

	Report	scaff10x	SALSA2
# contigs (>= 0 bp)	1805	1012	515
# contigs (>= 1000 bp)	1805	1012	515
# contigs (>= 5000 bp)	1805	1012	515
# contigs (>= 10000 bp)	1805	1012	515
# contigs (>= 25000 bp)	1800	1007	511
# contigs (>= 50000 bp)	1773	985	500
Total length (>= 0 bp)	436920153	436999453	437264453
Total length (>= 1000 bp)	436920153	436999453	437264453
Total length (>= 5000 bp)	436920153	436999453	437264453
Total length (>= 10000 bp)	436920153	436999453	437264453
Total length (>= 25000 bp)	436829068	436908368	437187275
Total length (>= 50000 bp)	435805794	436091683	436774790
# contigs	1805	1012	515
Largest contig	3341941	12331747	18206164
Total length	436920153	436999453	437264453
Reference length	437273953	437273953	437273953
Estimated reference length	-	-	-
GC (%)	44.99	44.99	44.99
Reference GC (%)	44.99	44.99	44.99
N50	418614	1392224	4383157
NG50	417868	1392224	4383157
N90	97153	148732	403116
NG90	97000	148448	403116
auN	668619.6	2113507.9	5815293.2
auNG	668078.6	2112181.2	5815166.8
L50	264	80	26
LG50	265	80	26
L90	1171	472	172
LG90	1175	474	172
# 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	22	32	11
# misassembled contigs	21	32	10
Misassembled contigs length	12800171	97154385	99932638
# local misassemblies	3	0	0
# scaffold gap ext. mis.	0	0	0
# scaffold gap loc. mis.	0	0	519
# structural variations	-	-	-
# possible TEs	2	2	2
# unaligned mis. contigs	0	0	0
# unaligned contigs	0 + 4 part	0 + 7 part	0 + 5 part
Unaligned length	26673	36041	28075
Genome fraction (%)	99.978	99.989	99.992
Duplication ratio	1.000	1.000	1.000
Avg contig read support	-	-	-
# N's per 100 kbp	0.07	18.21	78.81
# mismatches per 100 kbp	0.04	0.00	0.00
# indels per 100 kbp	0.01	0.00	0.00
# 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	3341941	10560250	13907510
Total aligned length	436863399	436954275	436966902
NA50	415714	1237961	3609294
NGA50	415714	1237961	3609294
NA90	96221	148359	403116
NGA90	96025	147444	403116
auNA	664713.0	1833412.6	4681223.9
auNGA	664175.2	1832261.7	4681122.2
LA50	266	91	32
LGA50	266	91	32
LA90	1180	501	183
LGA90	1183	503	183
K-mer-based compl. (%)	100.00	100.00	100.00
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).

Kmers report

	ipa	scaff10x	SALSA2
K-mer-based compl. (%)	100.00	100.00	100.00
K-mer-based cor. length (%)	-	-	-
K-mer-based mis. length (%)	-	-	-
# k-mer-based misjoins	-	-	-

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

	ipa	scaff10x	SALSA2
# misassemblies	22	32	11
# contig misassemblies	22	31	0
# c. relocations	1	1	0
# c. translocations	21	30	0
# c. inversions	0	0	0
# scaffold misassemblies	0	1	11
# s. relocations	0	0	9
# s. translocations	0	1	2
# s. inversions	0	0	0
# misassembled contigs	21	32	10
Misassembled contigs length	12800171	97154385	99932638
# local misassemblies	3	0	0
# scaffold gap ext. mis.	0	0	0
# scaffold gap loc. mis.	0	0	519
# structural variations	-	-	-
# possible TEs	2	2	2
# unaligned mis. contigs	0	0	0
# mismatches	169	8	8
# indels	55	1	0
# indels (<= 5 bp)	52	0	0
# indels (> 5 bp)	3	1	0
Indels length	216	100	0

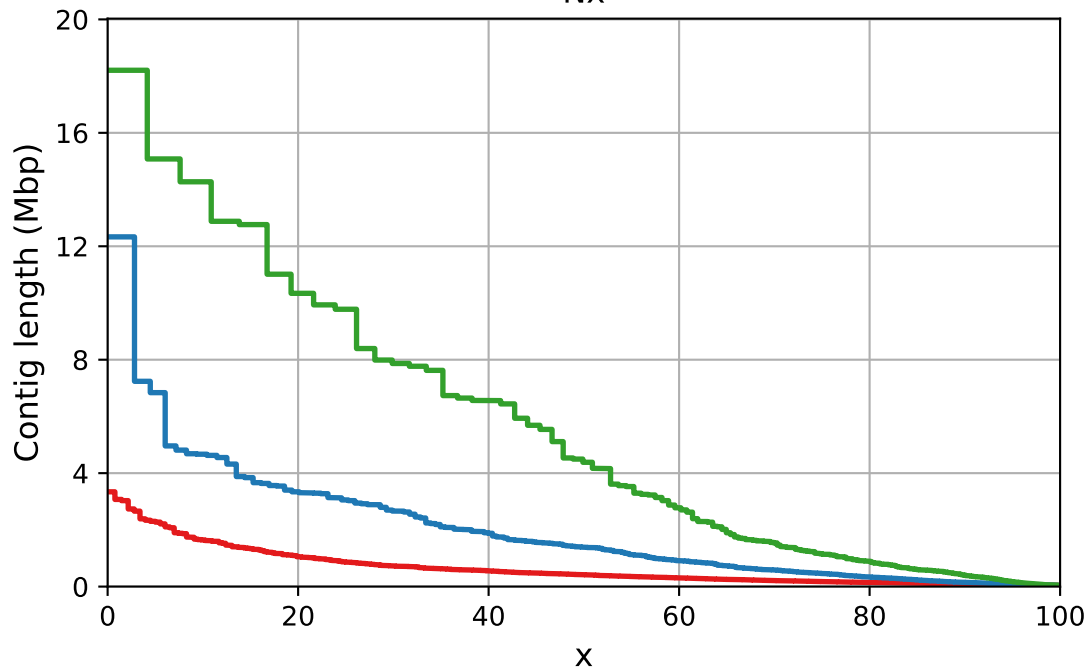
All statistics are based on contigs of size ≥ 3000 bp, unless otherwise noted (e.g., "# contigs (≥ 0 bp)" and "Total length (≥ 0 bp)" include all contigs).

Unaligned report

	ipa	scaff10x	SALSA2
# fully unaligned contigs	0	0	0
Fully unaligned length	0	0	0
# partially unaligned contigs	4	7	5
Partially unaligned length	26673	36041	28075
# N's	299	79599	344599

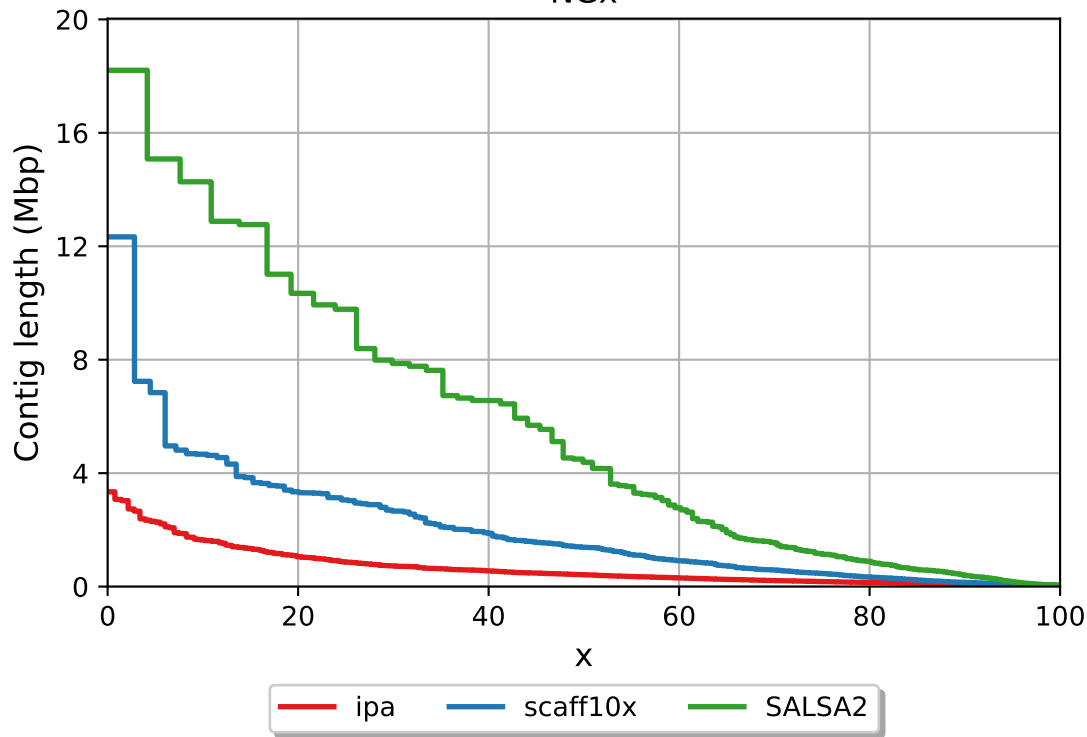
All statistics are based on contigs of size ≥ 3000 bp, unless otherwise noted (e.g., "# contigs (≥ 0 bp)" and "Total length (≥ 0 bp)" include all contigs).

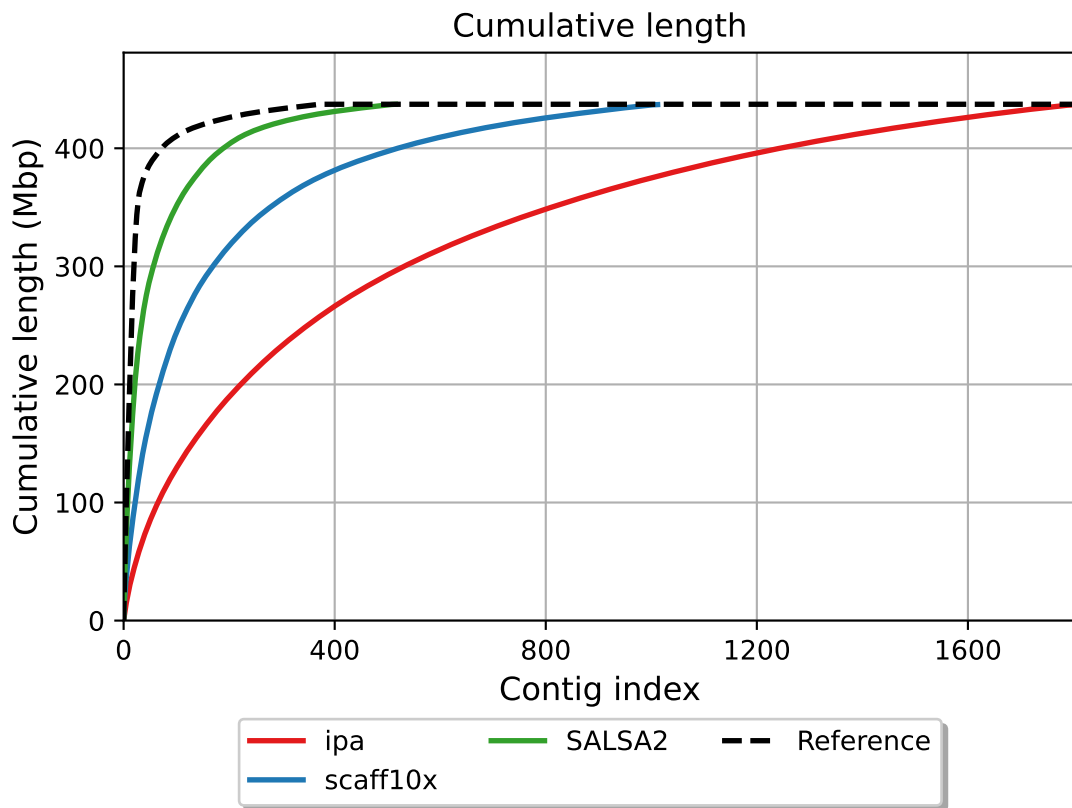
Nx



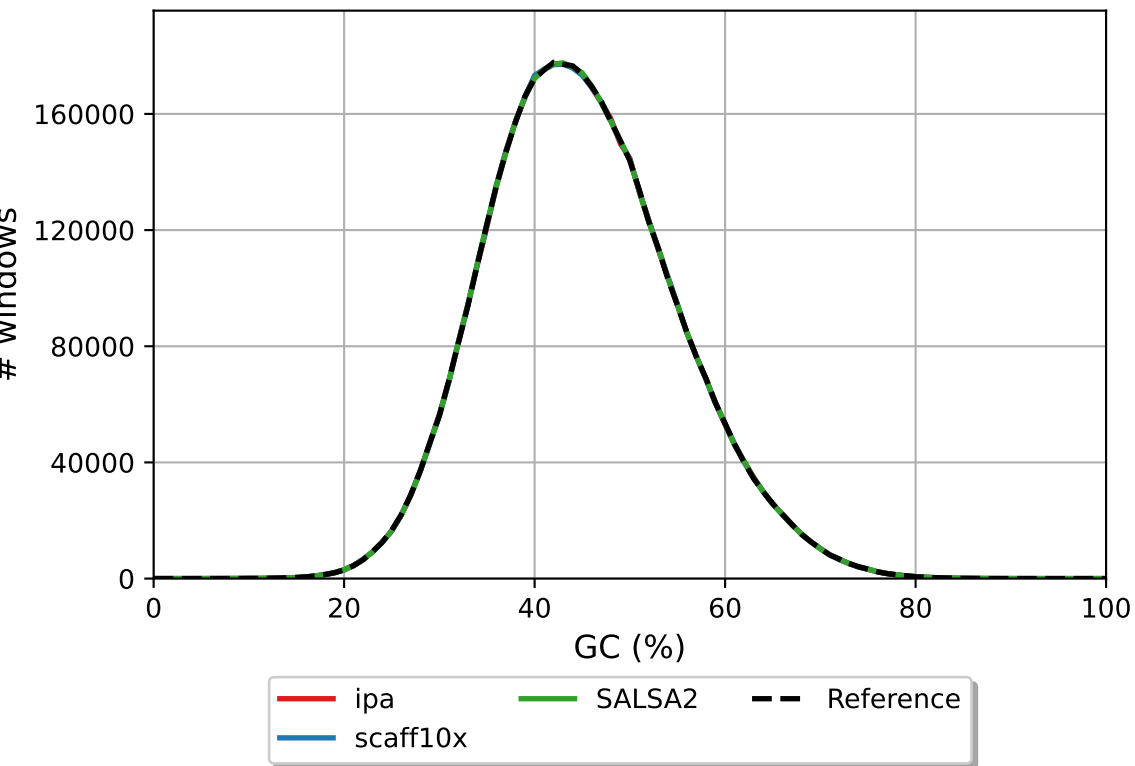
— ipa — scaff10x — SALSA2

NGx

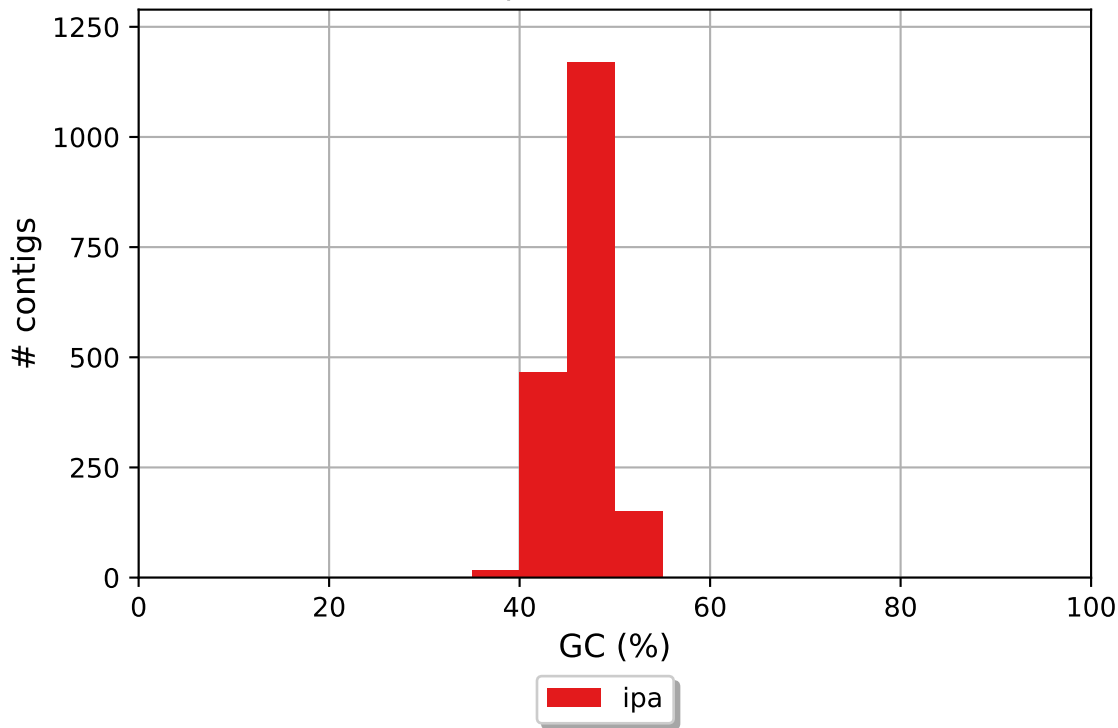




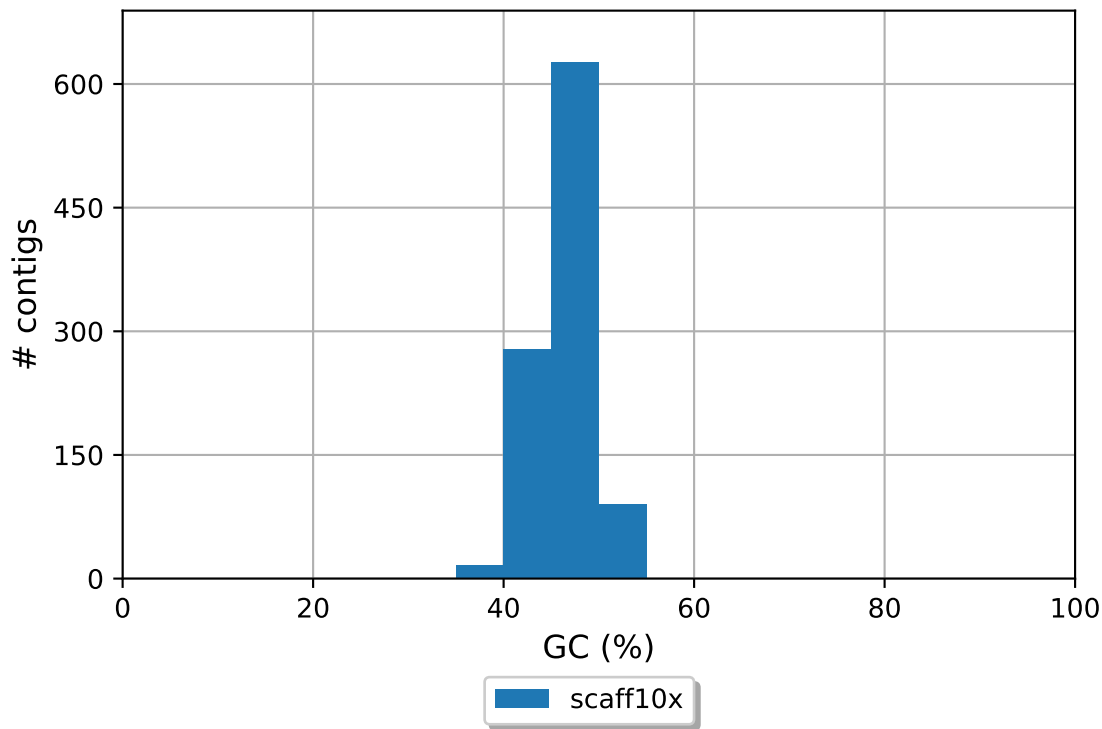
GC content



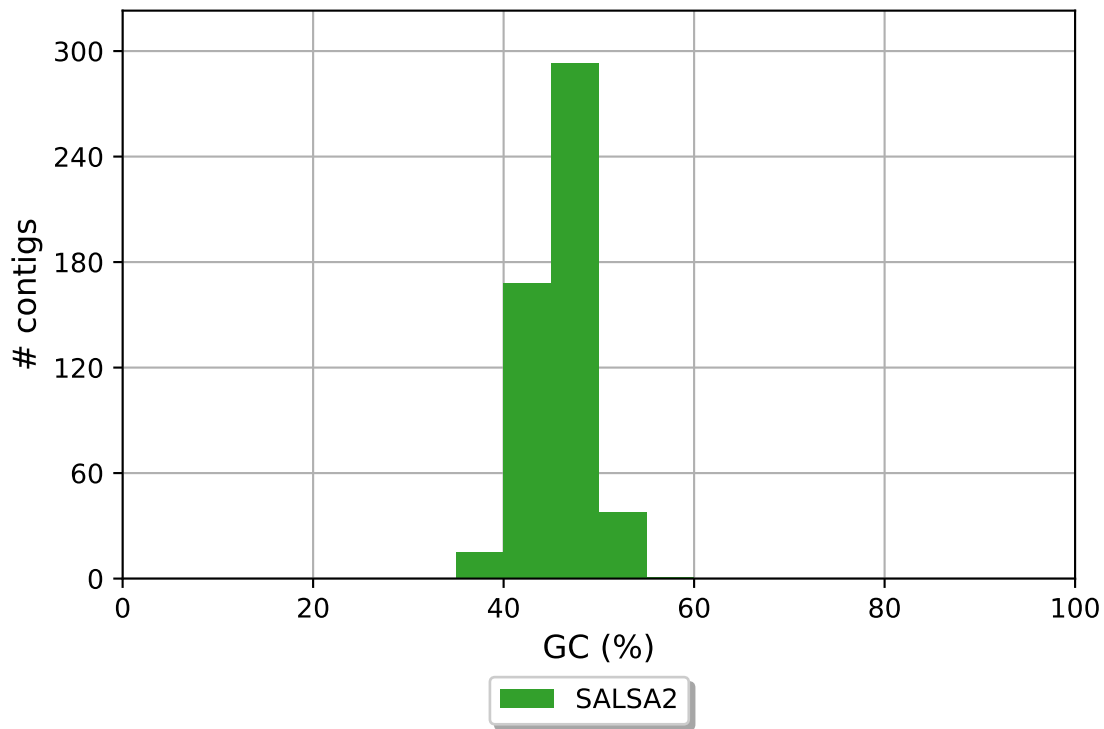
ipa GC content



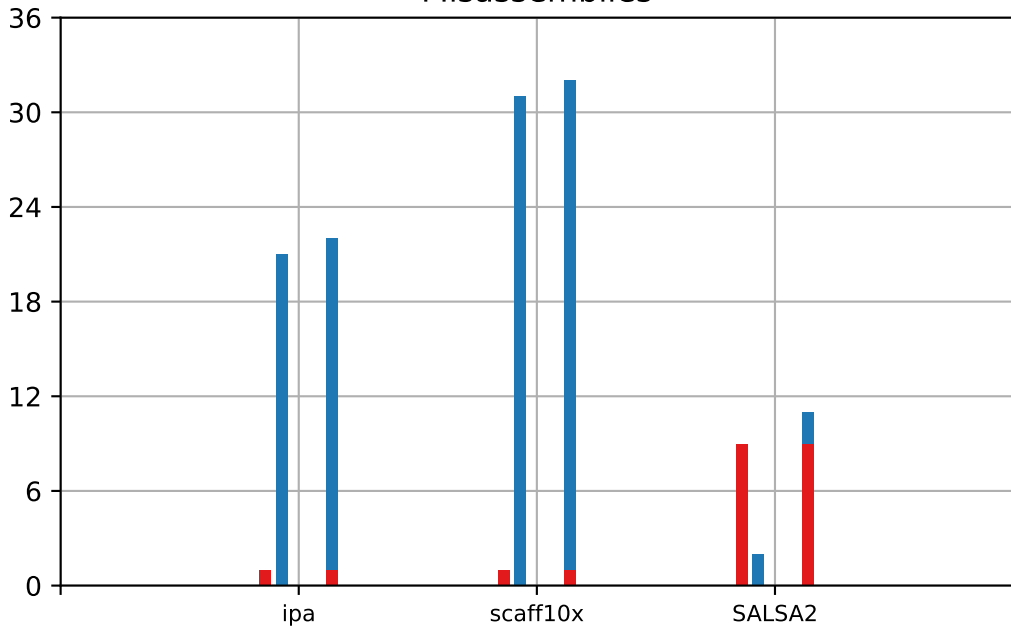
scaff10x GC content



SALSA2 GC content



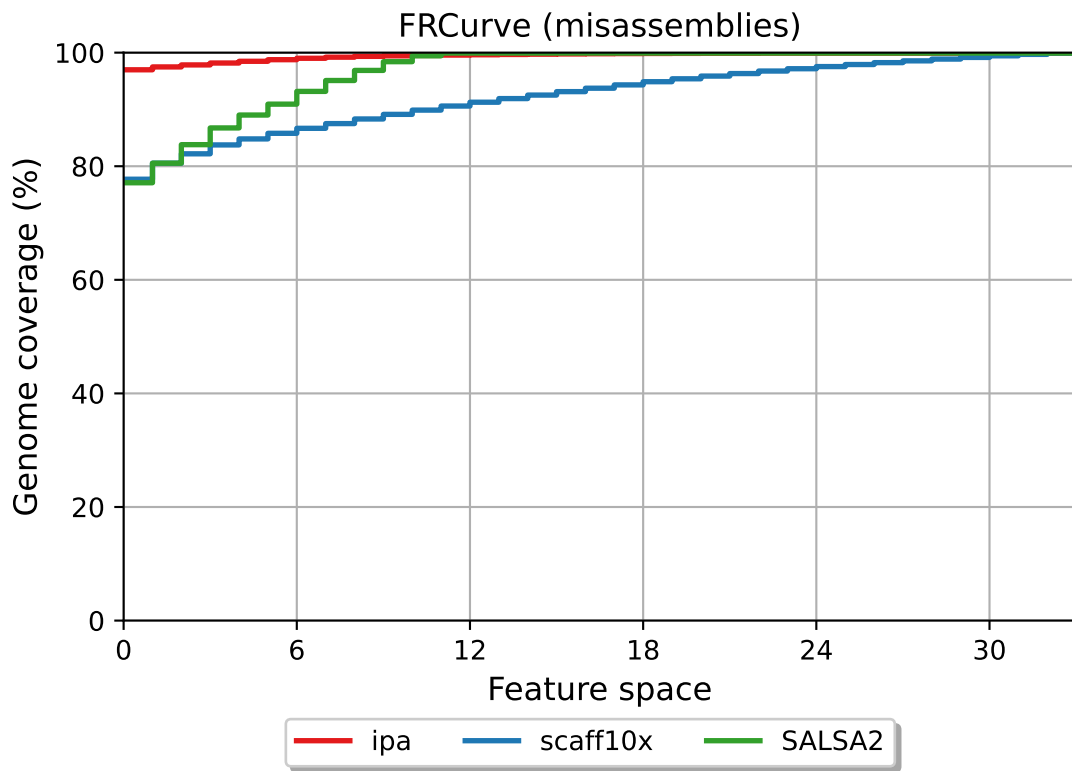
Misassemblies



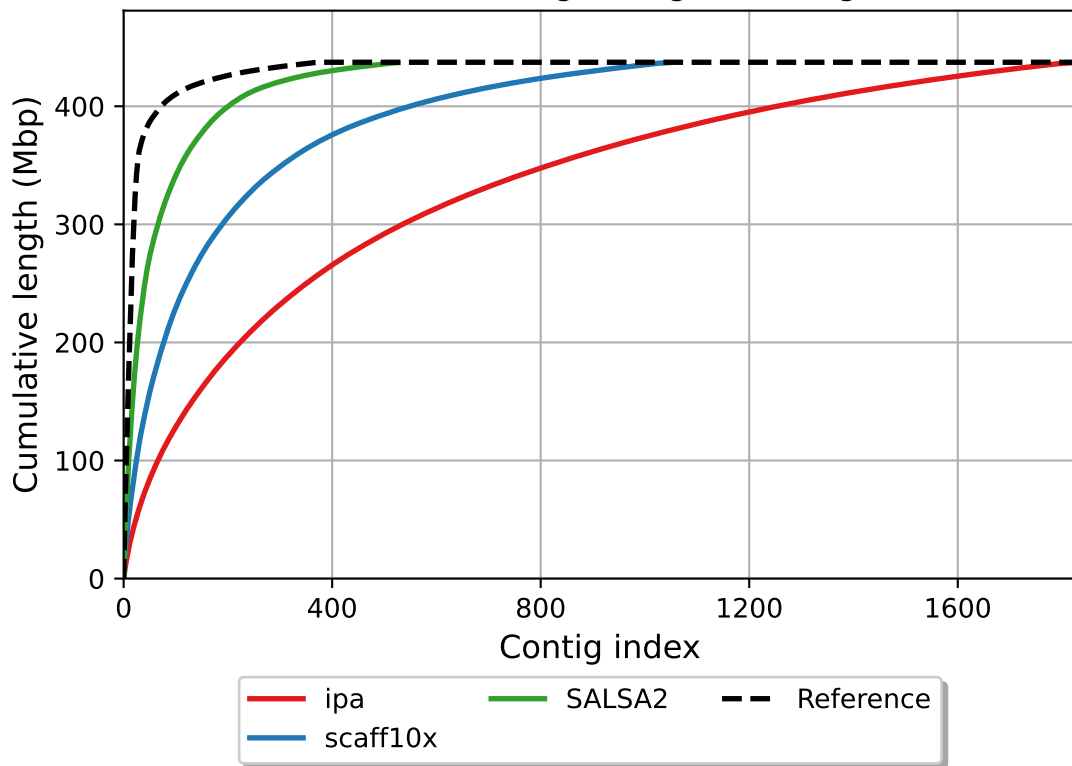
relocations



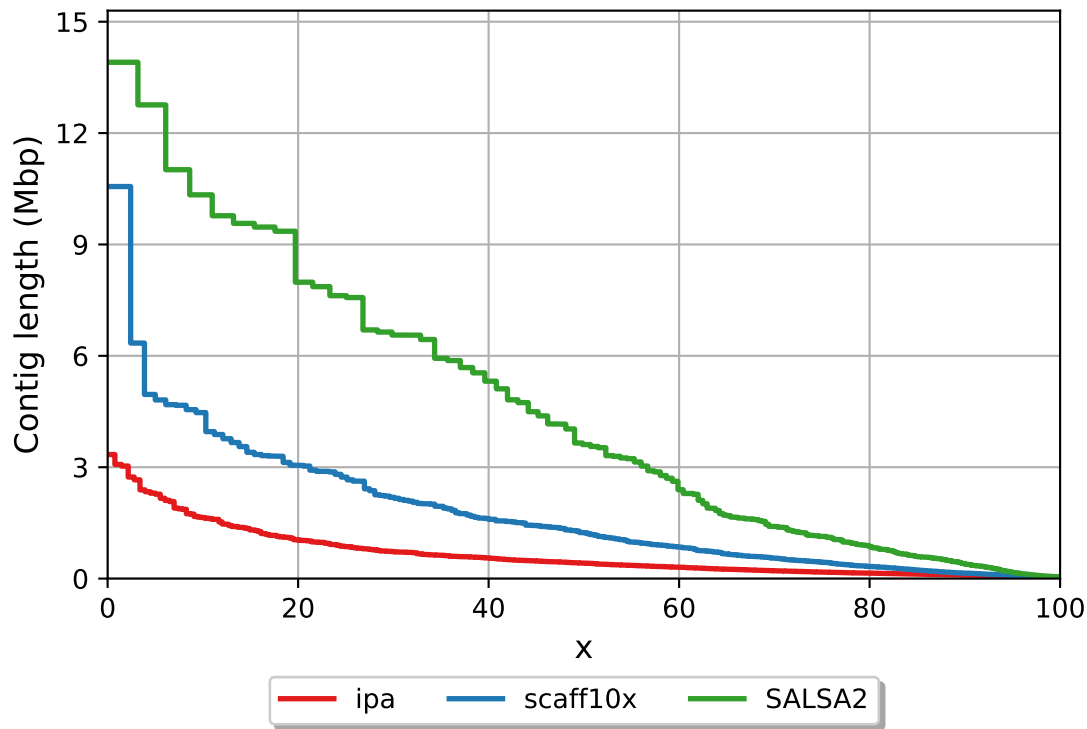
translocations



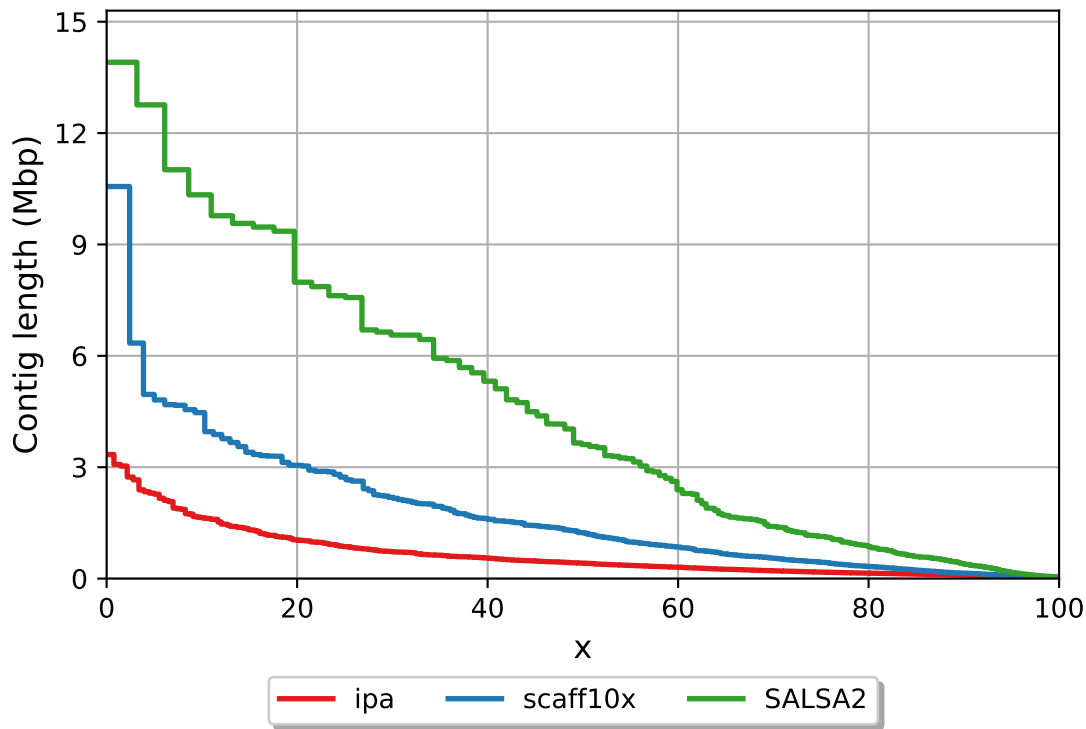
Cumulative length (aligned contigs)



NAx



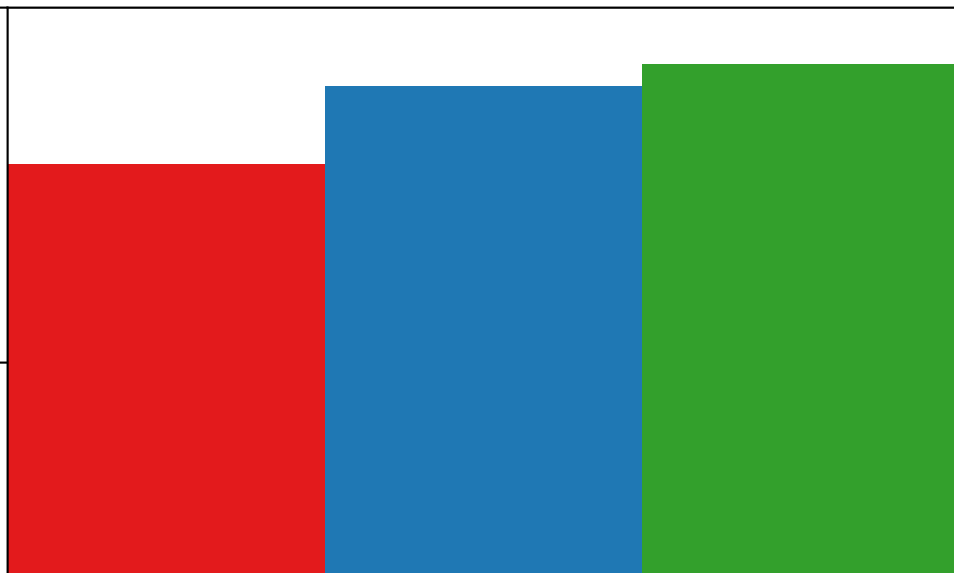
NGAx



Genome fraction, %

100.00

99.95



ipa

scaff10x

SALSA2