Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/30 12:15:38

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR975241.sorted.bam -c -nw 400 -hm 3
```

1.2. Alignment

Command line:	/home/luna/Desktop/Software/bwa/bwa mem -t 16 -k 30 -R @RG\tID:Singlecell2022\tLB:Library\tPL:ILLUMINA\tSM:sample_SRR975241 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR975241_1.fastq.gz SRR975241_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Fri Aug 30 12:15:22 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR975241.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	2,359,882
Mapped reads	2,333,452 / 98.88%
Unmapped reads	26,430 / 1.12%
Mapped paired reads	2,333,452 / 98.88%
Mapped reads, first in pair	1,166,571 / 49.43%
Mapped reads, second in pair	1,166,881 / 49.45%
Mapped reads, both in pair	2,324,706 / 98.51%
Mapped reads, singletons	8,746 / 0.37%
Secondary alignments	0
Supplementary alignments	9,592 / 0.41%
Read min/max/mean length	30 / 101 / 101.16
Duplicated reads (estimated)	96,604 / 4.09%
Duplication rate	2.33%
Clipped reads	1,461,414 / 61.93%

2.2. ACGT Content

Number/percentage of A's	62,118,679 / 29.19%
Number/percentage of C's	40,185,445 / 18.88%
Number/percentage of T's	65,424,598 / 30.75%
Number/percentage of G's	45,060,696 / 21.18%
Number/percentage of N's	2,848 / 0%

GC Percentage	40.06%

2.3. Coverage

Mean	0.0688
Standard Deviation	0.7642

2.4. Mapping Quality

Mean Mapping Quality	52.87

2.5. Insert size

Mean	39,975.66
Standard Deviation	1,878,842.51
P25/Median/P75	138 / 170 / 214

2.6. Mismatches and indels

General error rate	0.83%
Mismatches	1,692,430
Insertions	36,398
Mapped reads with at least one insertion	1.52%
Deletions	69,601
Mapped reads with at least one deletion	2.92%
Homopolymer indels	45.78%

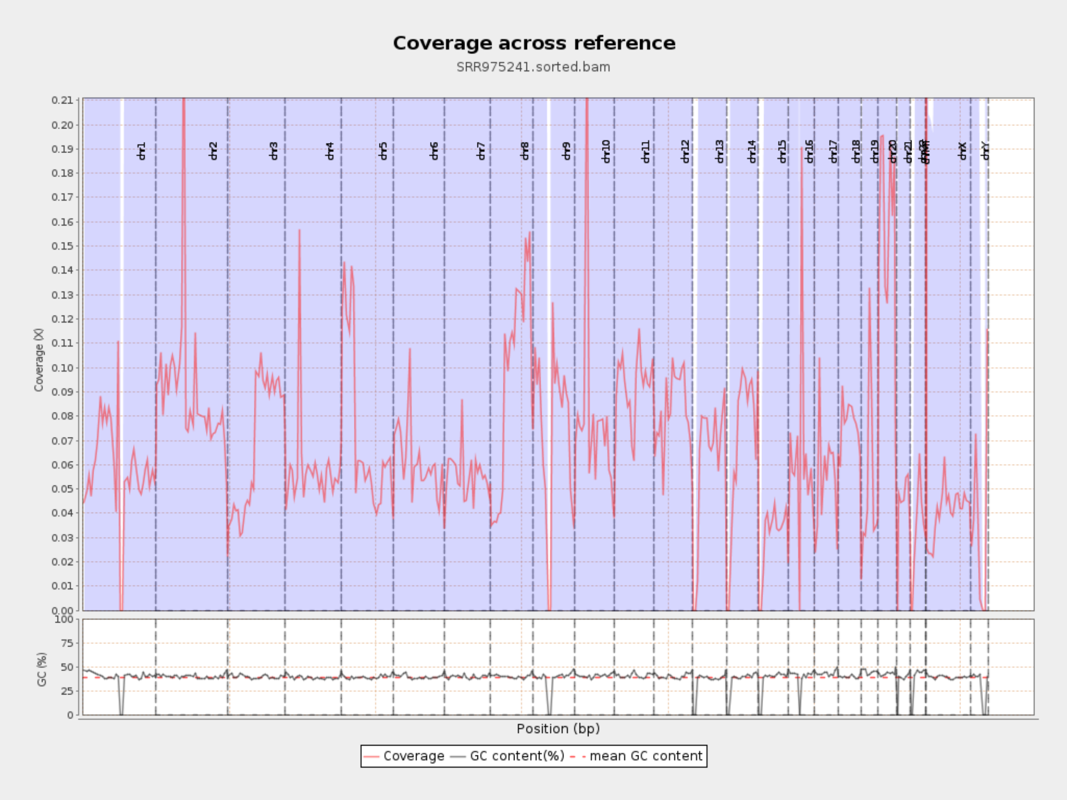
2.7. Chromosome stats

Name	**Length**	**Mapped**	**Mean**	**Standard**

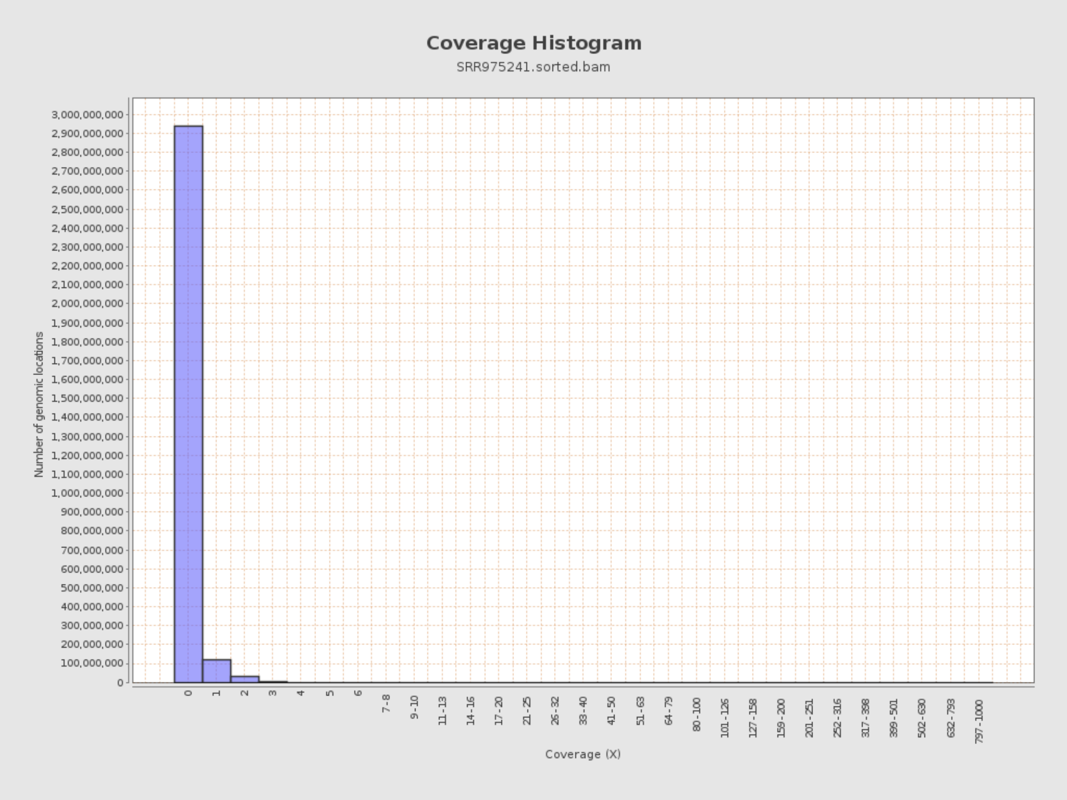
		bases	coverage	deviation
chr1	249250621	14514114	0.0582	1.023
chr2	243199373	22312588	0.0917	1.1575
chr3	198022430	13522435	0.0683	0.3273
chr4	191154276	11227772	0.0587	0.7031
chr5	180915260	13227475	0.0731	0.3346
chr6	171115067	10670470	0.0624	0.4367
chr7	159138663	8867394	0.0557	0.6671
chr8	146364022	14143527	0.0966	0.4861
chr9	141213431	10554343	0.0747	1.2969
chr10	135534747	10837824	0.08	1.4085
chr11	135006516	12429983	0.0921	0.5828
chr12	133851895	11047860	0.0825	0.3502
chr13	115169878	7110496	0.0617	0.2989
chr14	107349540	7370435	0.0687	0.3569
chr15	102531392	3103112	0.0303	0.2086
chr16	90354753	5625865	0.0623	0.9645
chr17	81195210	4515769	0.0556	0.9666
chr18	78077248	6000155	0.0768	1.096
chr19	59128983	3186257	0.0539	0.5035
chr20	63025520	10255359	0.1627	0.5335
chr21	48129895	2081520	0.0432	0.3147
chr22	51304566	1688366	0.0329	0.2305
chrMT	16571	86972	5.2484	4.2674
chrX	155270560	6299305	0.0406	0.321

chrY	59373566	2235822	0.0377	0.7963

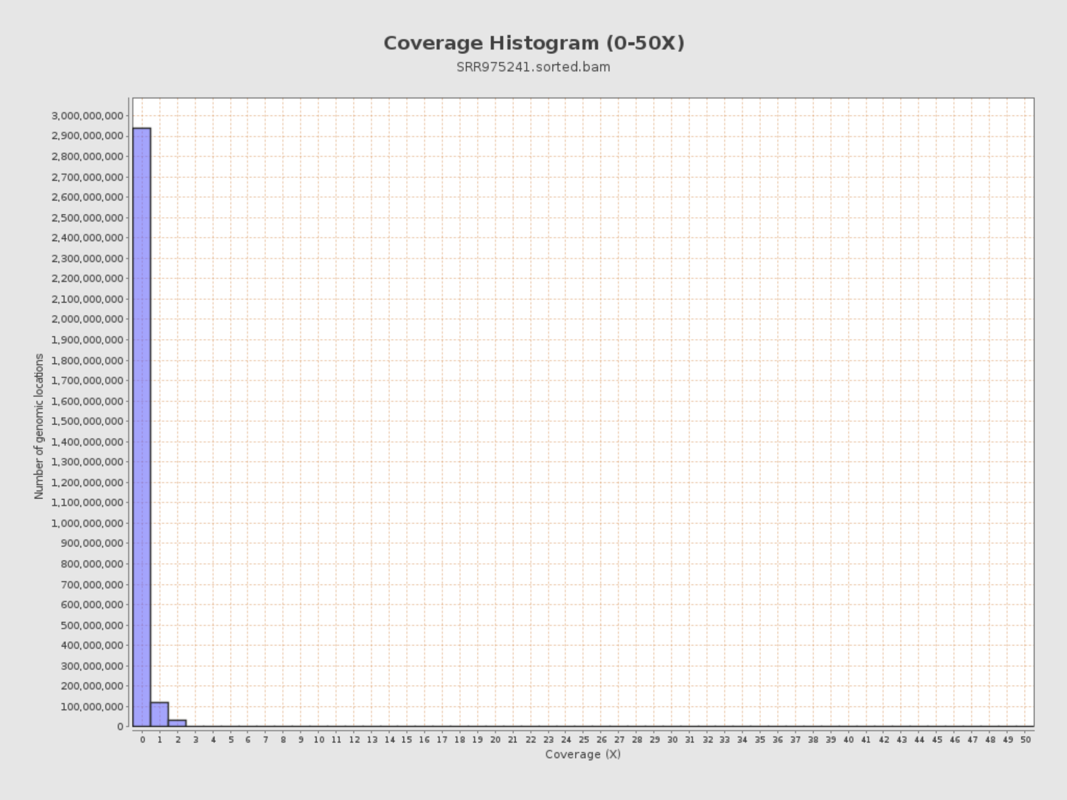
3. Results : Coverage across reference



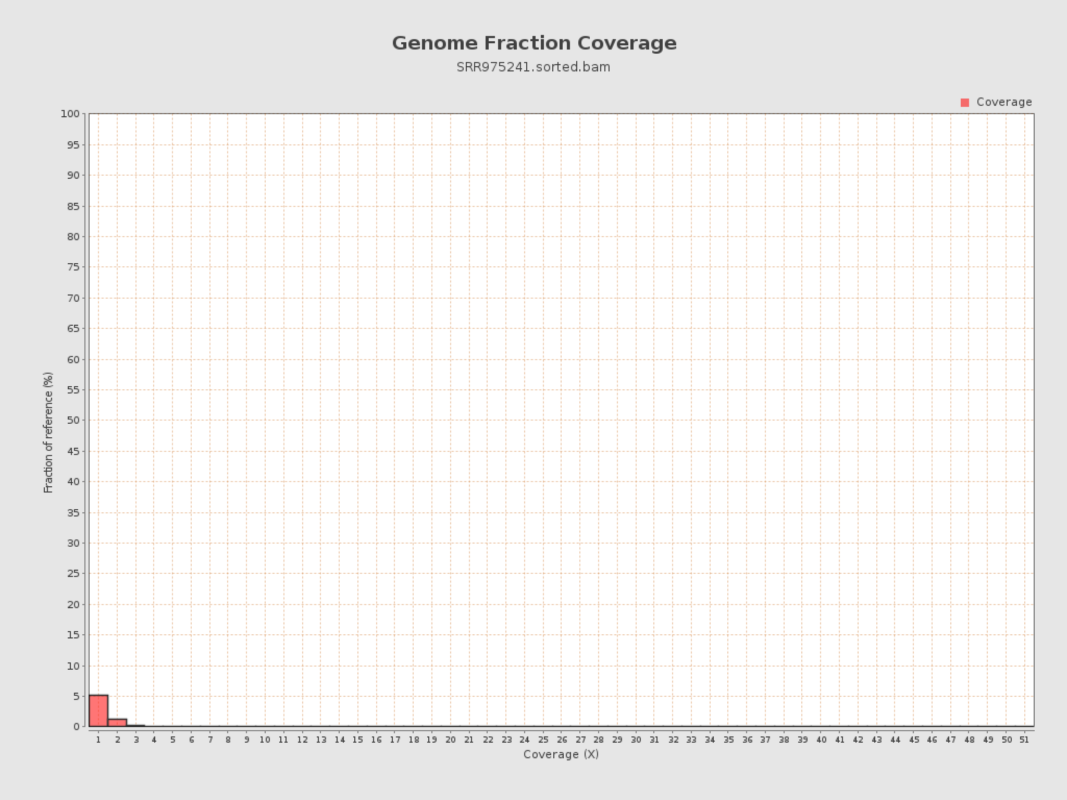
4. Results : Coverage Histogram



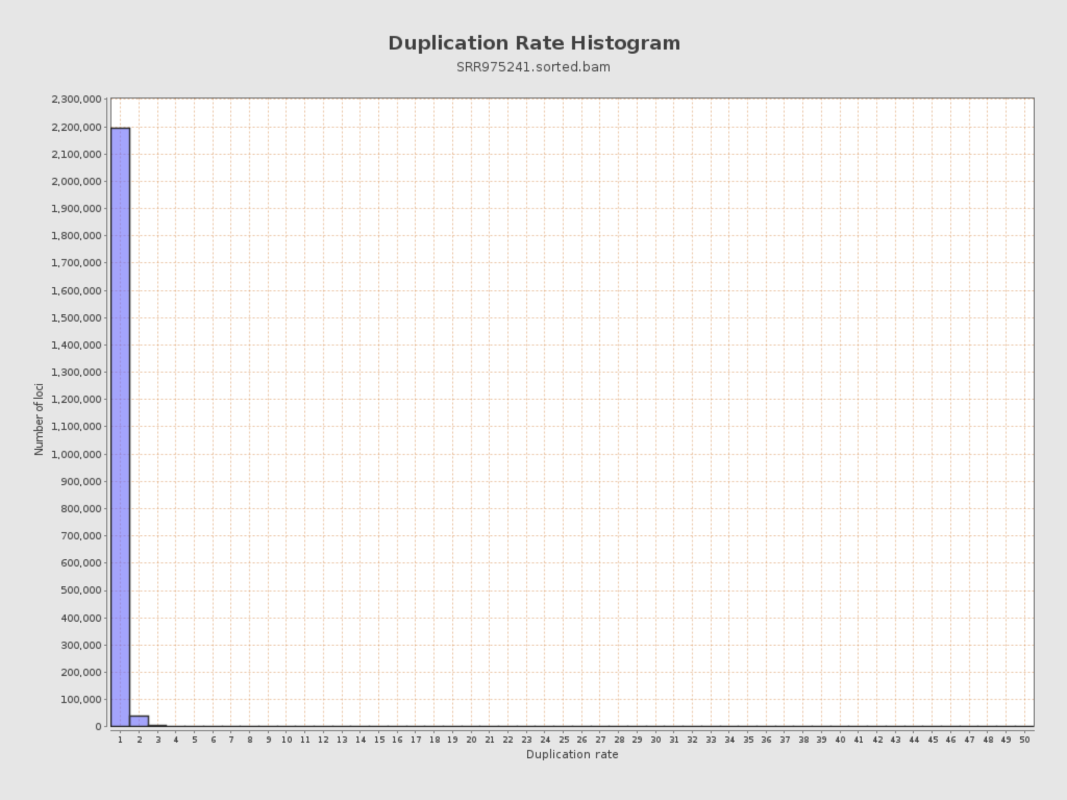
5. Results : Coverage Histogram (0-50X)



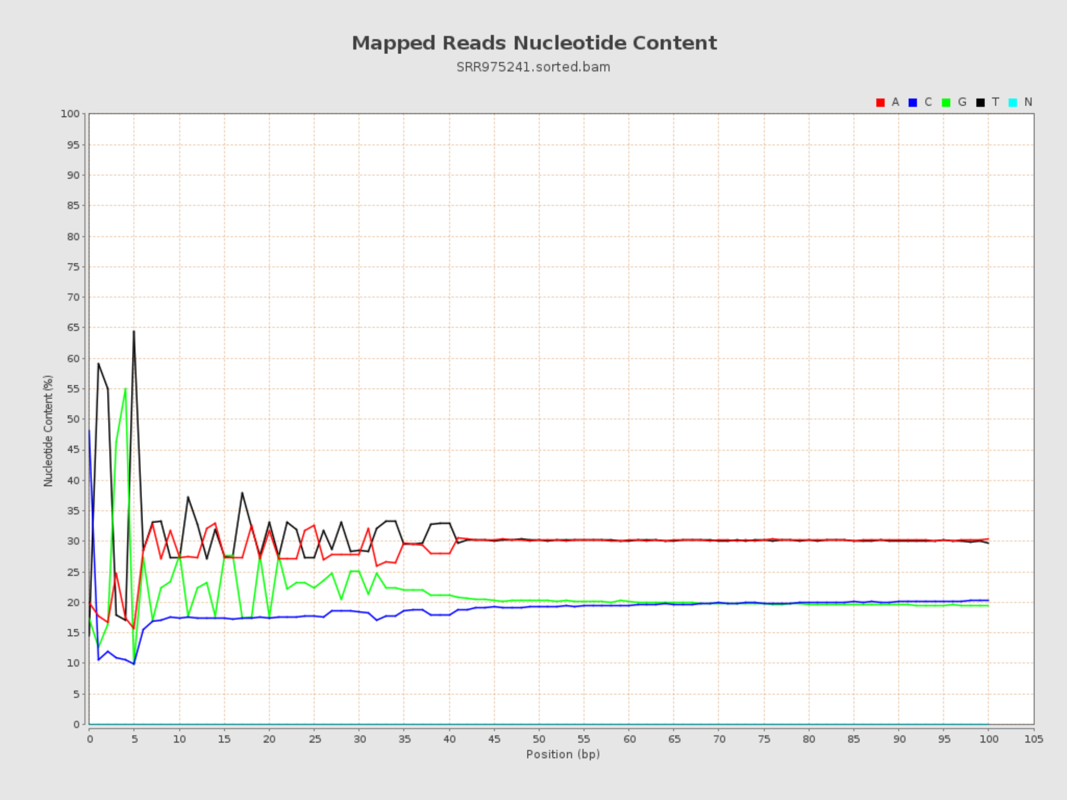
6. Results : Genome Fraction Coverage



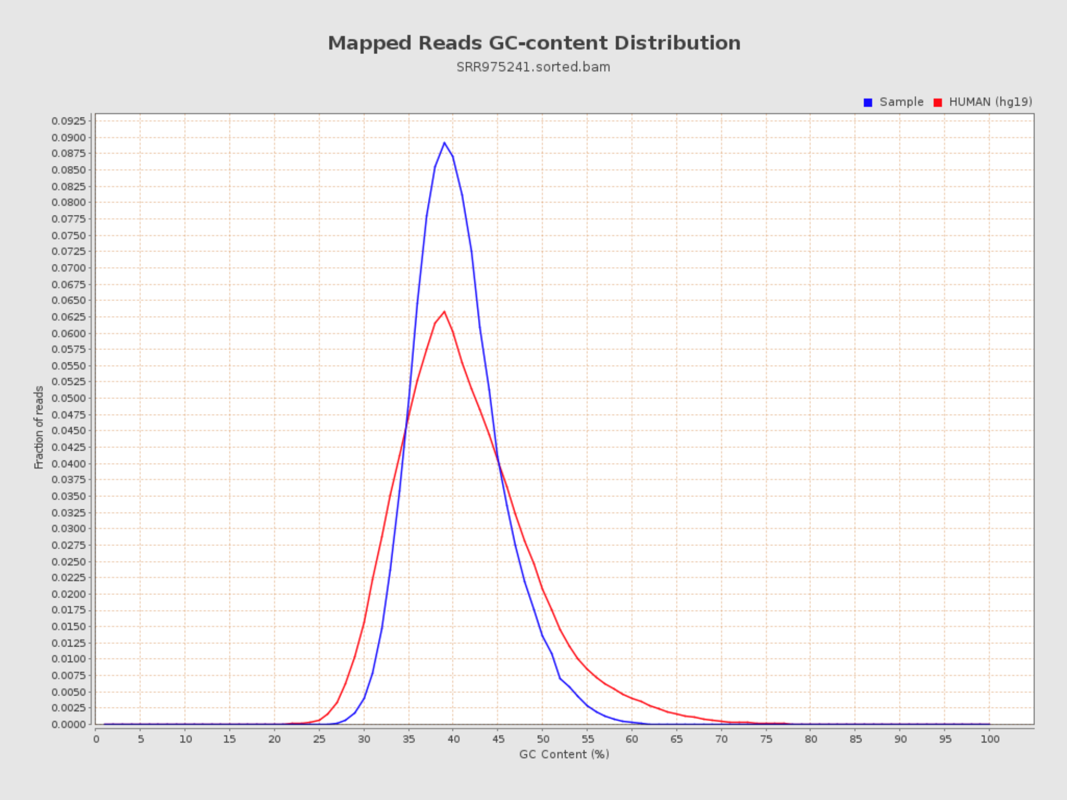
7. Results : Duplication Rate Histogram



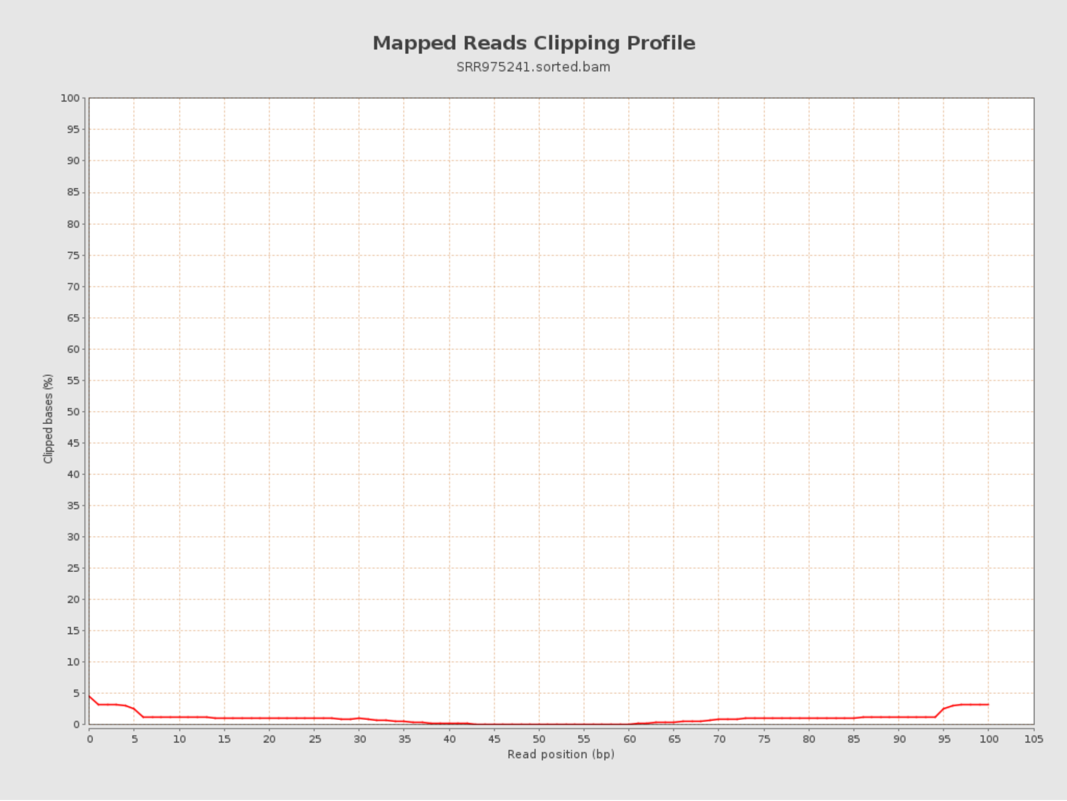
8. Results : Mapped Reads Nucleotide Content



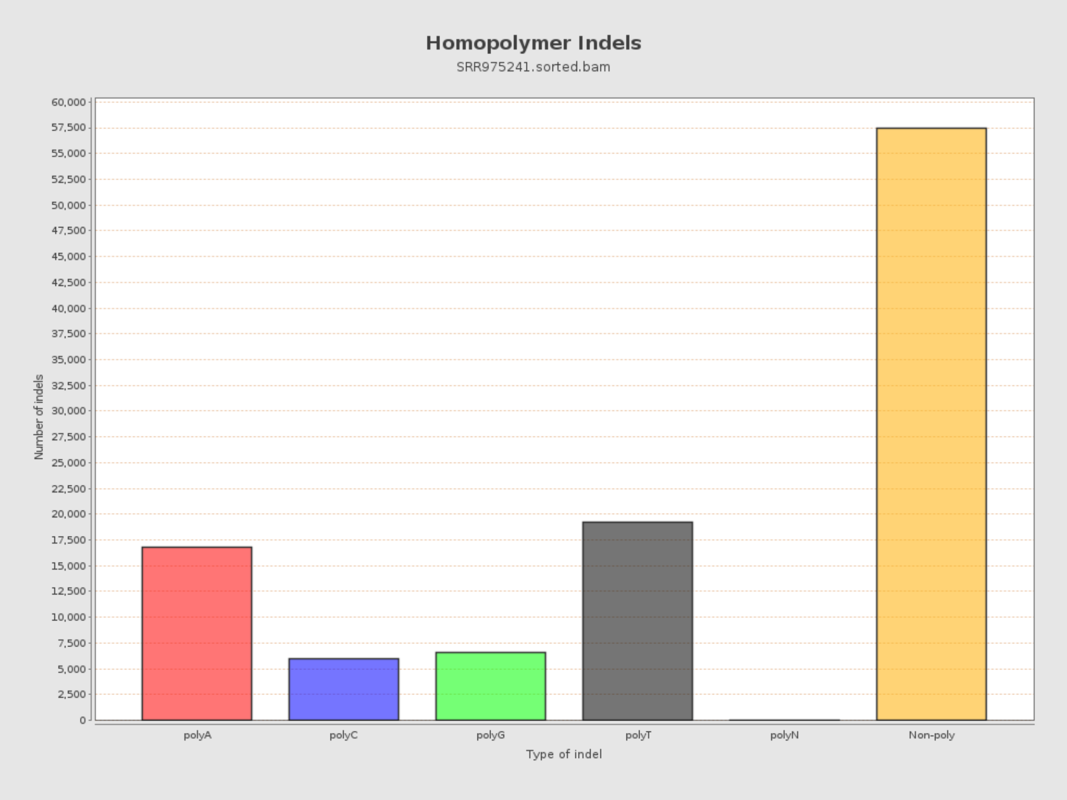
9. Results : Mapped Reads GC-content Distribution



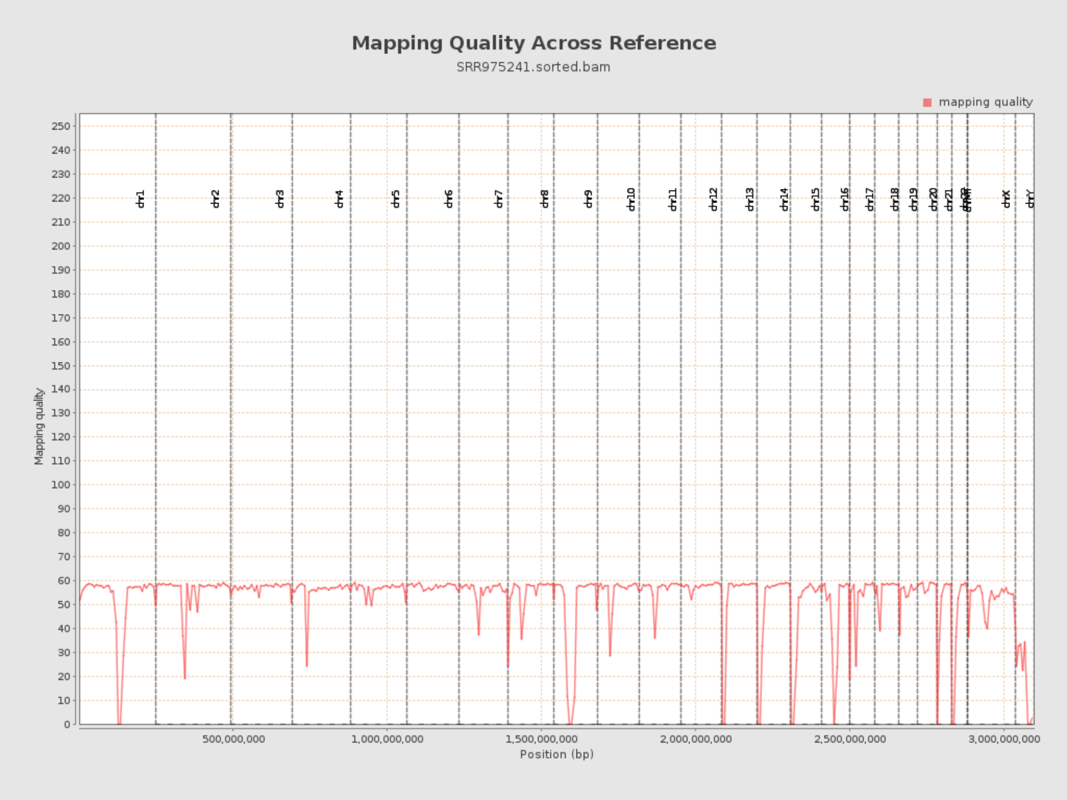
10. Results : Mapped Reads Clipping Profile



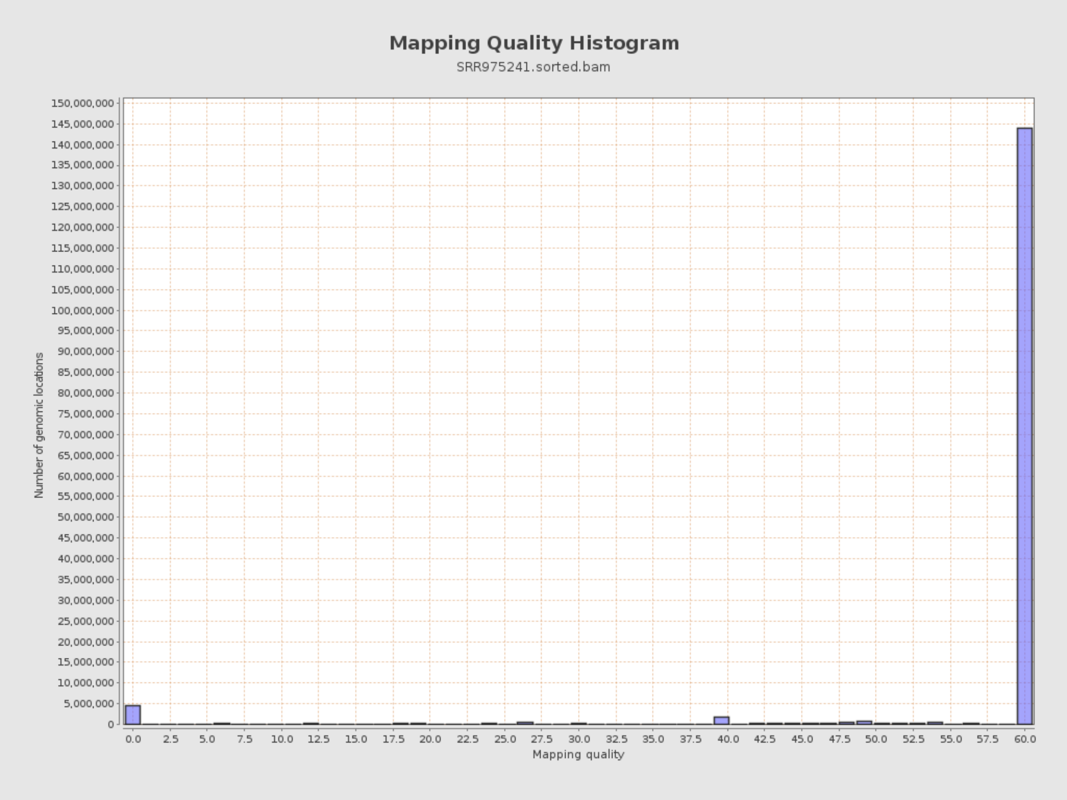
11. Results : Homopolymer Indels



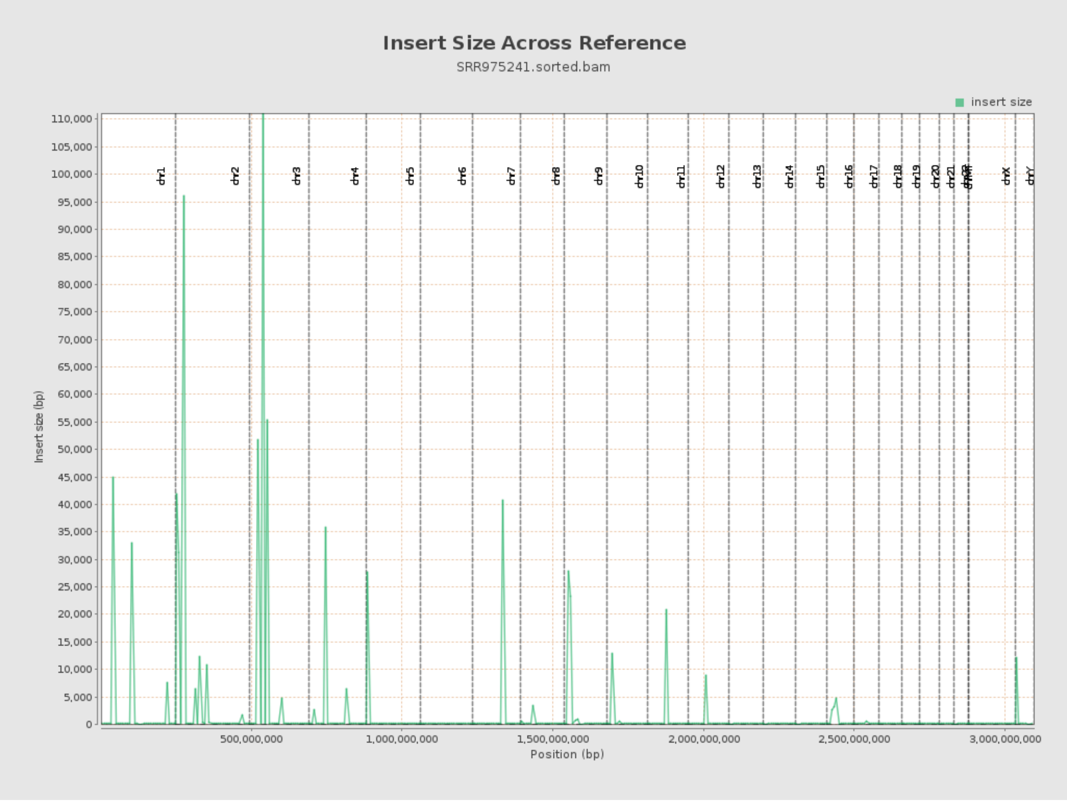
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram