Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/06 23:42:39

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR975300.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_SRR975300 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR975300_1.fastq.gz SRR975300_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Fri Sep 06 23:42:38 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR975300.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	2,254,124
Mapped reads	2,222,281 / 98.59%
Unmapped reads	31,843 / 1.41%
Mapped paired reads	2,222,281 / 98.59%
Mapped reads, first in pair	1,113,045 / 49.38%
Mapped reads, second in pair	1,109,236 / 49.21%
Mapped reads, both in pair	2,213,972 / 98.22%
Mapped reads, singletons	8,309 / 0.37%
Secondary alignments	0
Supplementary alignments	34,009 / 1.51%
Read min/max/mean length	30 / 151 / 151.71
Duplicated reads (estimated)	379,581 / 16.84%
Duplication rate	15.73%
Clipped reads	1,655,763 / 73.45%

2.2. ACGT Content

Number/percentage of A's	86,965,993 / 29.48%
Number/percentage of C's	58,315,329 / 19.77%
Number/percentage of T's	87,329,280 / 29.6%
Number/percentage of G's	62,400,135 / 21.15%
Number/percentage of N's	17,269 / 0.01%

GC Percentage	40.92%

2.3. Coverage

Mean	0.0954
Standard Deviation	1.2573

2.4. Mapping Quality

Mean Mapping Quality	53.28

2.5. Insert size

Mean	88,385.69
Standard Deviation	2,806,098.08
P25/Median/P75	134 / 167 / 214

2.6. Mismatches and indels

General error rate	1.05%
Mismatches	2,924,703
Insertions	61,373
Mapped reads with at least one insertion	2.56%
Deletions	99,817
Mapped reads with at least one deletion	4.28%
Homopolymer indels	44.43%

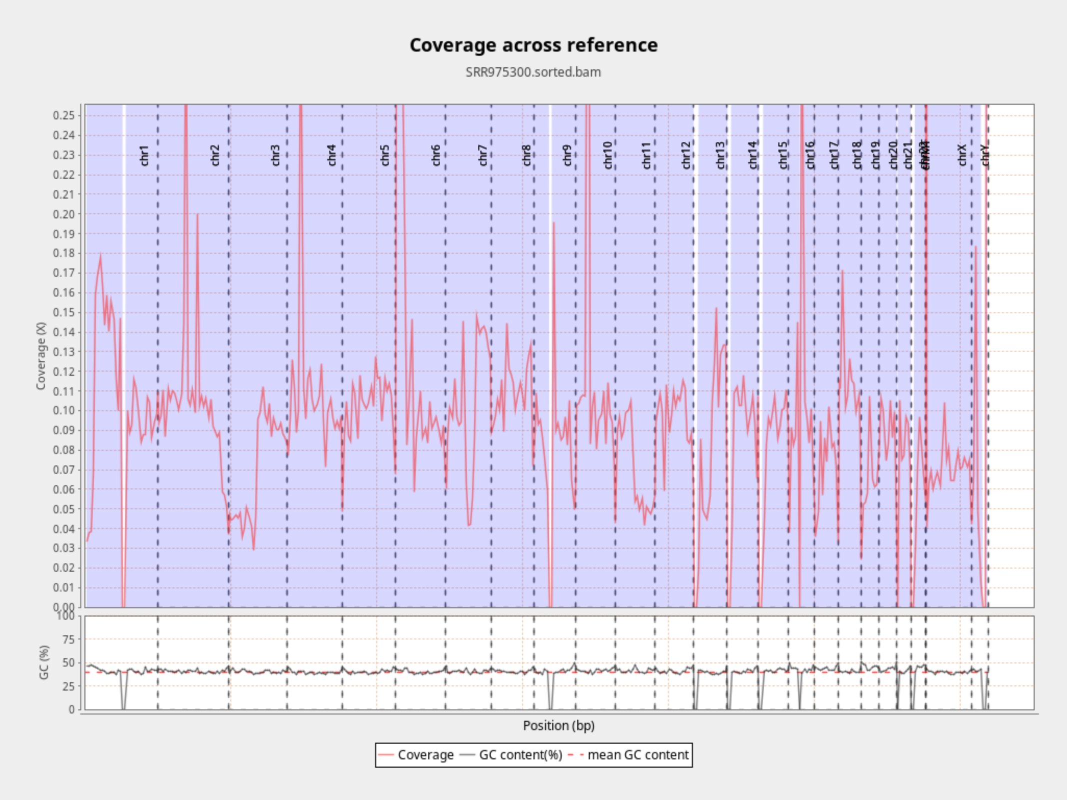
2.7. Chromosome stats

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

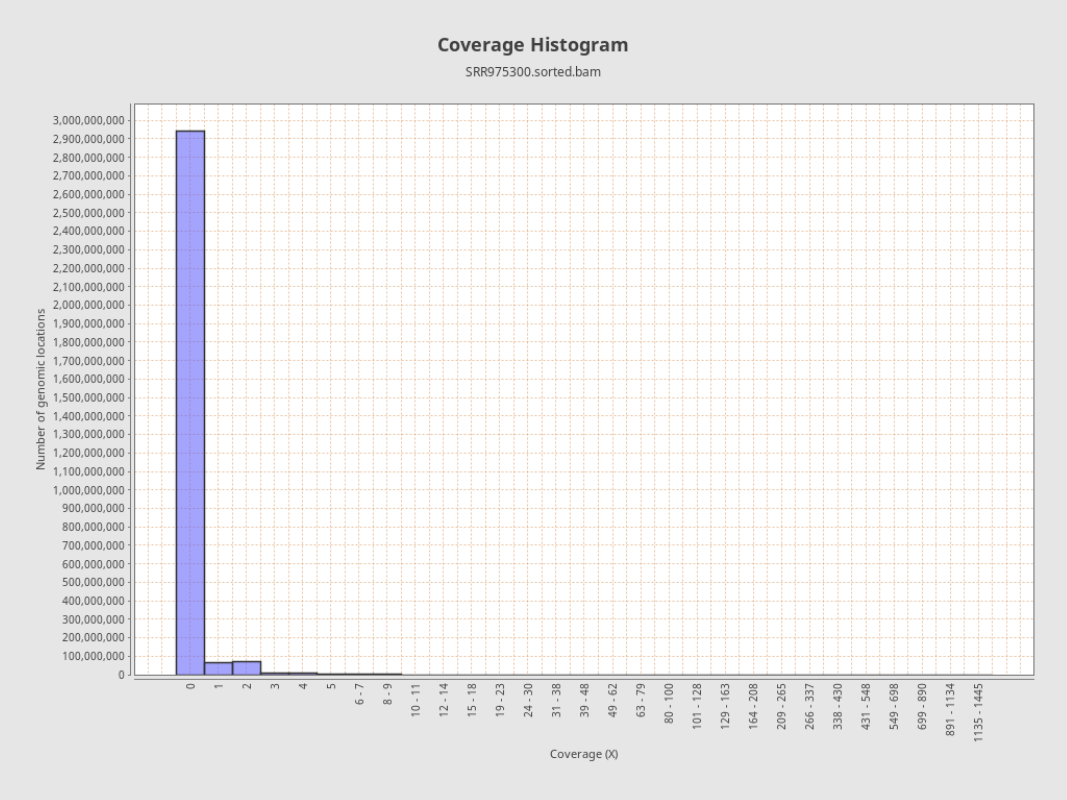
		bases	coverage	deviation
chr1	249250621	25821568	0.1036	0.9625
chr2	243199373	26128257	0.1074	1.7182
chr3	198022430	13839508	0.0699	0.3978
chr4	191154276	21032303	0.11	1.3127
chr5	180915260	18853374	0.1042	0.4793
chr6	171115067	22582583	0.132	0.8175
chr7	159138663	16410061	0.1031	1.057
chr8	146364022	16091956	0.1099	0.6457
chr9	141213431	11530551	0.0817	2.1354
chr10	135534747	16443843	0.1213	2.8841
chr11	135006516	9459893	0.0701	0.722
chr12	133851895	13057000	0.0975	0.4602
chr13	115169878	9275133	0.0805	0.4193
chr14	107349540	8946789	0.0833	0.4579
chr15	102531392	8098159	0.079	0.4128
chr16	90354753	9310394	0.103	1.6612
chr17	81195210	5817464	0.0716	0.8973
chr18	78077248	9000921	0.1153	1.9609
chr19	59128983	3766006	0.0637	0.6942
chr20	63025520	5642495	0.0895	0.6423
chr21	48129895	3814814	0.0793	0.7974
chr22	51304566	2774218	0.0541	0.3568
chrMT	16571	74300	4.4837	4.3501
chrX	155270560	11010514	0.0709	0.4759

chrY	59373566	6477382	0.1091	2.9459

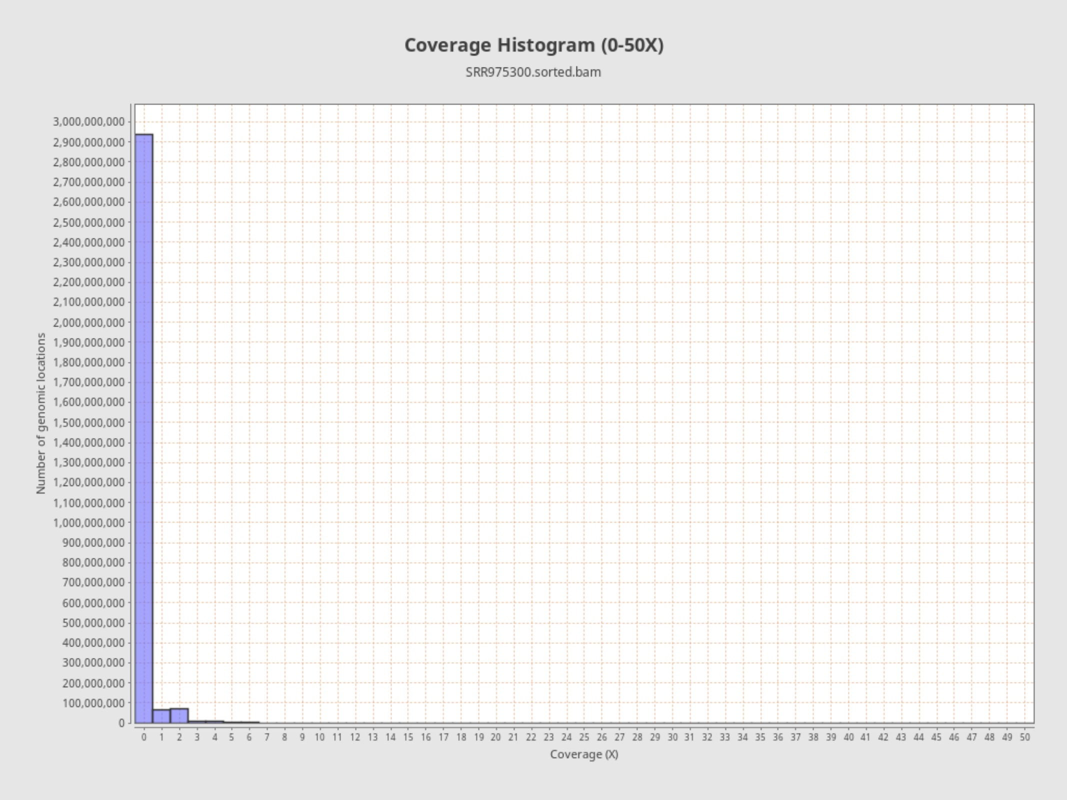
3. Results : Coverage across reference



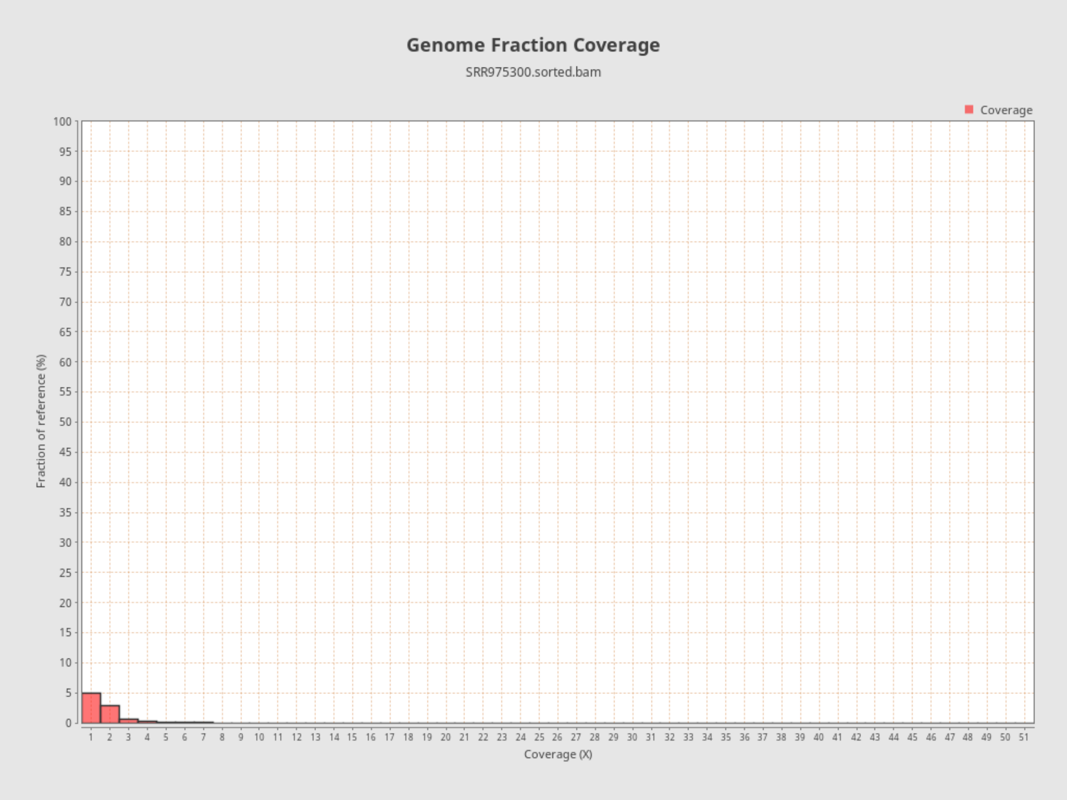
4. Results : Coverage Histogram



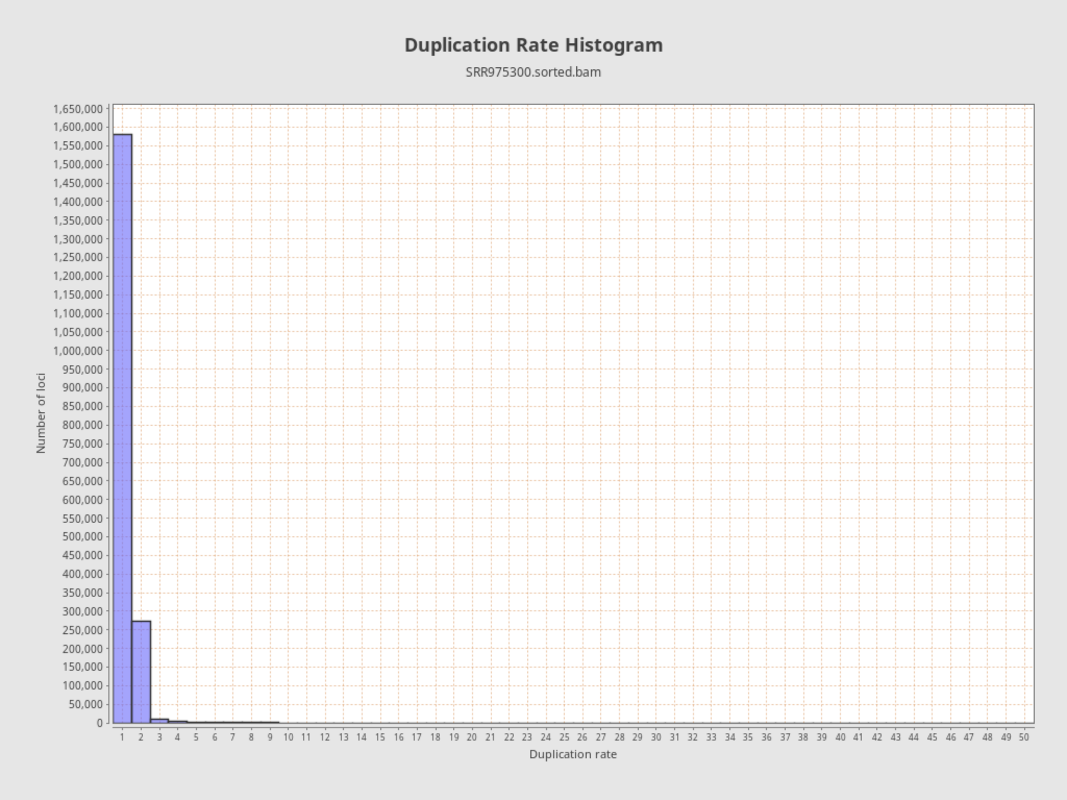
5. Results : Coverage Histogram (0-50X)



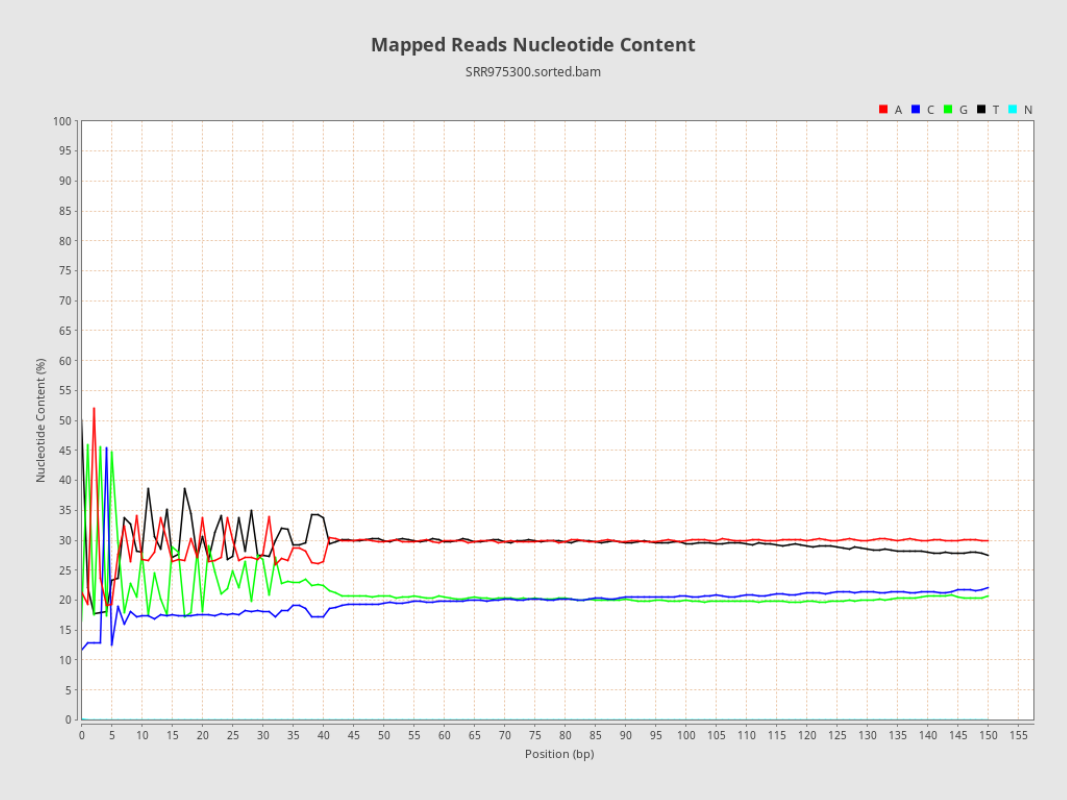
6. Results : Genome Fraction Coverage



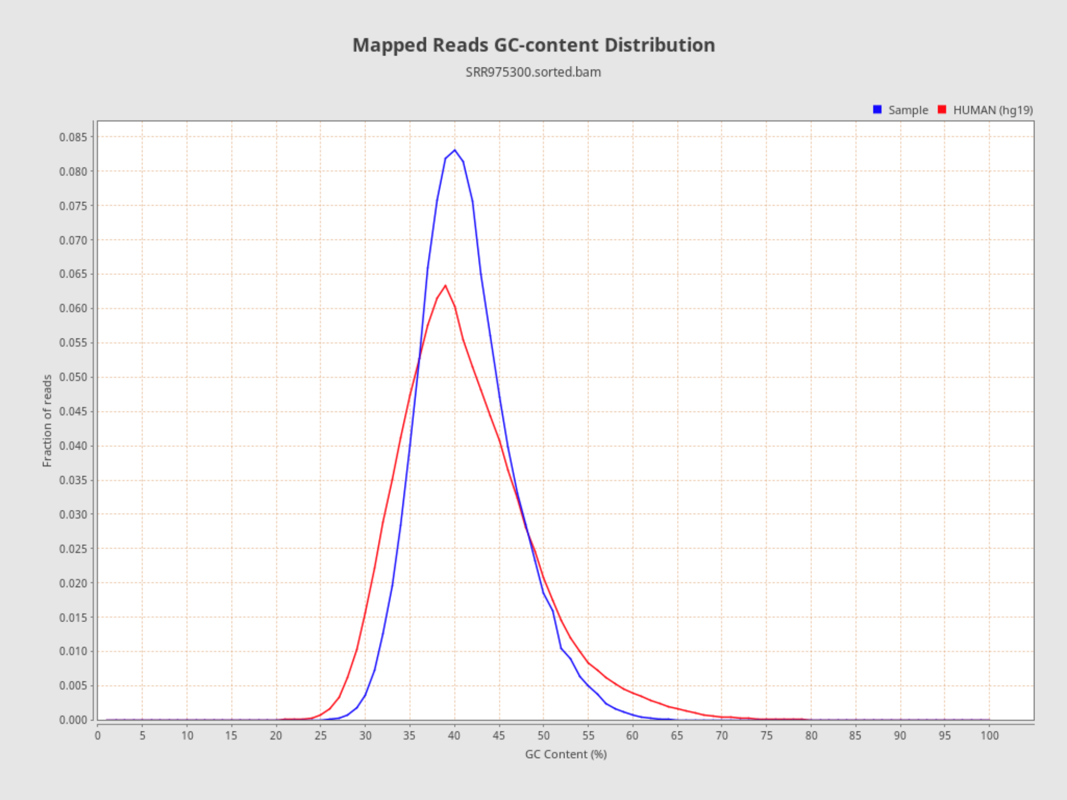
7. Results : Duplication Rate Histogram



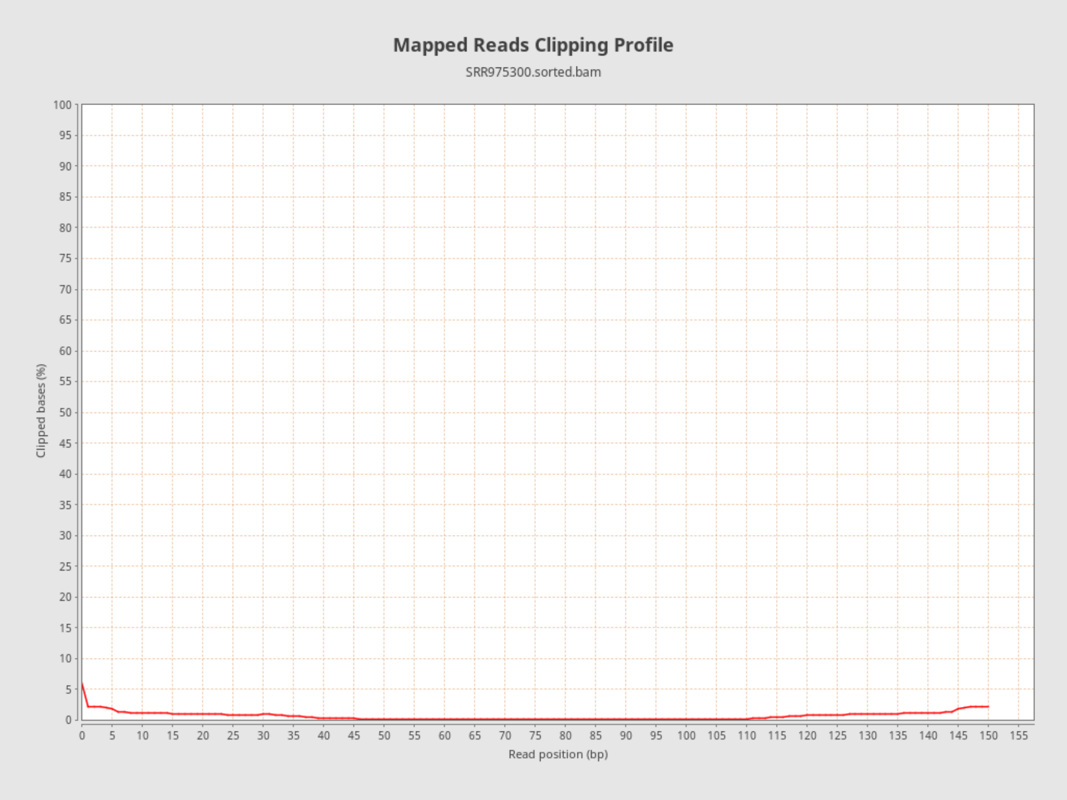
8. Results : Mapped Reads Nucleotide Content



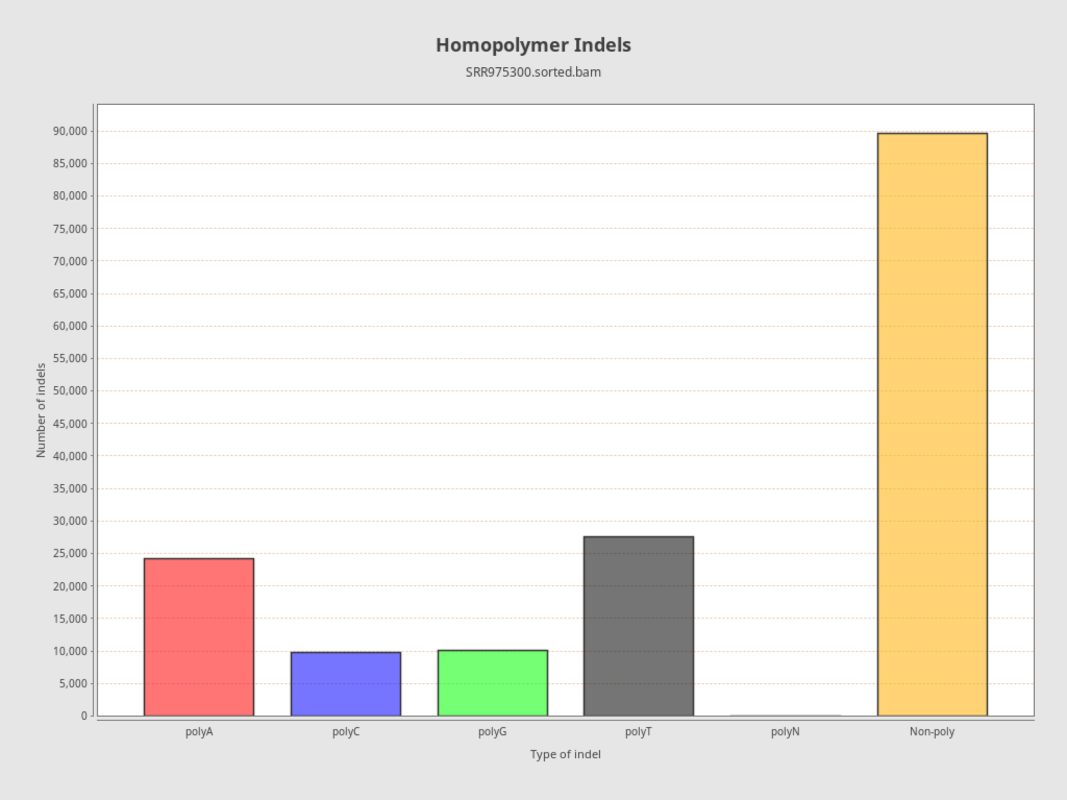
9. Results : Mapped Reads GC-content Distribution



10. Results : Mapped Reads Clipping Profile

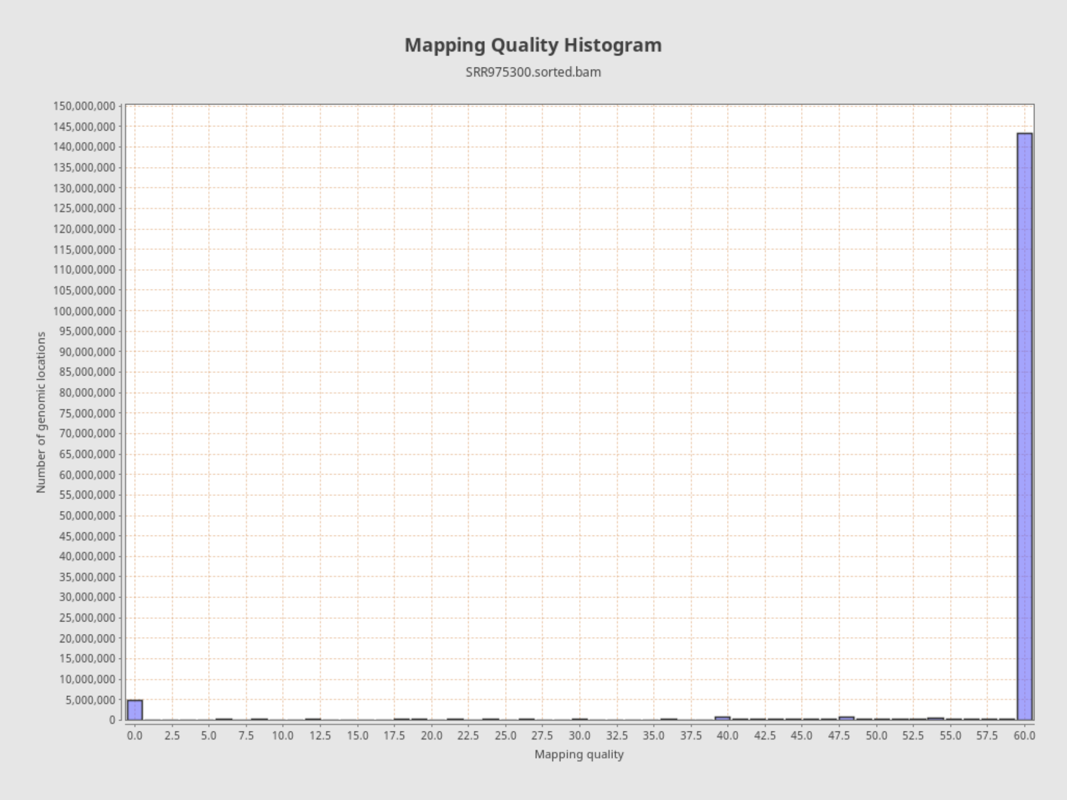


11. Results : Homopolymer Indels

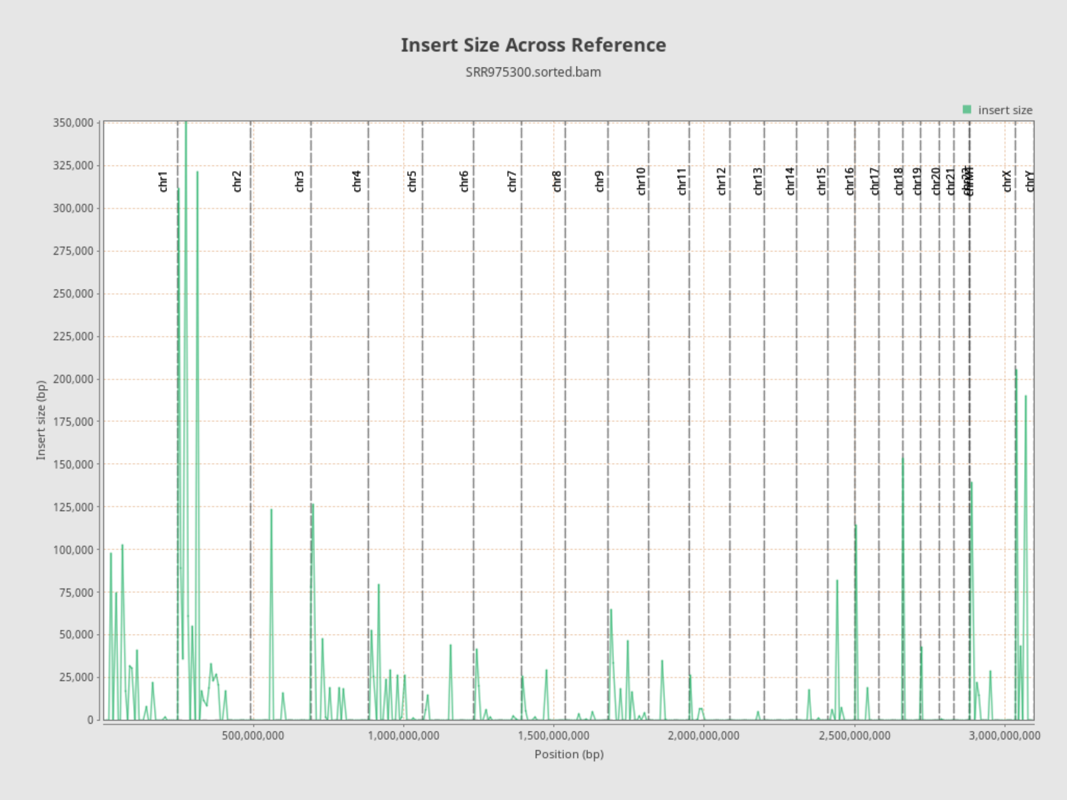


12. Results : Mapping Quality Across Reference

13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram