Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/03 19:23:31

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR9716939.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_SRR9716939 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR9716939.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Tue Sep 03 19:23:30 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR9716939.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	637,297
Mapped reads	493,807 / 77.48%
Unmapped reads	143,490 / 22.52%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	661 / 0.1%
Read min/max/mean length	30 / 76 / 76.03
Duplicated reads (estimated)	24,772 / 3.89%
Duplication rate	4.51%
Clipped reads	493,577 / 77.45%

2.2. ACGT Content

Number/percentage of A's	5,304,675 / 20.21%
Number/percentage of C's	4,445,781 / 16.94%
Number/percentage of T's	8,910,508 / 33.95%
Number/percentage of G's	7,581,321 / 28.89%
Number/percentage of N's	509 / 0%
GC Percentage	45.83%

2.3. Coverage

Mean	0.0085

Standard Deviation	0.1066

2.4. Mapping Quality

Mean Mapping Quality	43.5

2.5. Mismatches and indels

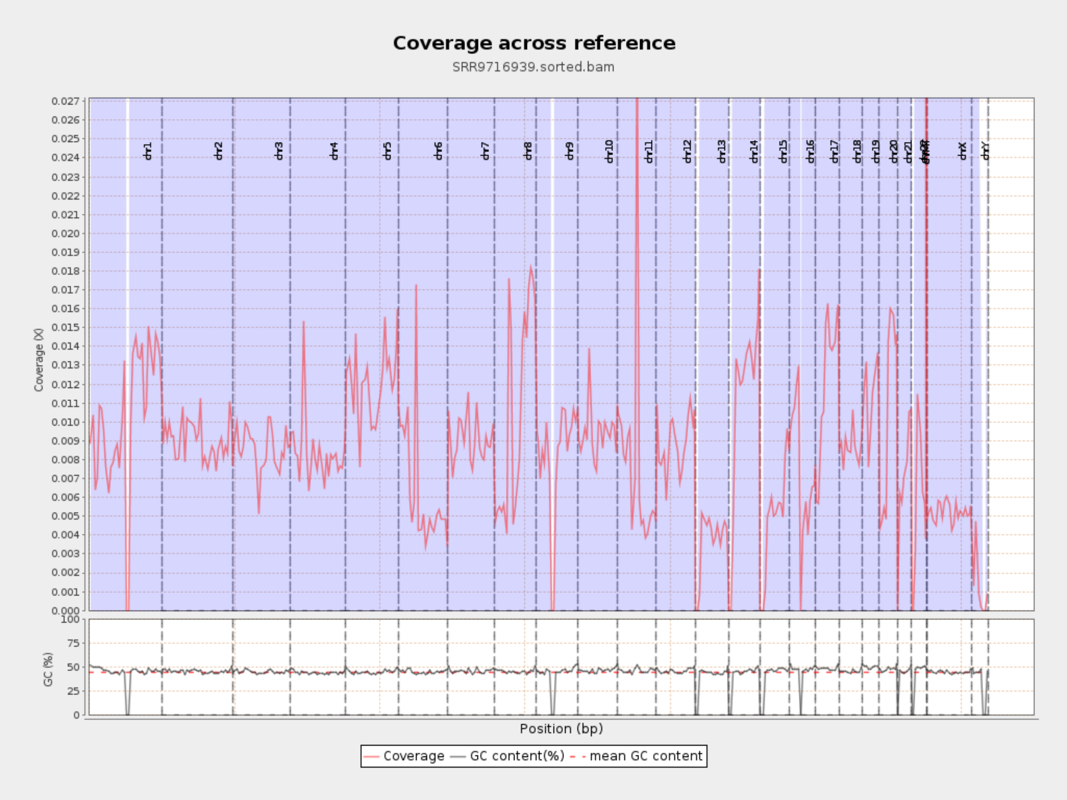
General error rate	0.67%
Mismatches	172,055
Insertions	1,590
Mapped reads with at least one insertion	0.32%
Deletions	3,716
Mapped reads with at least one deletion	0.75%
Homopolymer indels	41.58%

2.6. Chromosome stats

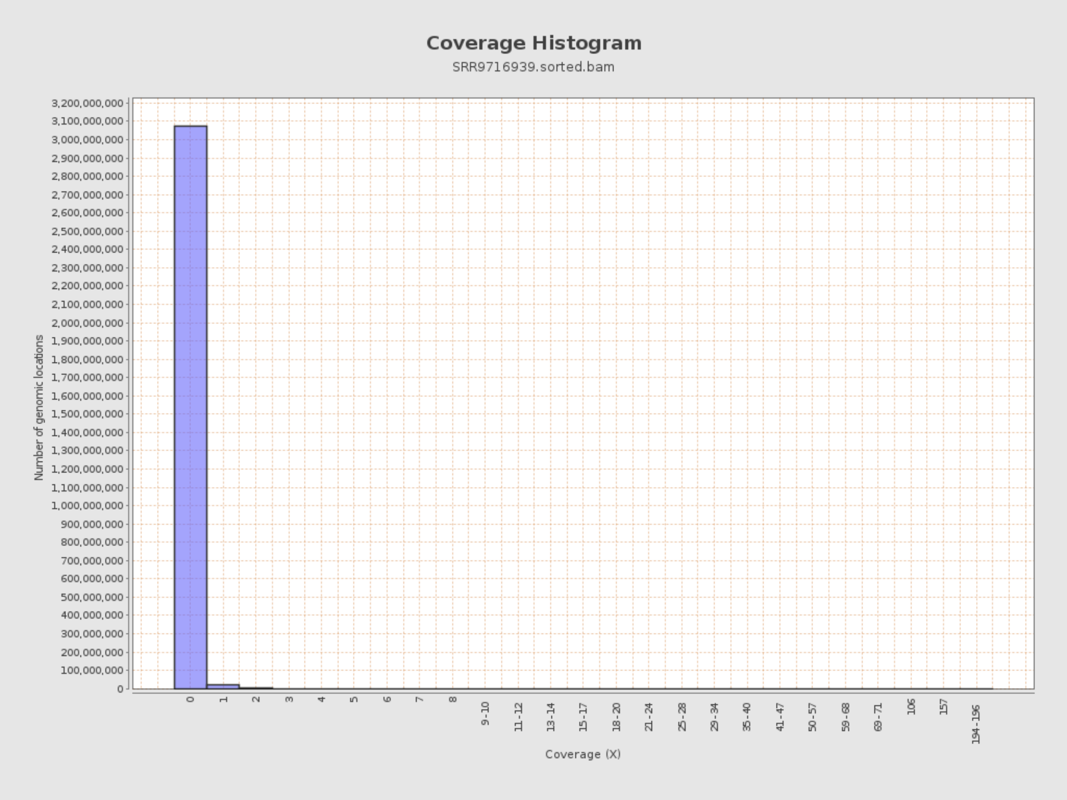
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	2534970	0.0102	0.1199
chr2	243199373	2205680	0.0091	0.132
chr3	198022430	1694438	0.0086	0.1004
chr4	191154276	1583768	0.0083	0.1024
chr5	180915260	2163353	0.012	0.1188
chr6	171115067	1097145	0.0064	0.091
chr7	159138663	1440073	0.009	0.1104

chr8	146364022	1549006	0.0106	0.1135
chr9	141213431	1128851	0.008	0.1028
chr10	135534747	1270569	0.0094	0.1156
chr11	135006516	1095354	0.0081	0.1035
chr12	133851895	1182211	0.0088	0.1022
chr13	115169878	421084	0.0037	0.0662
chr14	107349540	1182069	0.011	0.1159
chr15	102531392	503189	0.0049	0.0781
chr16	90354753	662340	0.0073	0.0977
chr17	81195210	1007894	0.0124	0.124
chr18	78077248	674654	0.0086	0.1118
chr19	59128983	668846	0.0113	0.1276
chr20	63025520	652621	0.0104	0.1138
chr21	48129895	342062	0.0071	0.0977
chr22	51304566	286184	0.0056	0.083
chrMT	16571	15145	0.9139	1.1191
chrX	155270560	810821	0.0052	0.0789
chrY	59373566	77039	0.0013	0.0469

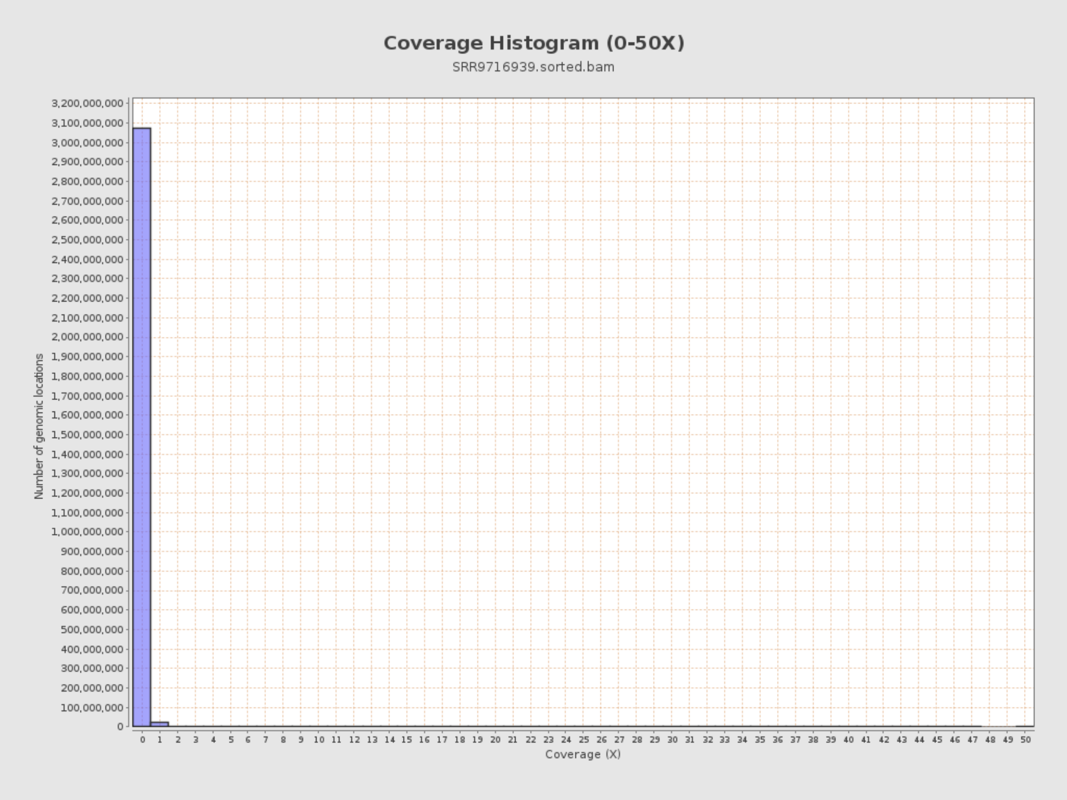
3. Results : Coverage across reference



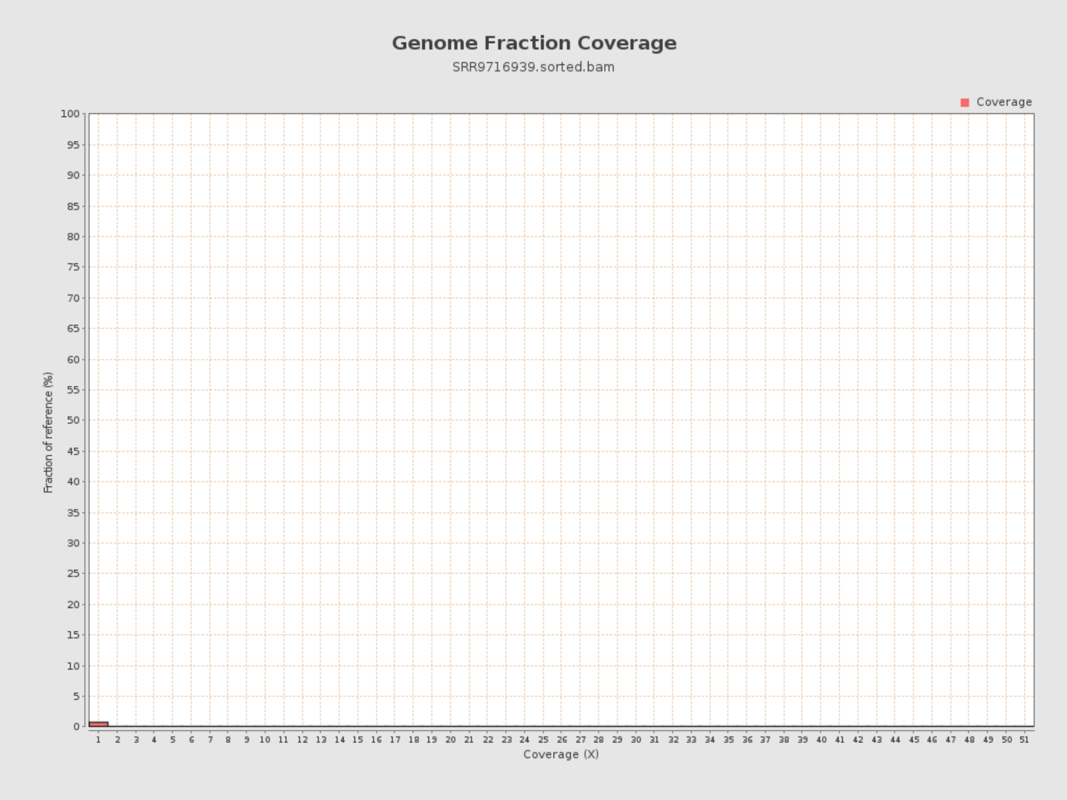
4. Results : Coverage Histogram



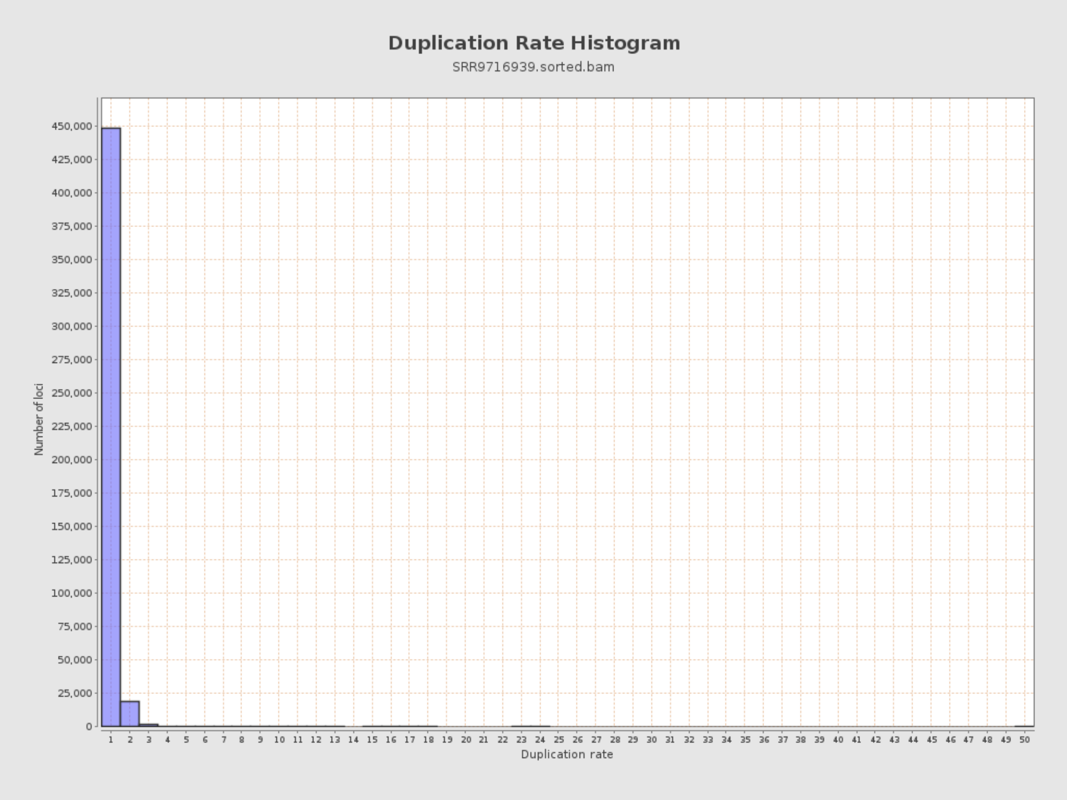
5. Results : Coverage Histogram (0-50X)



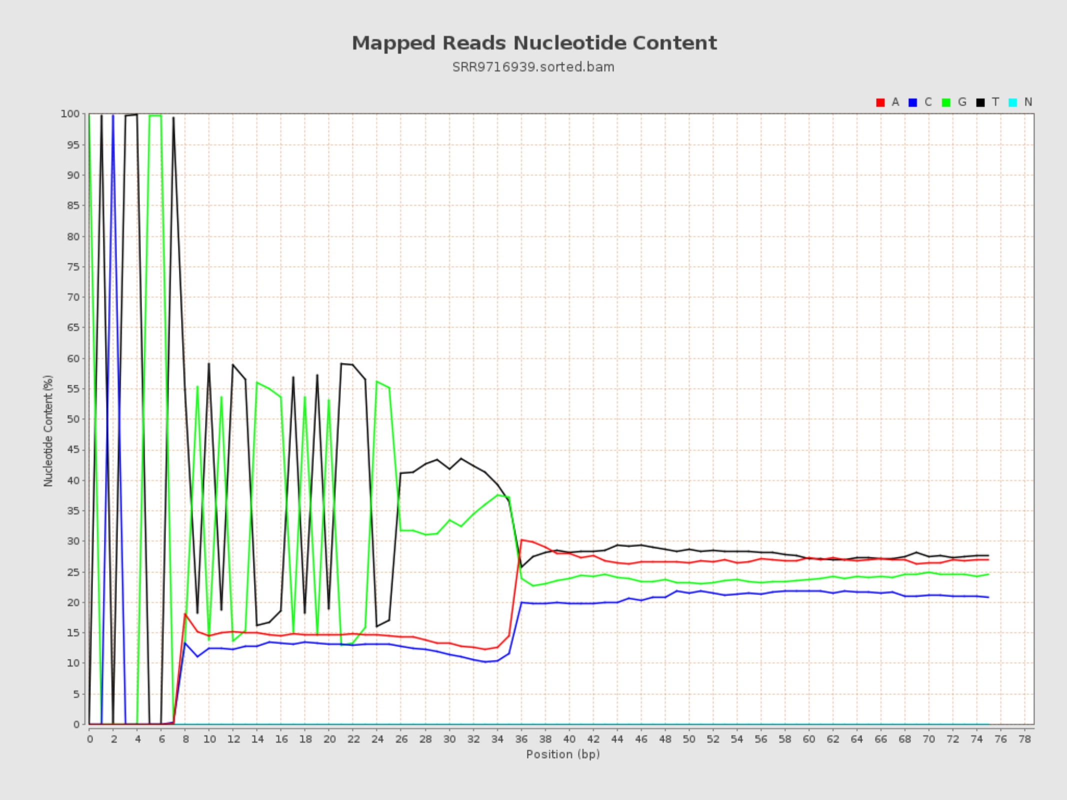
6. Results : Genome Fraction Coverage



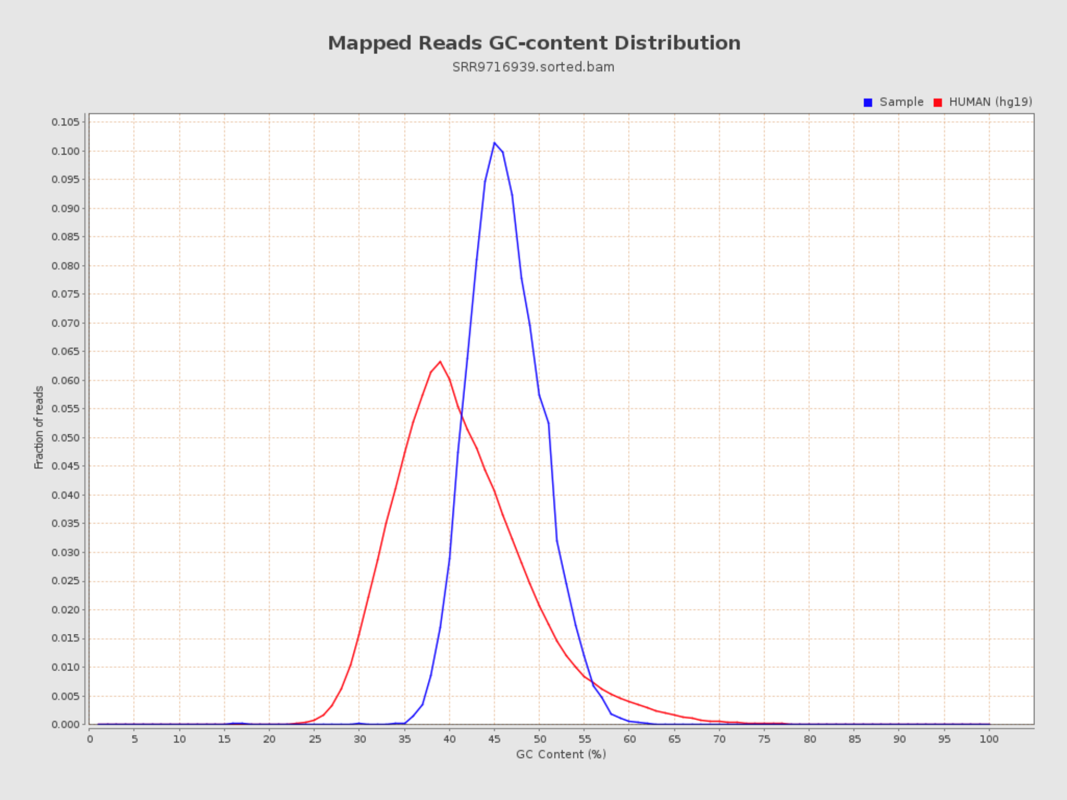
7. Results : Duplication Rate Histogram



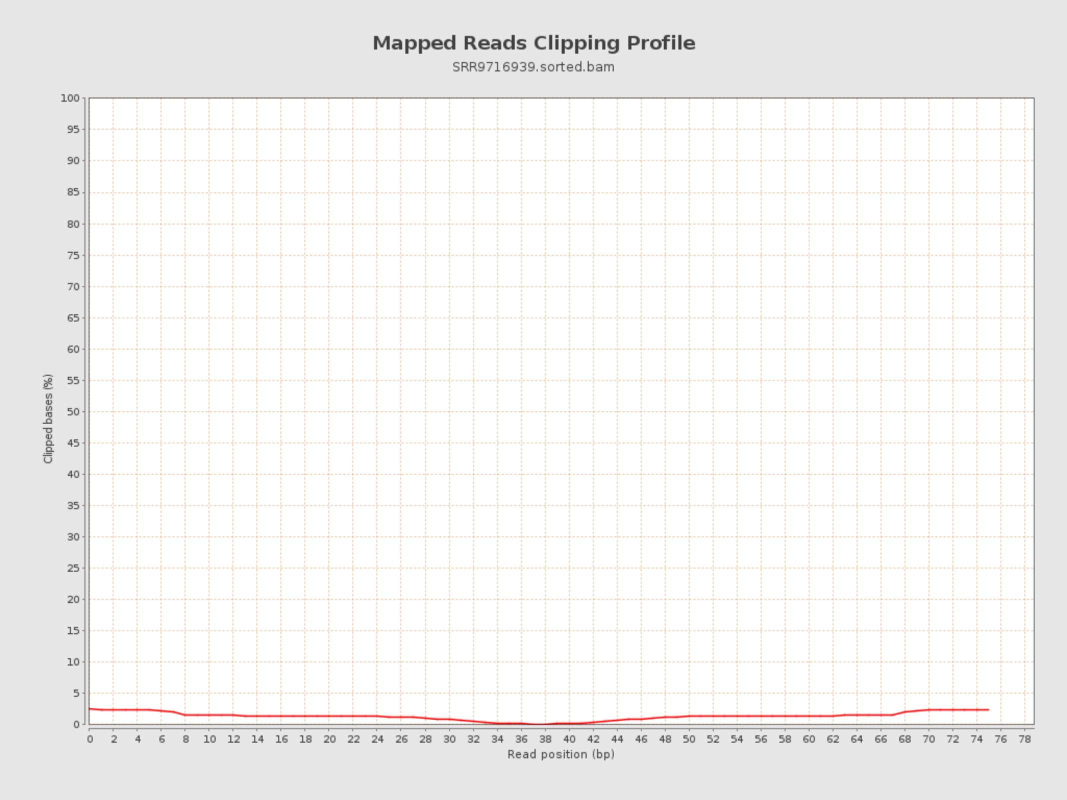
8. Results : Mapped Reads Nucleotide Content



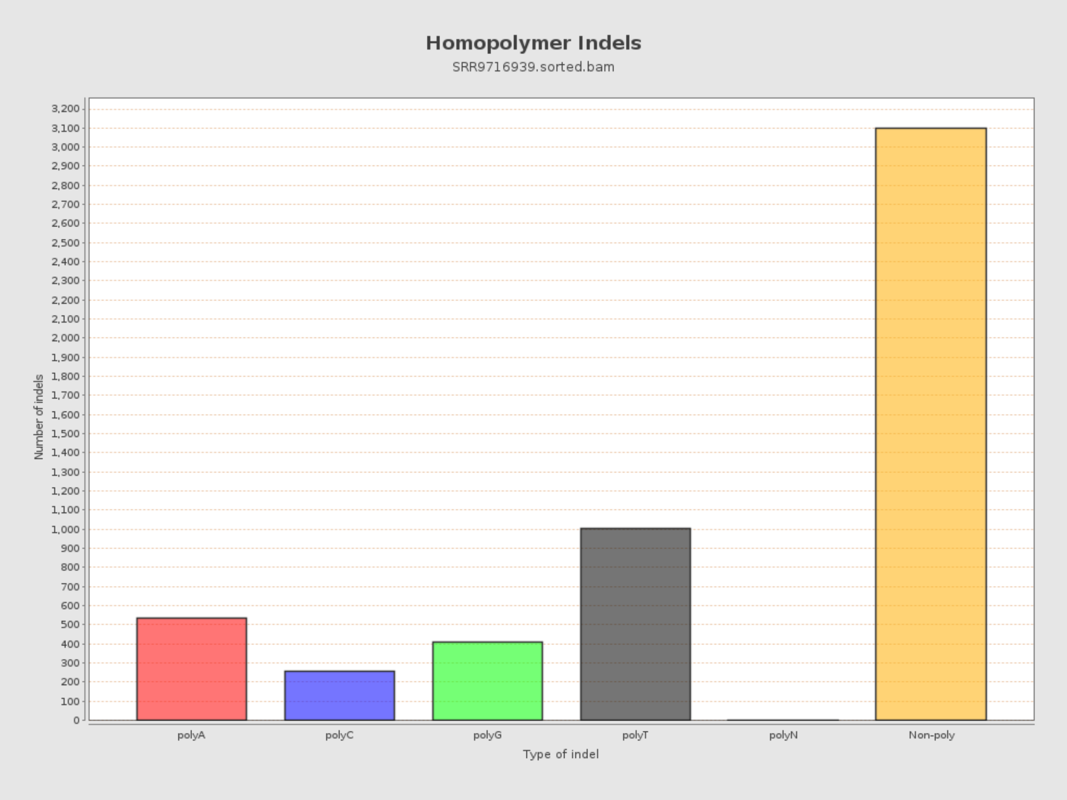
9. Results : Mapped Reads GC-content Distribution



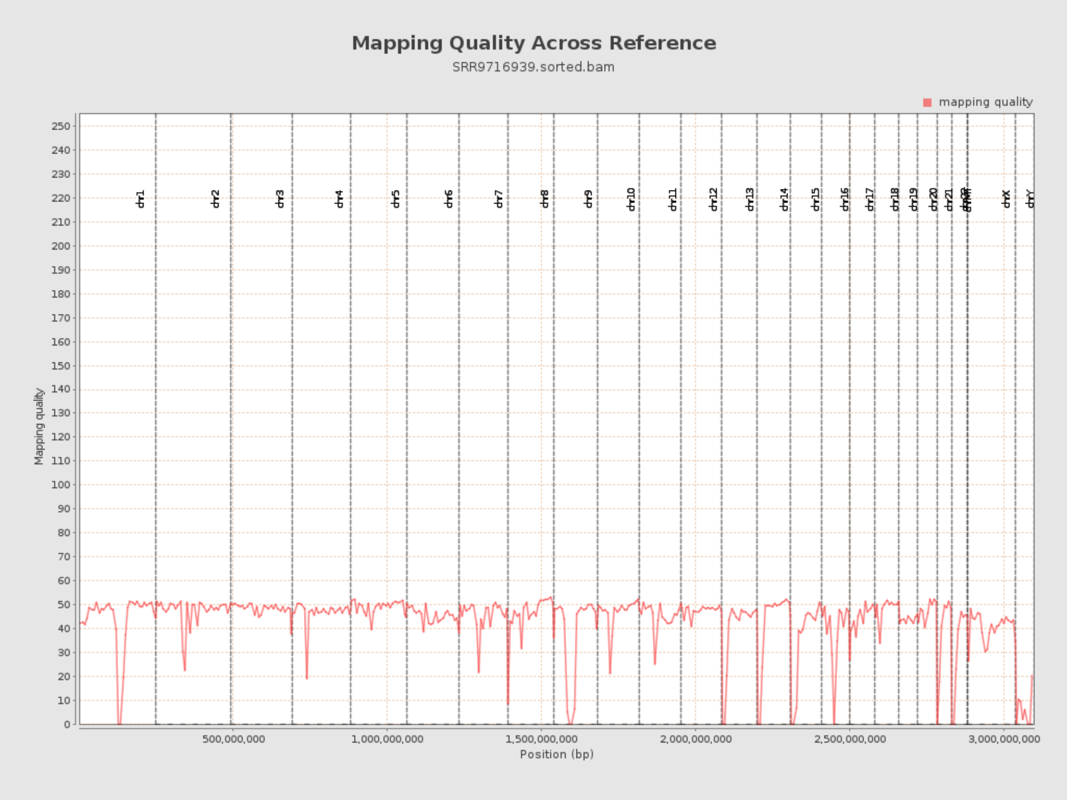
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram