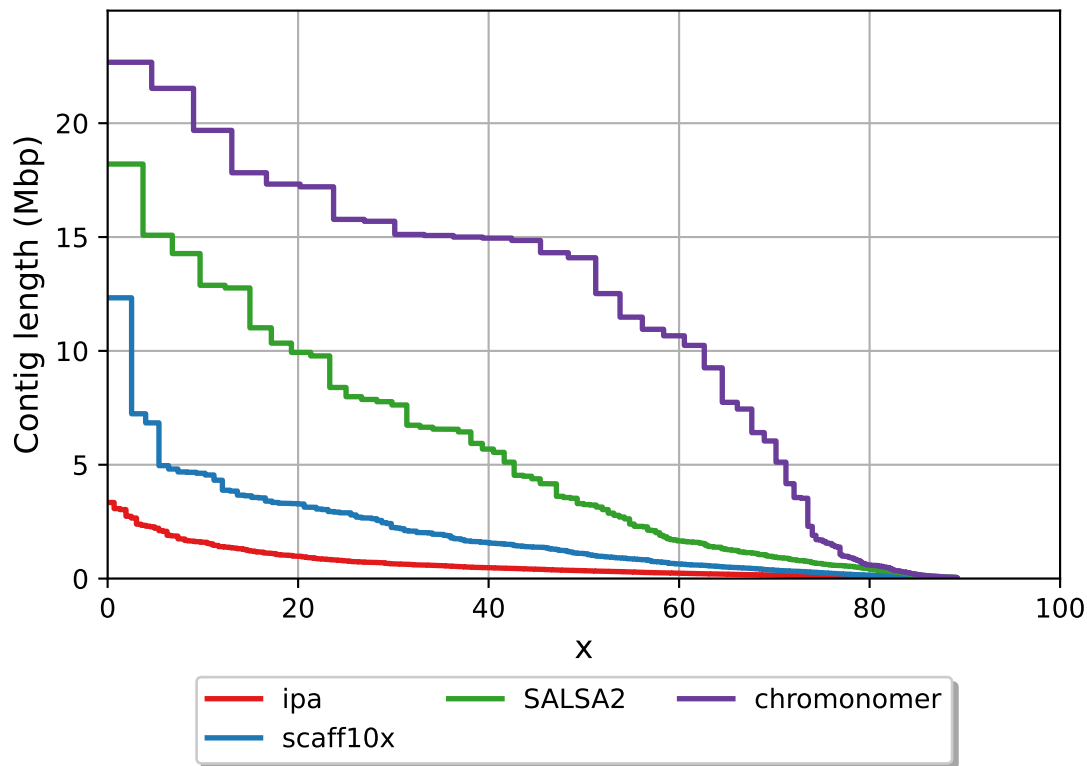
	ipa	scaff10x	SALSA2	chromonomer
Report				
# contigs (>= 0 bp)	1805	1012	515	376
# contigs (>= 1000 bp)	1805	1012	515	376
# contigs (>= 5000 bp)	1805	1012	515	376
# contigs (>= 10000 bp)	1805	1012	515	376
# contigs (>= 25000 bp)	1800	1007	511	372
# contigs (>= 50000 bp)	1773	985	500	361
Total length (>= 0 bp)	436920153	436999453	437264453	437273953
Total length (>= 1000 bp)	436920153	436999453	437264453	437273953
Total length (>= 5000 bp)	436920153	436999453	437264453	437273953
Total length (>= 10000 bp)	436920153	436999453	437264453	437273953
Total length (>= 25000 bp)	436829068	436908368	437187275	437196775
Total length (>= 50000 bp)	435805794	436091683	436774790	436784290
# contigs	1805	1012	515	376
Largest contig	3341941	12331747	18206164	22675904
Total length	436920153	436999453	437264453	437273953
Reference length	-	-	-	-
Estimated reference length	490000000	490000000	490000000	490000000
GC (%)	44.99	44.99	44.99	44.99
Reference GC (%)	-	-	-	-
N50	418614	1392224	4383157	14850352
NG50	346609	1094608	3252074	14090550
N90	97153	148732	403116	583287
NG90	-	-	-	-
auN	668619.6	2113507.9	5815293.2	12187194.5
auNG	596190.5	1884901.7	5189430.6	10875801.4
L50	264	80	26	13
LG50	334	102	33	15
L90	1171	472	172	61
LG90	-	-	-	-
# 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	0.07	18.21	78.81	80.98
# 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).

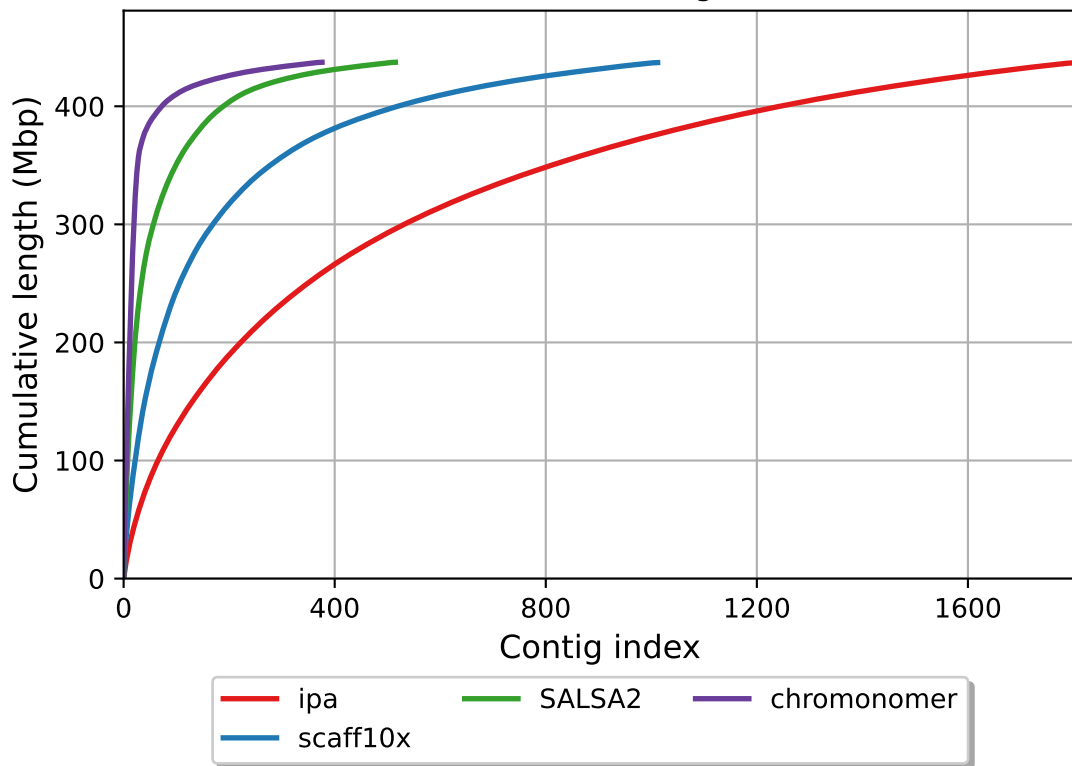
Nx



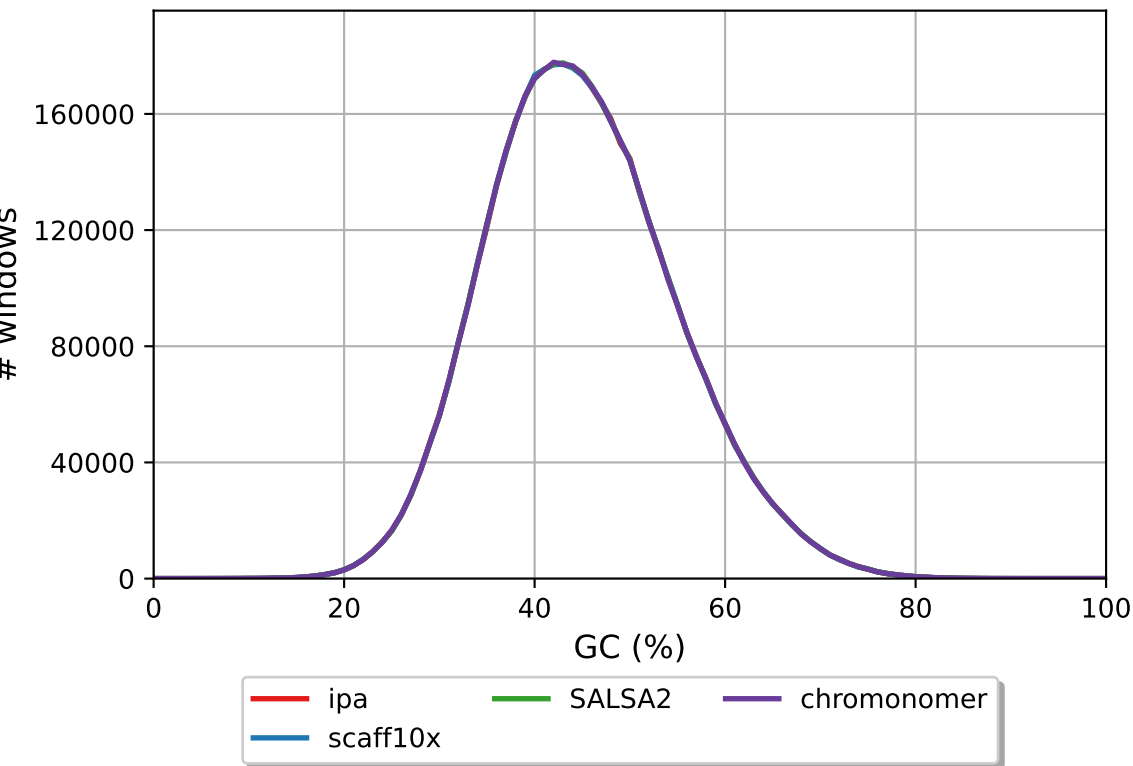
NGx



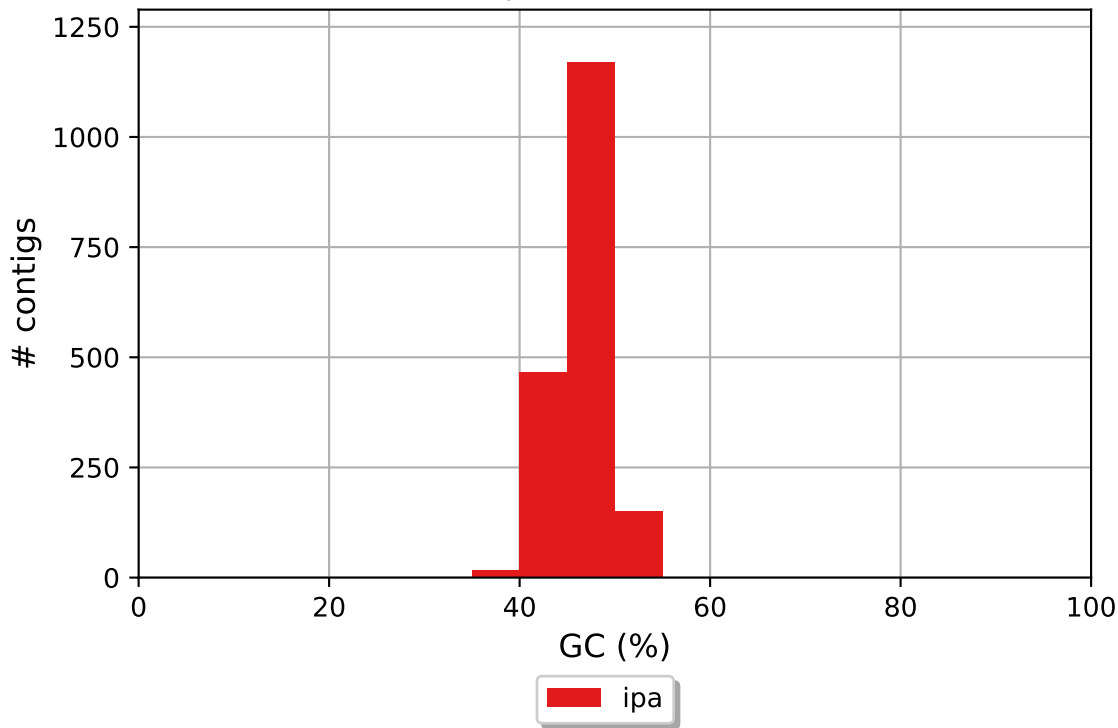
Cumulative length



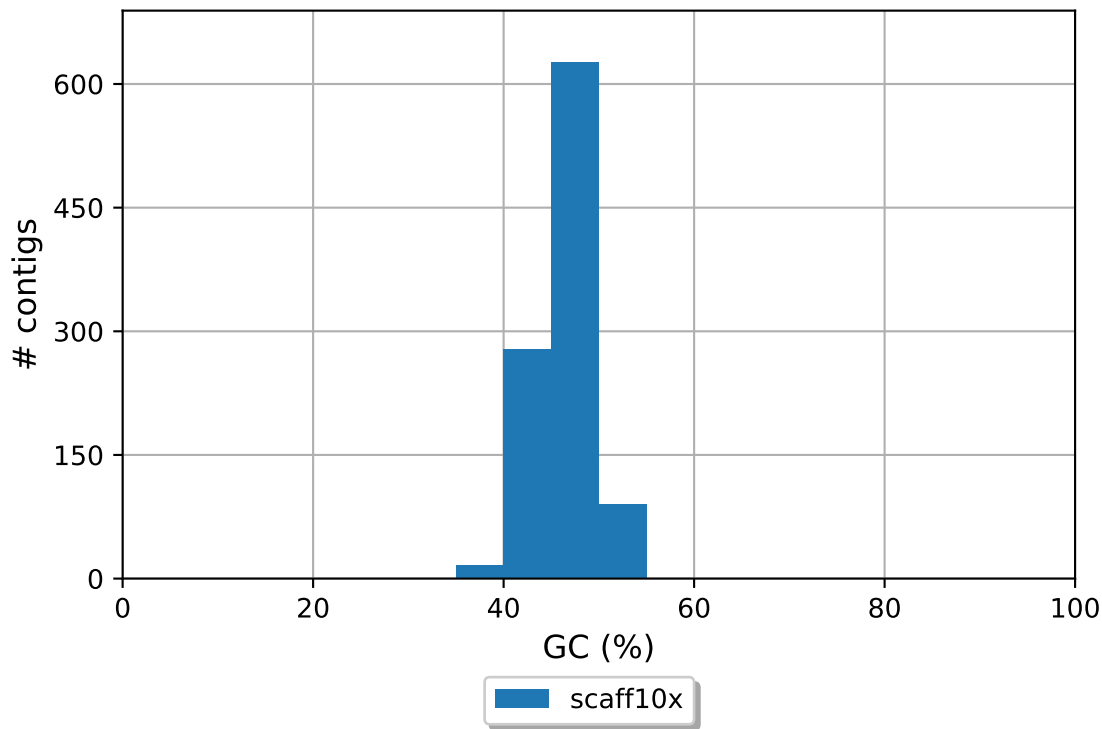
GC content



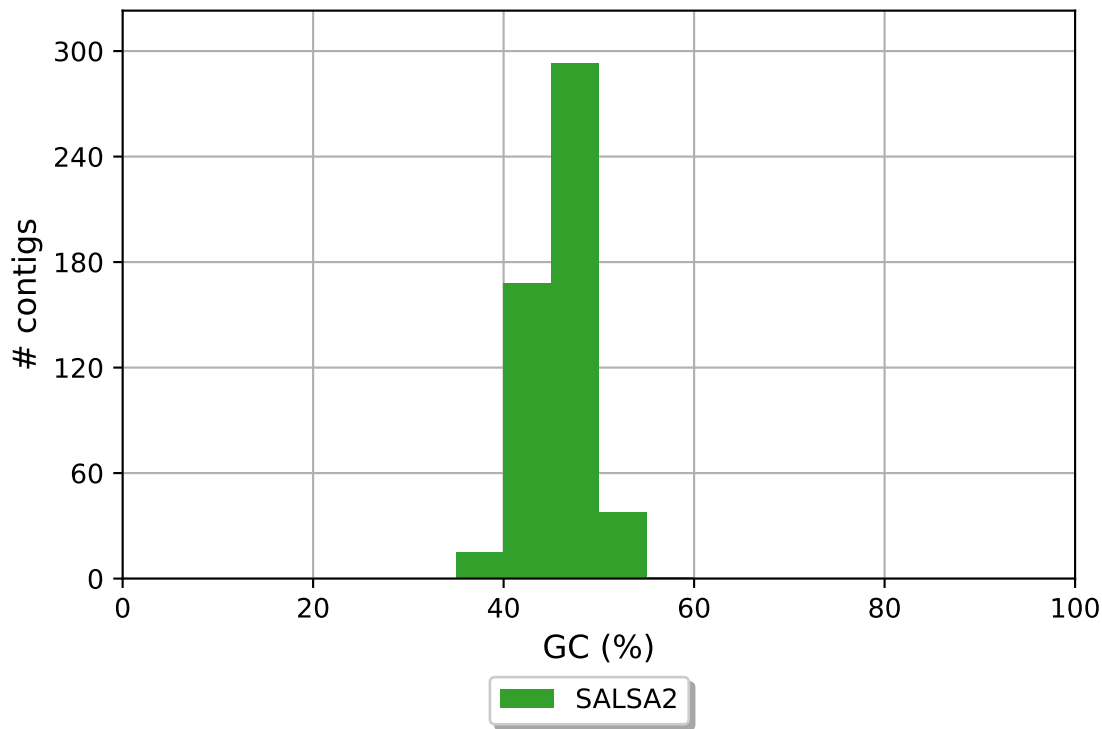
ipa GC content



scaff10x GC content



SALSA2 GC content



chromonomer GC content

