Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/02 23:23:31

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR9716590.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_SRR9716590 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR9716590.fastq.gz`
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Mon Sep 02 23:23:30 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR9716590.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	413,875
Mapped reads	360,440 / 87.09%
Unmapped reads	53,435 / 12.91%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	940 / 0.23%
Read min/max/mean length	30 / 76 / 76.08
Duplicated reads (estimated)	5,497 / 1.33%
Duplication rate	1.24%
Clipped reads	360,100 / 87.01%

2.2. ACGT Content

Number/percentage of A's	5,500,788 / 26.19%
Number/percentage of C's	3,968,890 / 18.89%
Number/percentage of T's	6,380,614 / 30.37%
Number/percentage of G's	5,156,121 / 24.55%
Number/percentage of N's	196 / 0%
GC Percentage	43.44%

2.3. Coverage

Mean	0.0068

Standard Deviation	0.0914

2.4. Mapping Quality

Mean Mapping Quality	45.33

2.5. Mismatches and indels

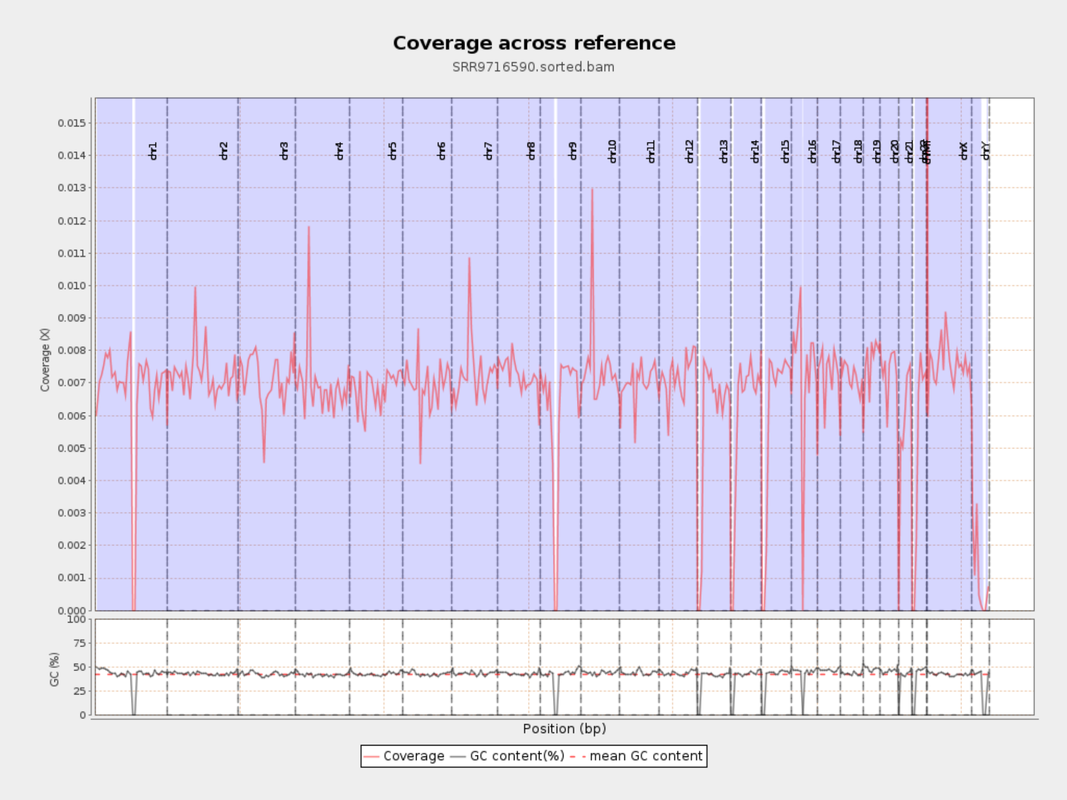
General error rate	0.5%
Mismatches	101,684
Insertions	1,742
Mapped reads with at least one insertion	0.48%
Deletions	4,231
Mapped reads with at least one deletion	1.16%
Homopolymer indels	41.84%

2.6. Chromosome stats

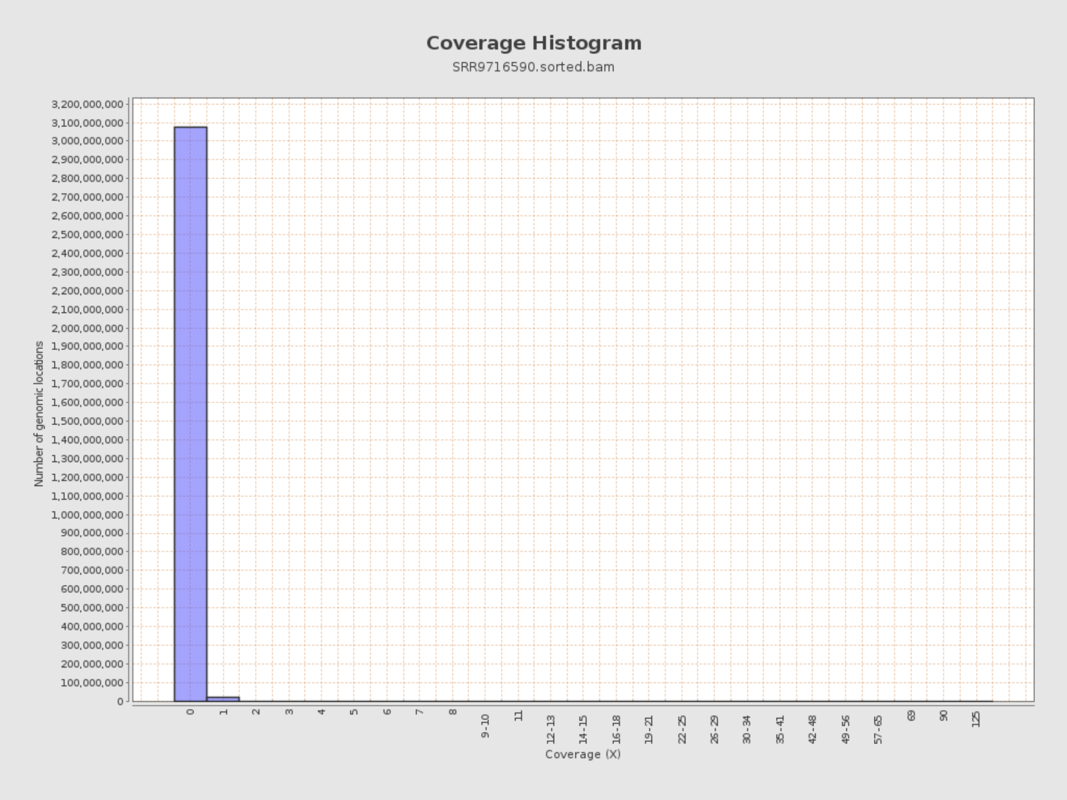
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	1674166	0.0067	0.0988
chr2	243199373	1766413	0.0073	0.1064
chr3	198022430	1405476	0.0071	0.0868
chr4	191154276	1329458	0.007	0.0881
chr5	180915260	1241852	0.0069	0.0852
chr6	171115067	1185410	0.0069	0.0895
chr7	159138663	1165093	0.0073	0.1092

chr8	146364022	1060861	0.0072	0.0919
chr9	141213431	865714	0.0061	0.0846
chr10	135534747	1019394	0.0075	0.1002
chr11	135006516	948266	0.007	0.091
chr12	133851895	962879	0.0072	0.087
chr13	115169878	661427	0.0057	0.0778
chr14	107349540	636055	0.0059	0.0801
chr15	102531392	611229	0.006	0.0793
chr16	90354753	651194	0.0072	0.0895
chr17	81195210	592439	0.0073	0.0892
chr18	78077248	561329	0.0072	0.1078
chr19	59128983	454252	0.0077	0.1016
chr20	63025520	457338	0.0073	0.088
chr21	48129895	270255	0.0056	0.0788
chr22	51304566	254770	0.005	0.0728
chrMT	16571	1857	0.1121	0.3282
chrX	155270560	1176500	0.0076	0.0913
chrY	59373566	59764	0.001	0.041

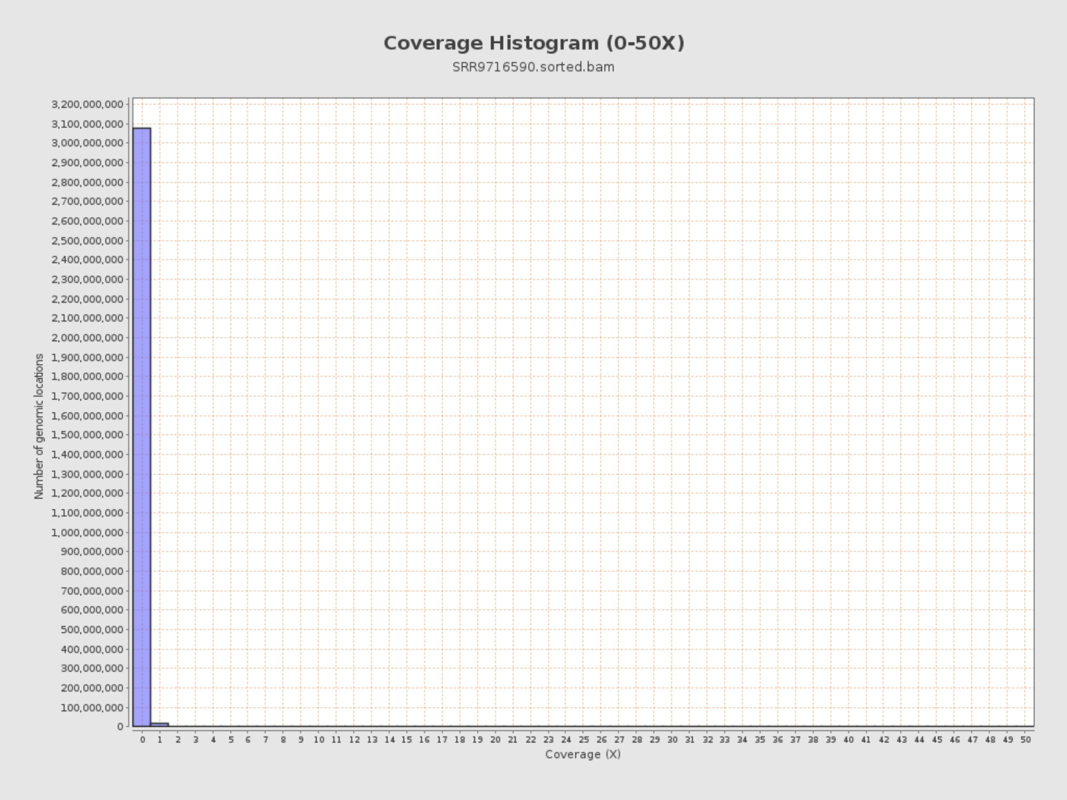
3. Results : Coverage across reference



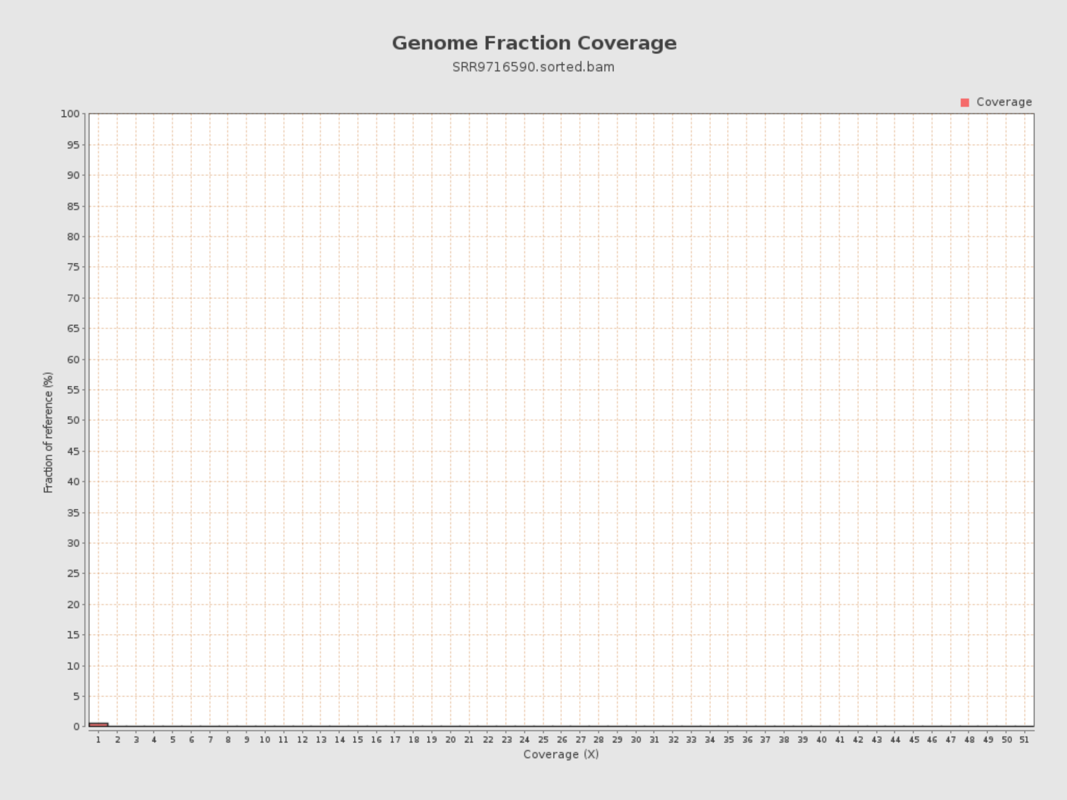
4. Results : Coverage Histogram



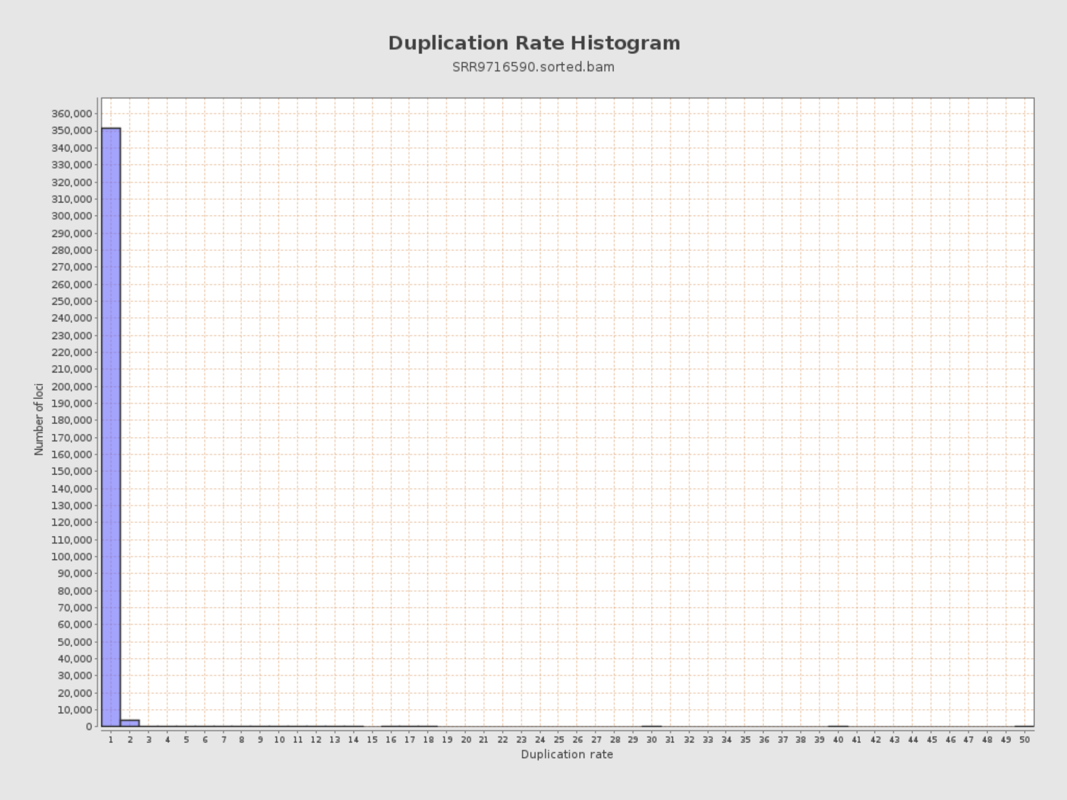
5. Results : Coverage Histogram (0-50X)



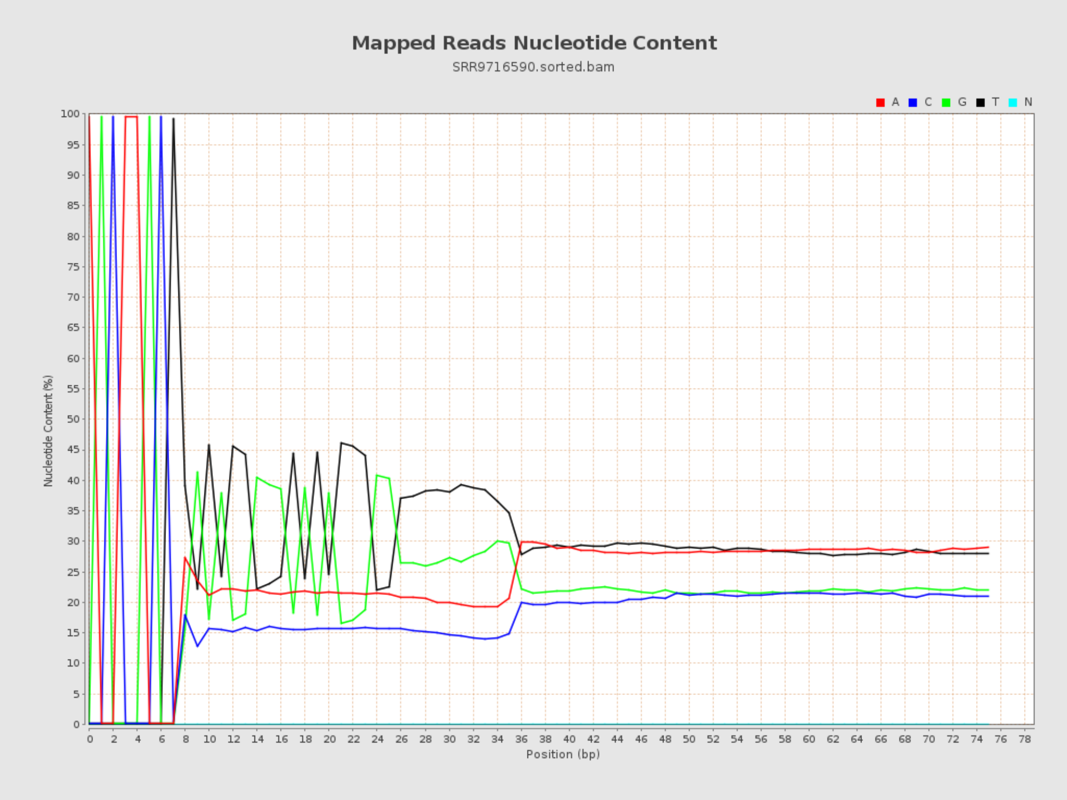
6. Results : Genome Fraction Coverage



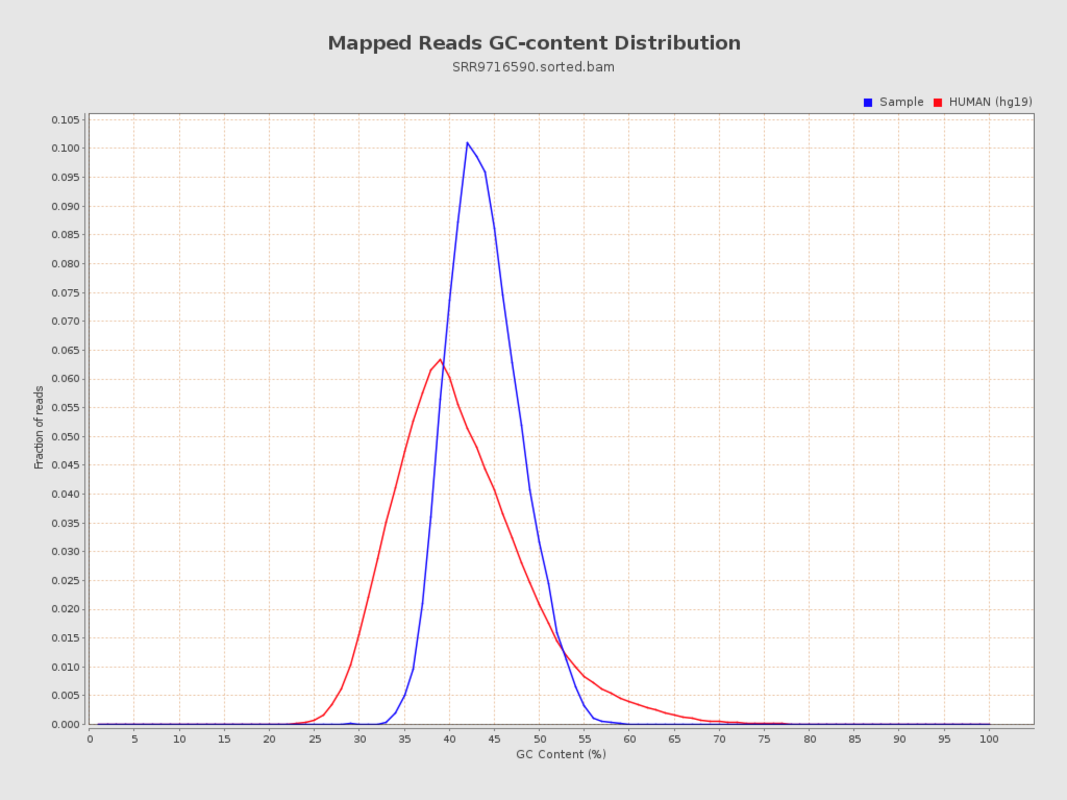
7. Results : Duplication Rate Histogram



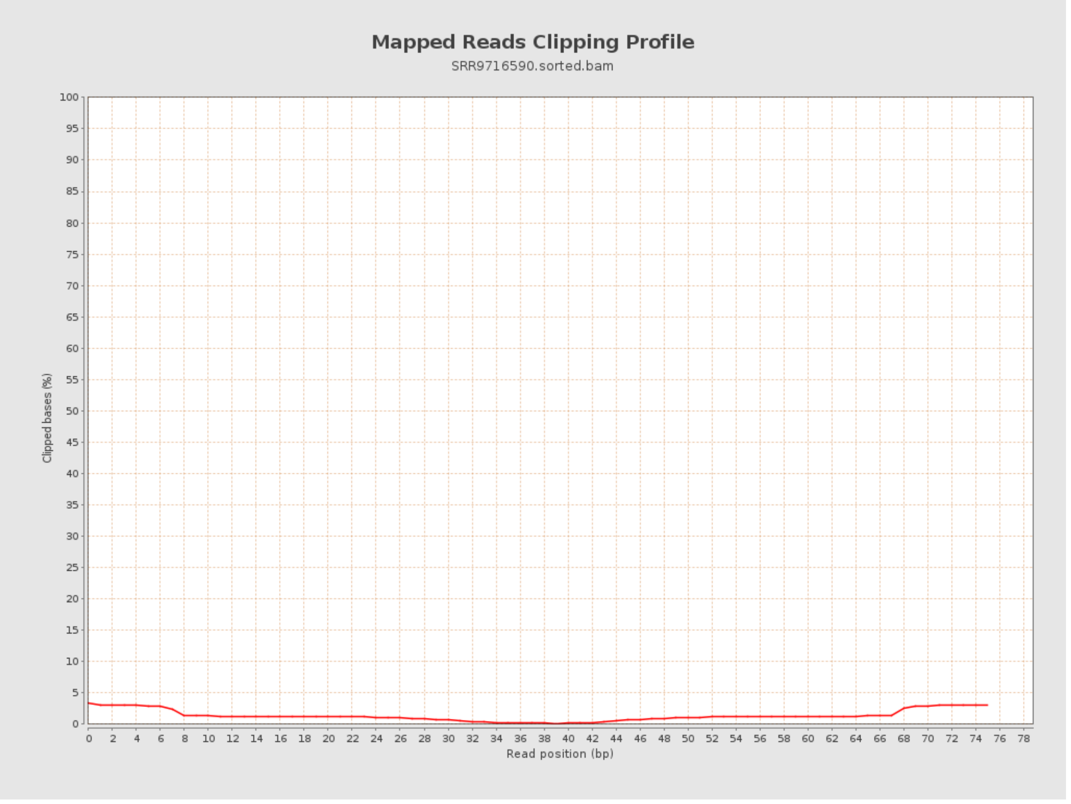
8. Results : Mapped Reads Nucleotide Content



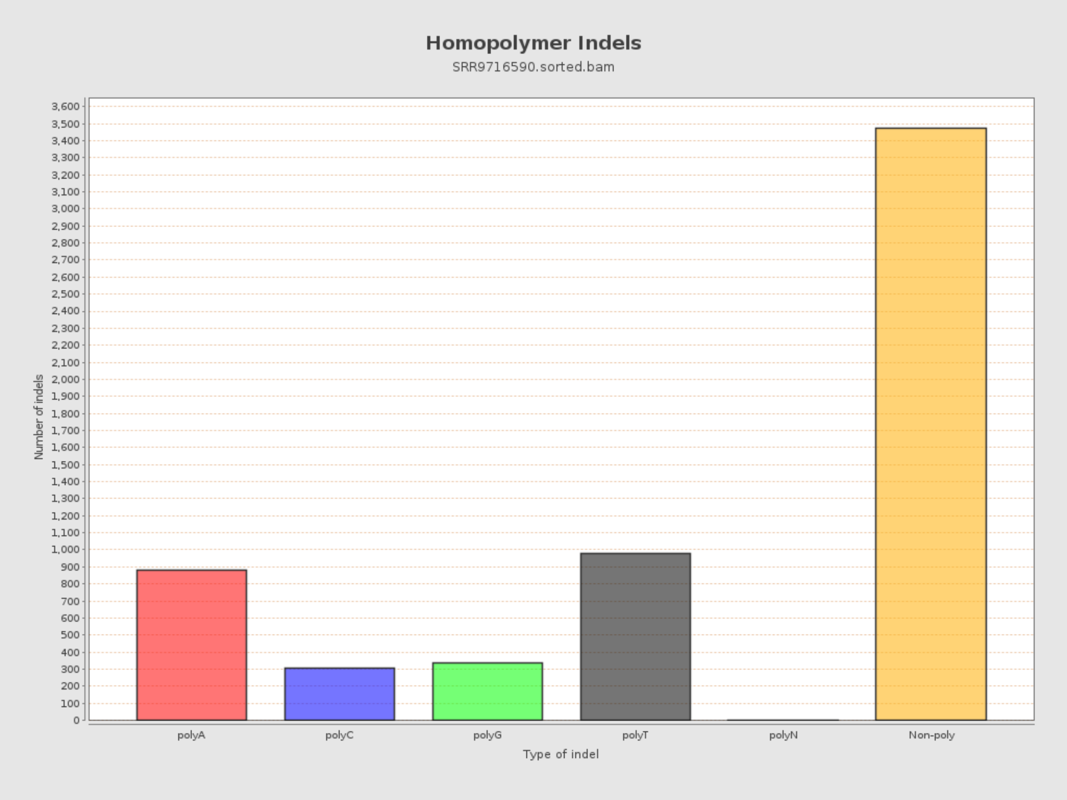
9. Results : Mapped Reads GC-content Distribution



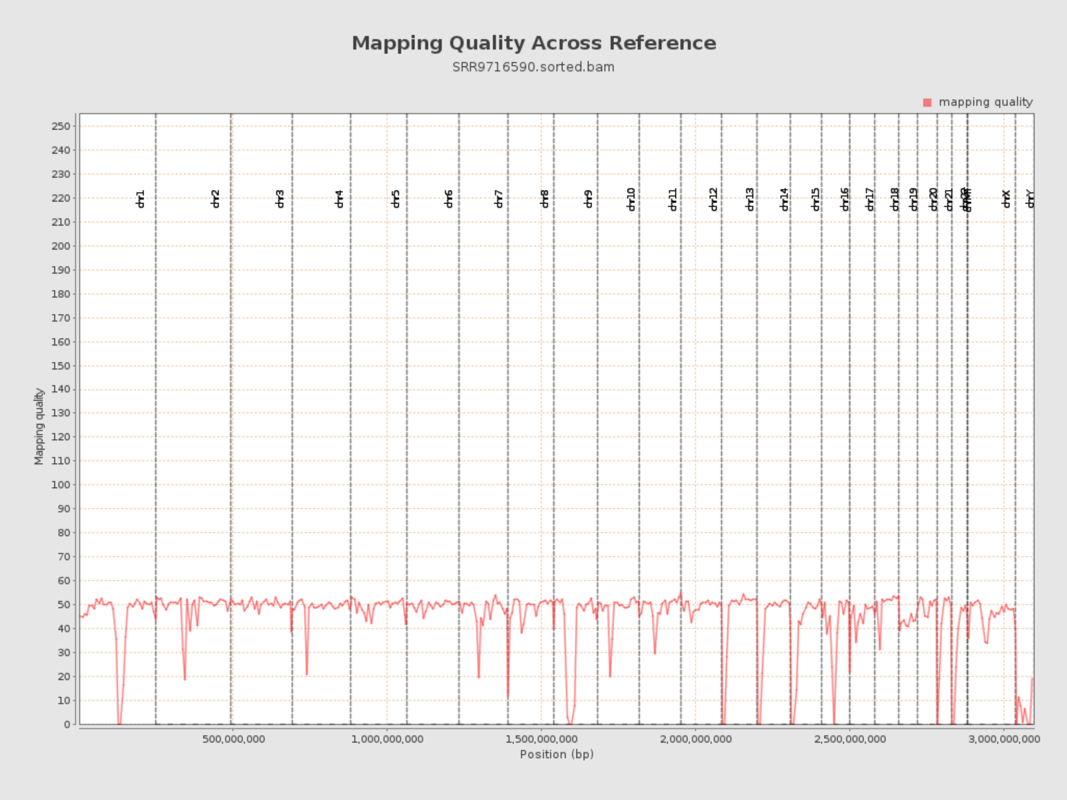
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram