Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/02 06:38:47

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR9716308.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_SRR9716308 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR9716308.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Mon Sep 02 06:38:46 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR9716308.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	394,210
Mapped reads	356,669 / 90.48%
Unmapped reads	37,541 / 9.52%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	1,491 / 0.38%
Read min/max/mean length	30 / 76 / 76.13
Duplicated reads (estimated)	6,378 / 1.62%
Duplication rate	1.31%
Clipped reads	357,239 / 90.62%

2.2. ACGT Content

Number/percentage of A's	5,385,618 / 25.79%
Number/percentage of C's	3,751,901 / 17.96%
Number/percentage of T's	6,542,787 / 31.33%
Number/percentage of G's	5,203,963 / 24.92%
Number/percentage of N's	430 / 0%
GC Percentage	42.88%

2.3. Coverage

Mean	0.0067

Standard Deviation	0.0977

2.4. Mapping Quality

Mean Mapping Quality	45.16

2.5. Mismatches and indels

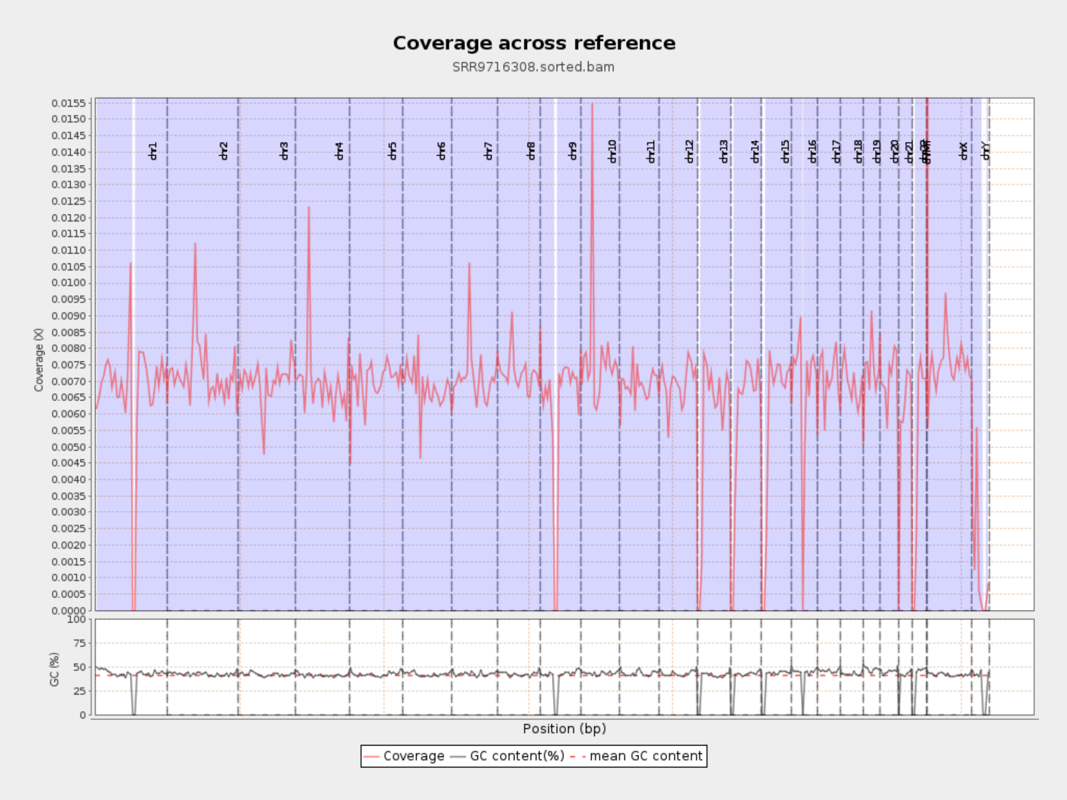
General error rate	0.52%
Mismatches	106,369
Insertions	1,539
Mapped reads with at least one insertion	0.43%
Deletions	4,271
Mapped reads with at least one deletion	1.19%
Homopolymer indels	41.86%

2.6. Chromosome stats

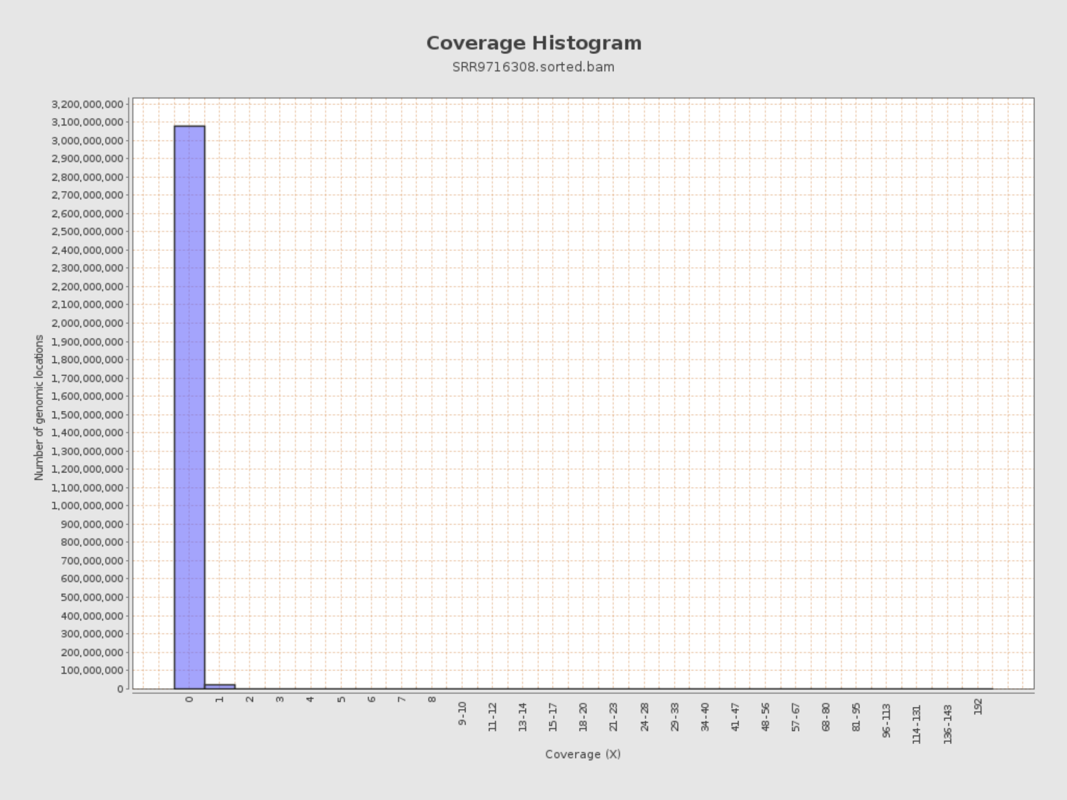
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	1662585	0.0067	0.1295
chr2	243199373	1772829	0.0073	0.1208
chr3	198022430	1385668	0.007	0.086
chr4	191154276	1341497	0.007	0.0919
chr5	180915260	1285103	0.0071	0.0866
chr6	171115067	1167577	0.0068	0.0887
chr7	159138663	1137137	0.0071	0.1053

chr8	146364022	1065597	0.0073	0.1121
chr9	141213431	864079	0.0061	0.0868
chr10	135534747	1052671	0.0078	0.1078
chr11	135006516	936563	0.0069	0.0916
chr12	133851895	927302	0.0069	0.0856
chr13	115169878	655410	0.0057	0.0775
chr14	107349540	630910	0.0059	0.0798
chr15	102531392	603180	0.0059	0.0785
chr16	90354753	604419	0.0067	0.0854
chr17	81195210	580299	0.0071	0.0884
chr18	78077248	539863	0.0069	0.1102
chr19	59128983	439500	0.0074	0.1132
chr20	63025520	444254	0.007	0.0875
chr21	48129895	283362	0.0059	0.083
chr22	51304566	254198	0.005	0.0724
chrMT	16571	4305	0.2598	0.5293
chrX	155270560	1171714	0.0075	0.091
chrY	59373566	81706	0.0014	0.0676

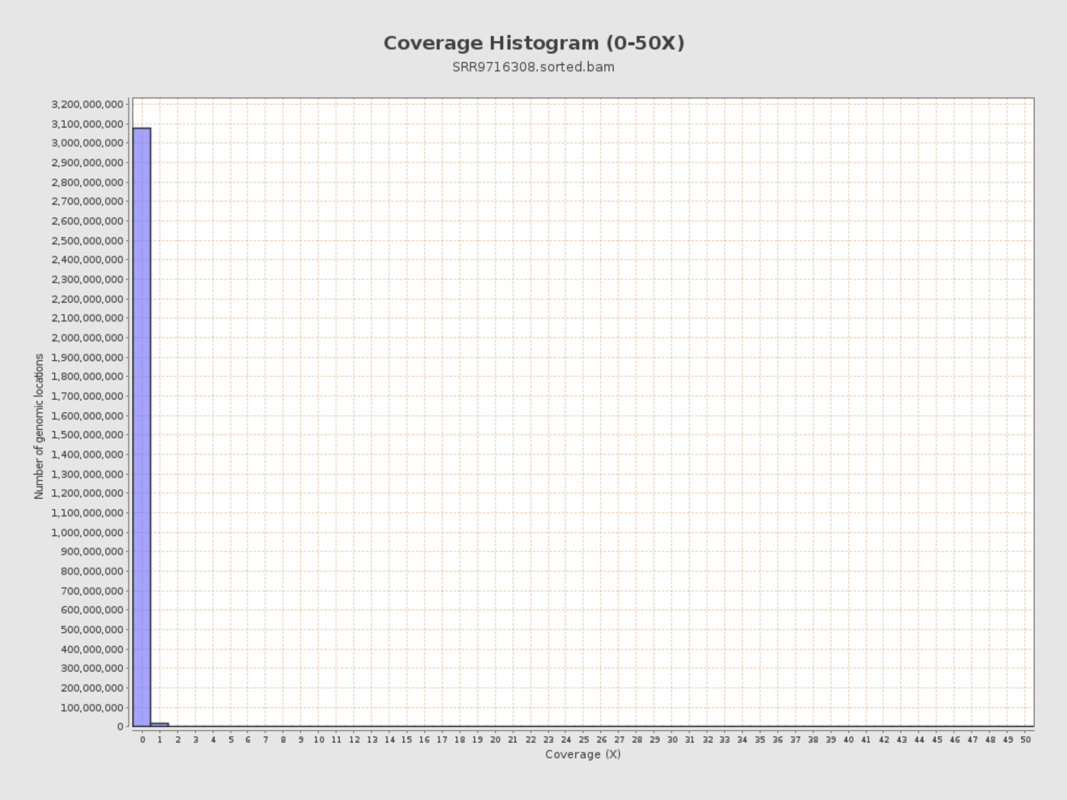
3. Results : Coverage across reference



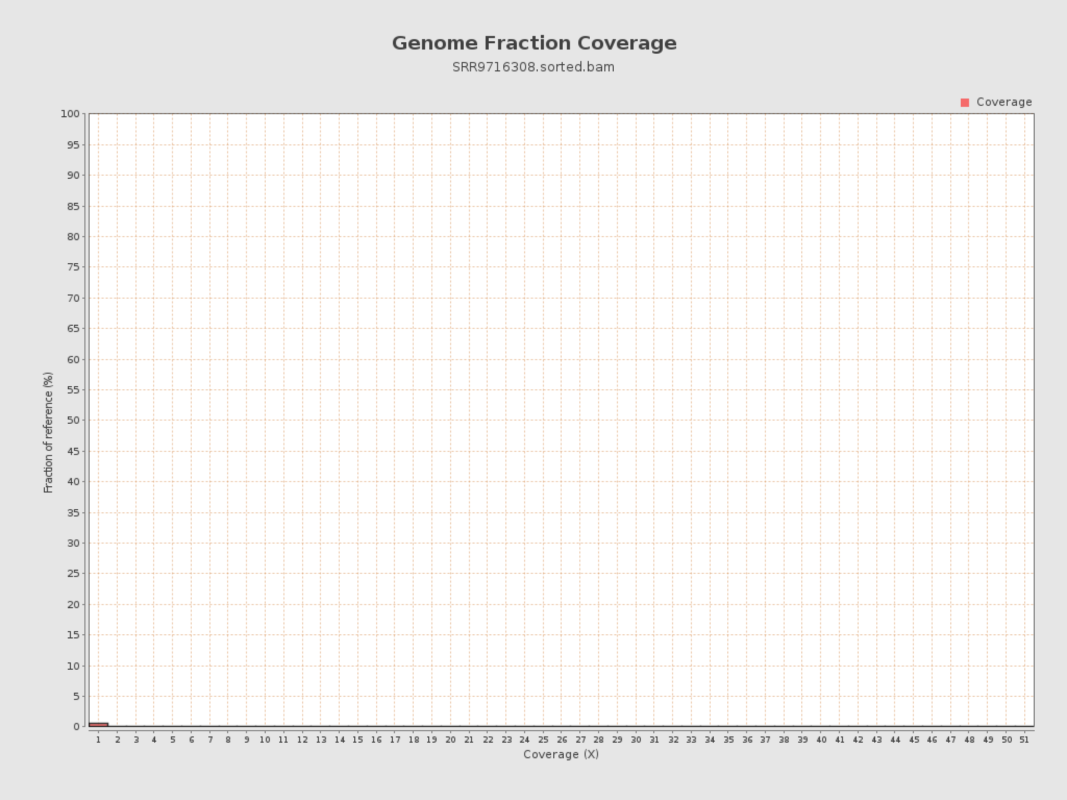
4. Results : Coverage Histogram



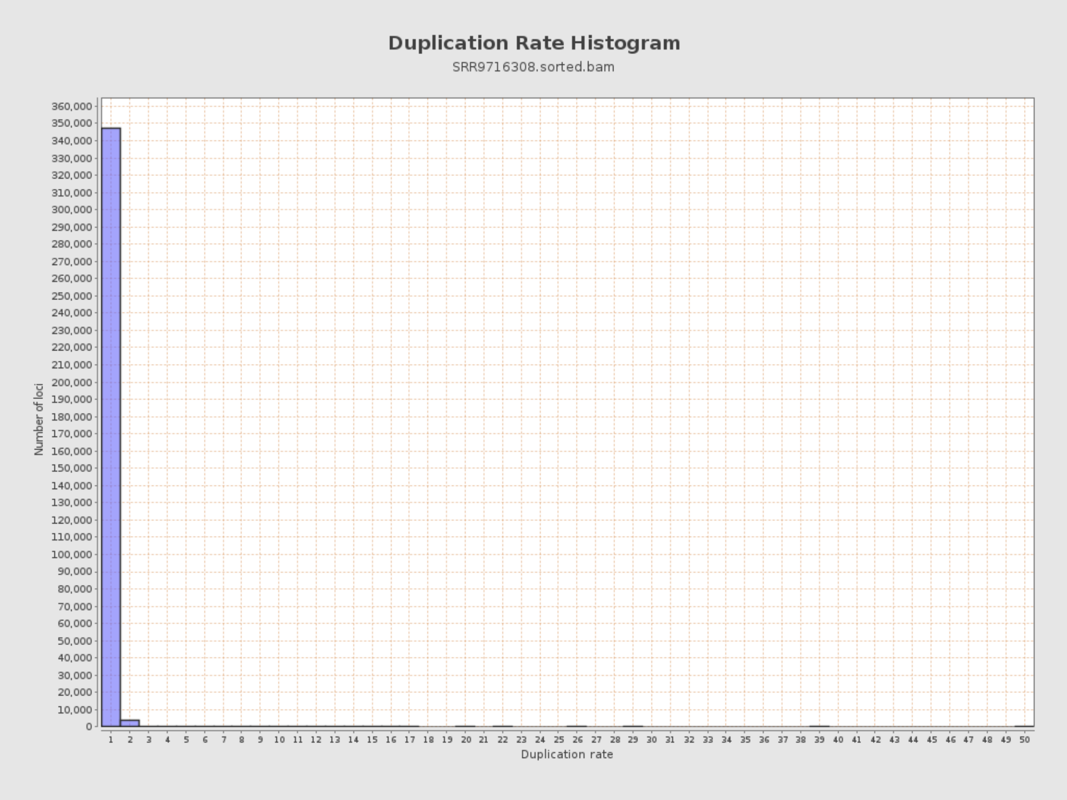
5. Results : Coverage Histogram (0-50X)



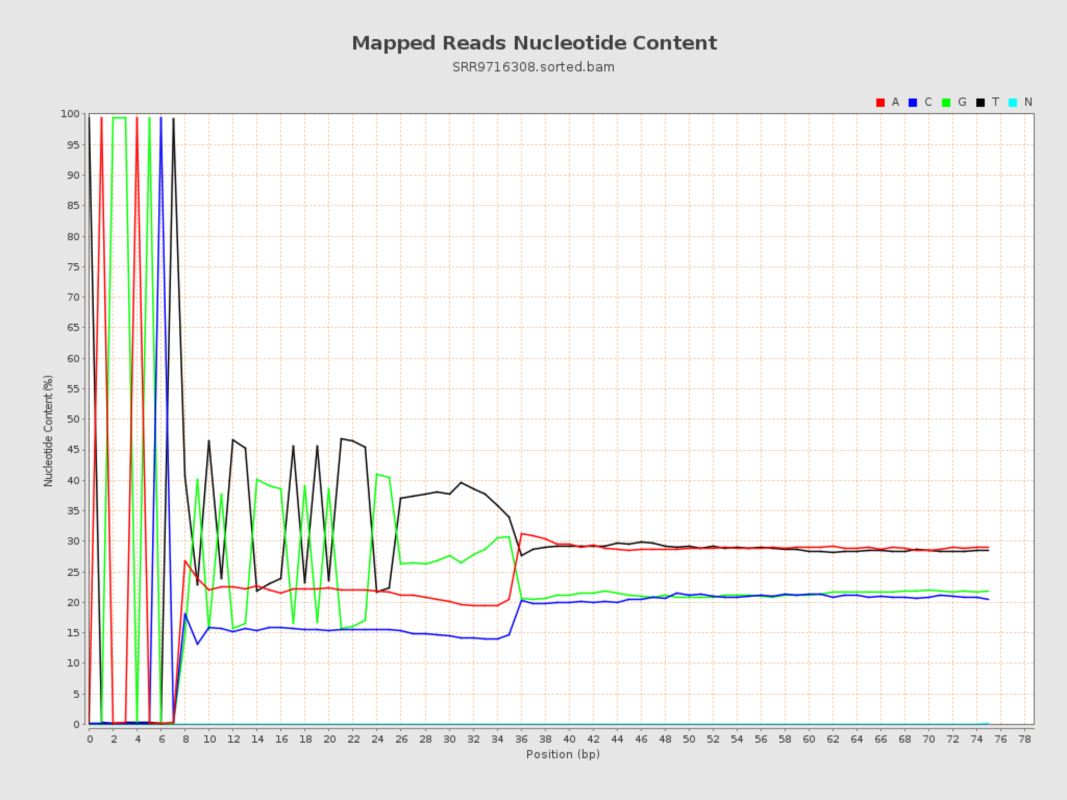
6. Results : Genome Fraction Coverage



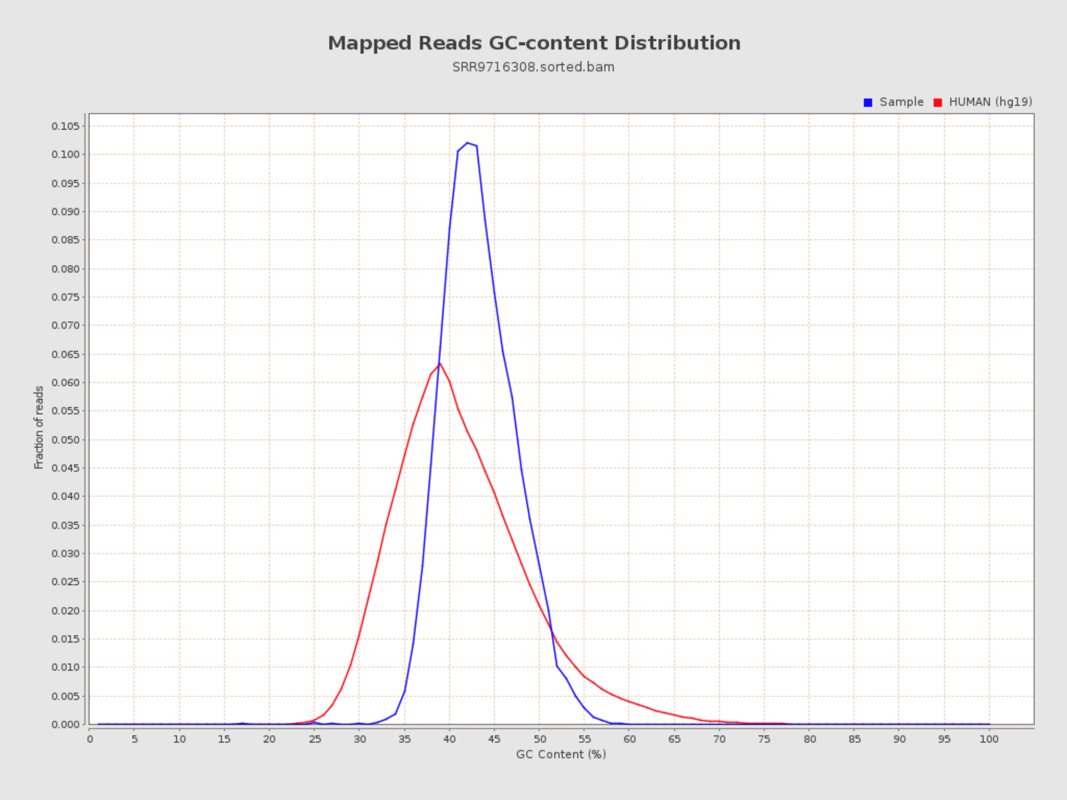
7. Results : Duplication Rate Histogram



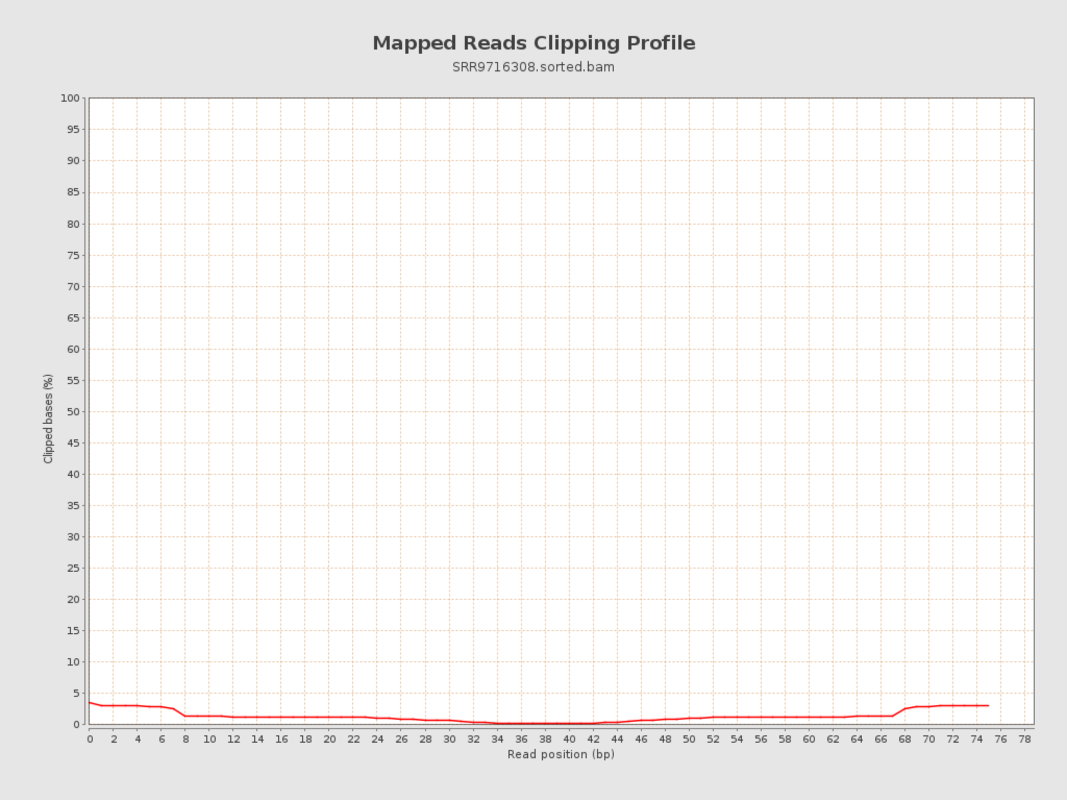
8. Results : Mapped Reads Nucleotide Content



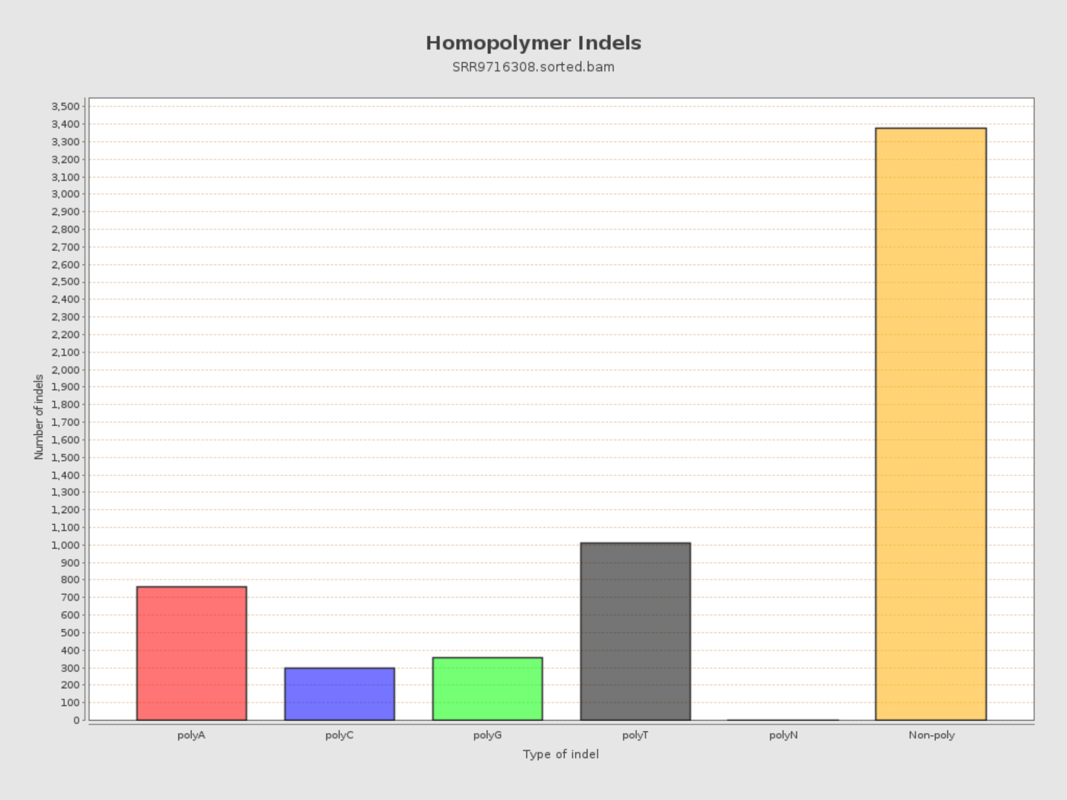
9. Results : Mapped Reads GC-content Distribution



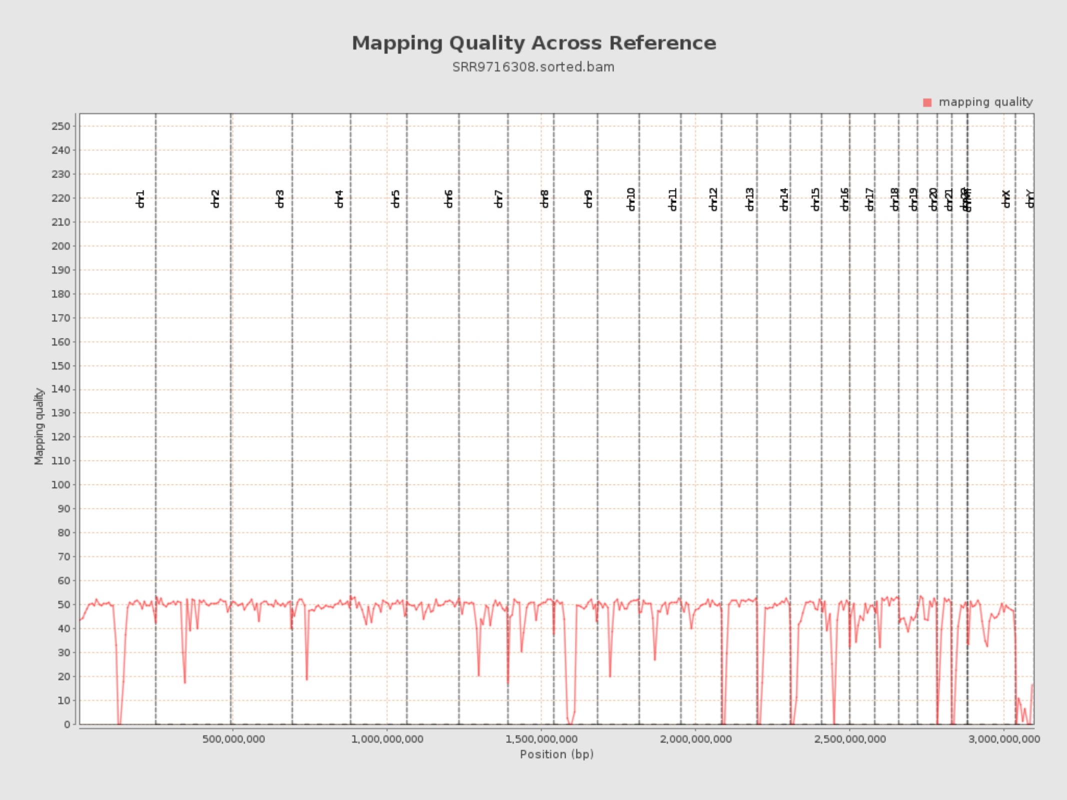
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram