Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/03 07:45:53

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR9716708.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_SRR9716708 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR9716708.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Tue Sep 03 07:45:52 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR9716708.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	2,324,754
Mapped reads	2,163,290 / 93.05%
Unmapped reads	161,464 / 6.95%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	60,226 / 2.59%
Read min/max/mean length	30 / 101 / 101.95
Duplicated reads (estimated)	125,706 / 5.41%
Duplication rate	4.37%
Clipped reads	2,219,625 / 95.48%

2.2. ACGT Content

Number/percentage of A's	40,809,510 / 24.6%
Number/percentage of C's	32,925,102 / 19.85%
Number/percentage of T's	50,621,903 / 30.51%
Number/percentage of G's	41,528,953 / 25.03%
Number/percentage of N's	6,748 / 0%
GC Percentage	44.88%

2.3. Coverage

Mean	0.0536

Standard Deviation	0.452

2.4. Mapping Quality

Mean Mapping Quality	45.36

2.5. Mismatches and indels

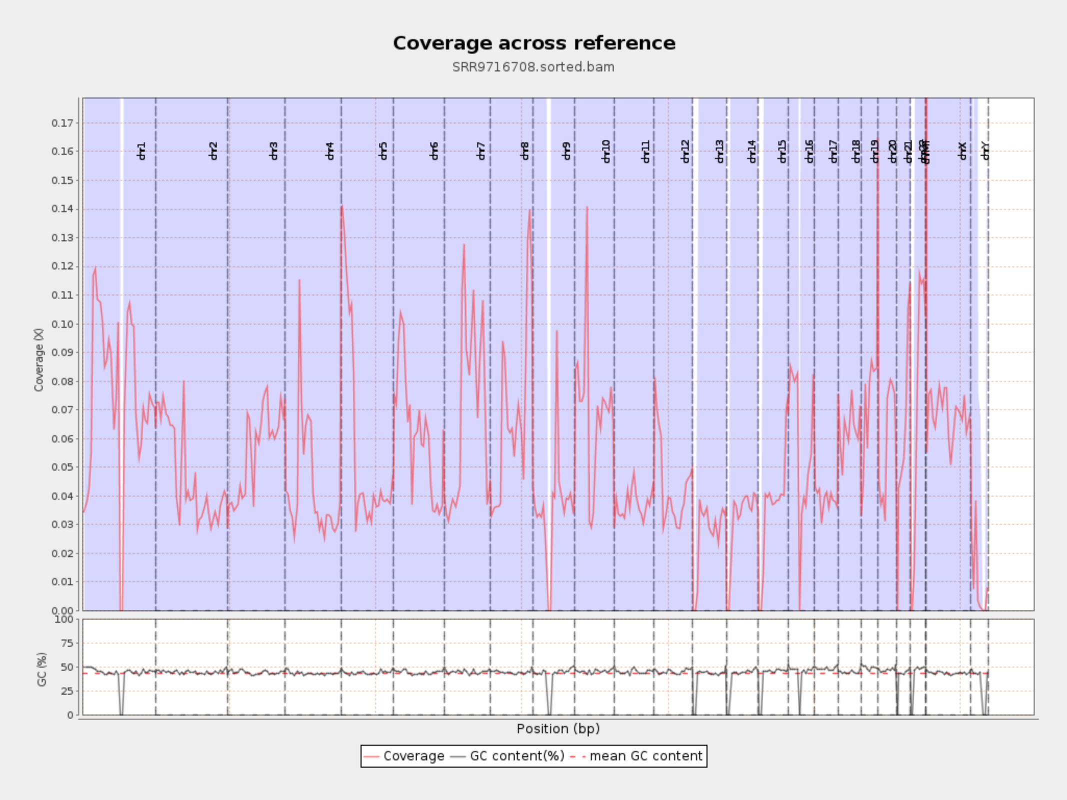
General error rate	0.71%
Mismatches	1,140,938
Insertions	15,981
Mapped reads with at least one insertion	0.73%
Deletions	32,349
Mapped reads with at least one deletion	1.47%
Homopolymer indels	38.37%

2.6. Chromosome stats

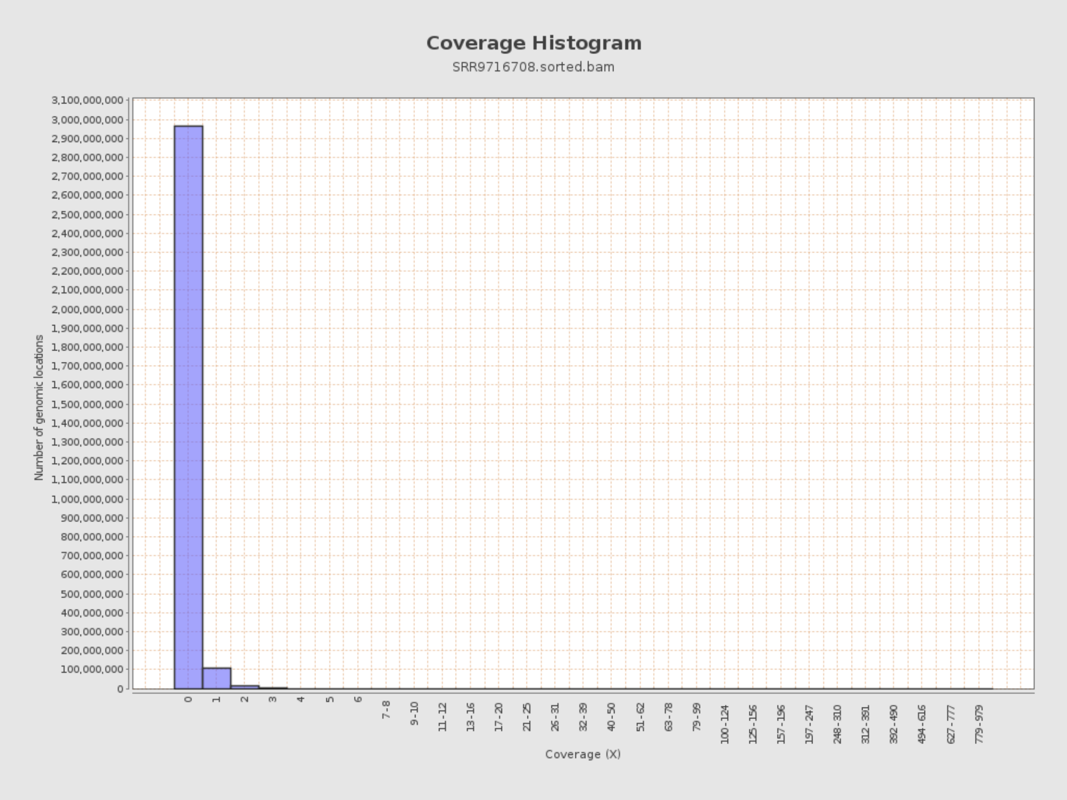
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	18654160	0.0748	0.8706
chr2	243199373	11457486	0.0471	0.4517
chr3	198022430	10979286	0.0554	0.2903
chr4	191154276	8215546	0.043	0.4078
chr5	180915260	10371719	0.0573	0.294
chr6	171115067	10516281	0.0615	0.3215
chr7	159138663	10883507	0.0684	0.6245

chr8	146364022	10086991	0.0689	0.4579
chr9	141213431	5063532	0.0359	0.3009
chr10	135534747	9387485	0.0693	0.6815
chr11	135006516	5013453	0.0371	0.3294
chr12	133851895	5923798	0.0443	0.2547
chr13	115169878	3062877	0.0266	0.1901
chr14	107349540	3387137	0.0316	0.2286
chr15	102531392	3580712	0.0349	0.2225
chr16	90354753	5195465	0.0575	0.3243
chr17	81195210	3161861	0.0389	0.265
chr18	78077248	4923273	0.0631	0.4874
chr19	59128983	4420964	0.0748	0.6264
chr20	63025520	3685438	0.0585	0.3258
chr21	48129895	3007464	0.0625	0.403
chr22	51304566	3626049	0.0707	0.3457
chrMT	16571	147893	8.9248	6.6185
chrX	155270560	10616075	0.0684	0.3342
chrY	59373566	591133	0.01	0.364

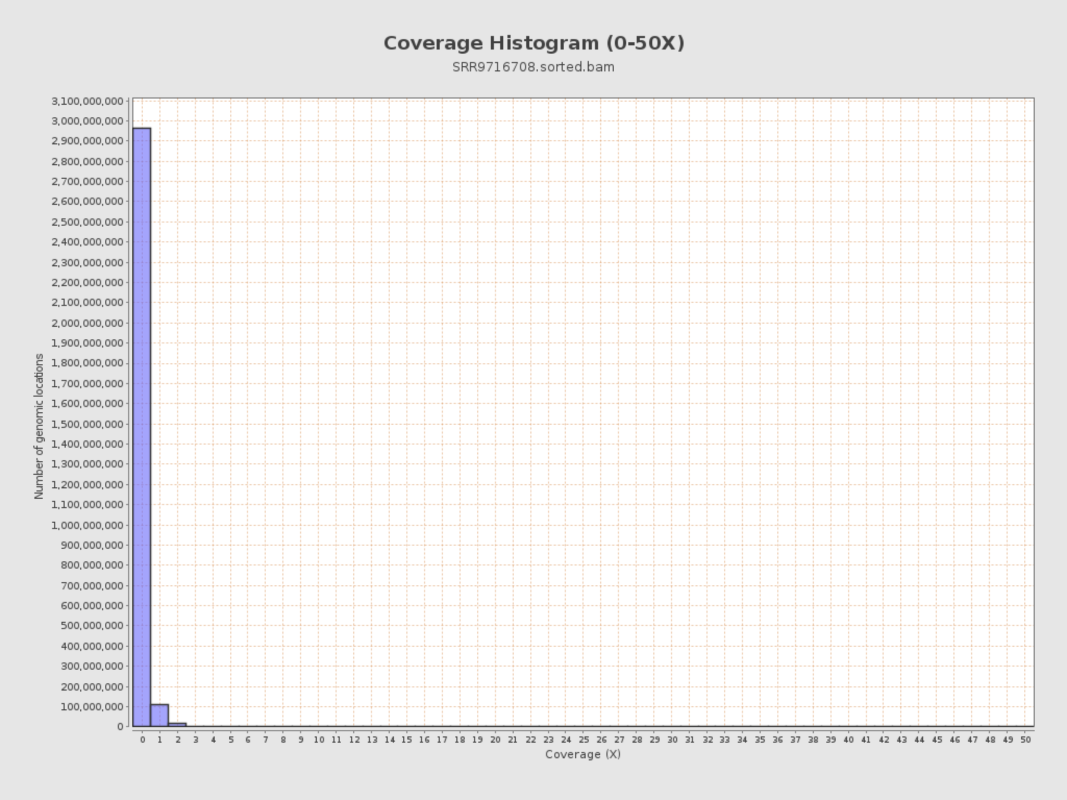
3. Results : Coverage across reference



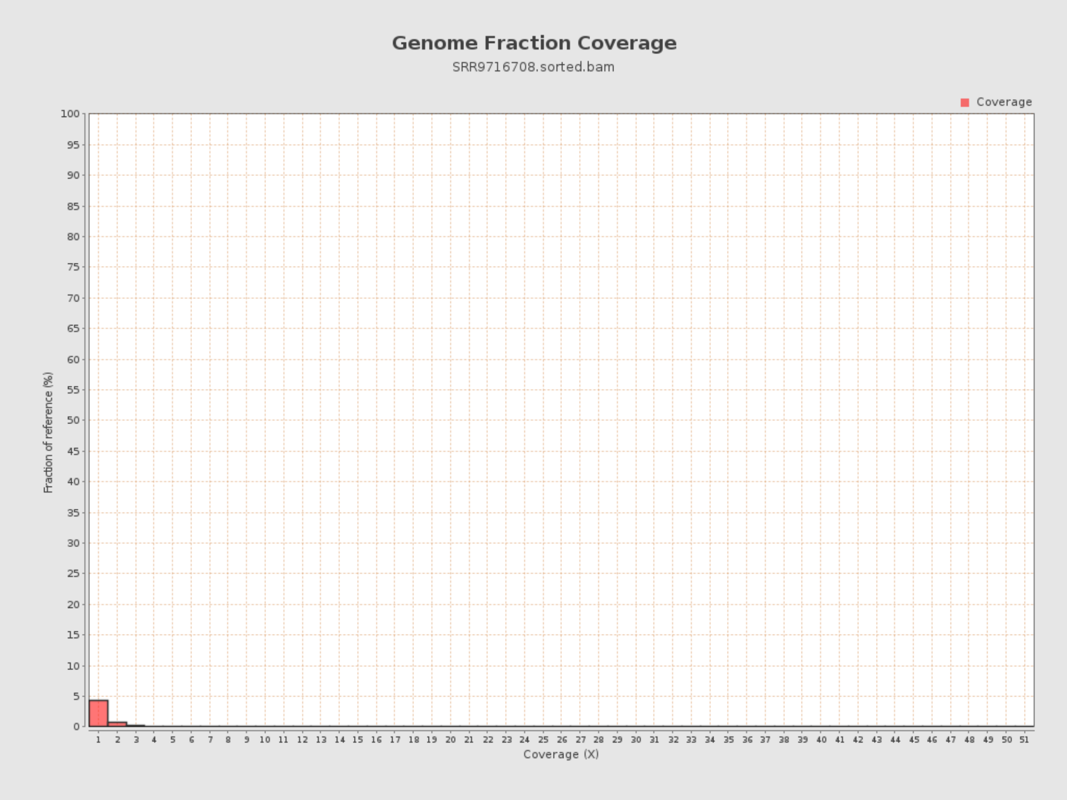
4. Results : Coverage Histogram



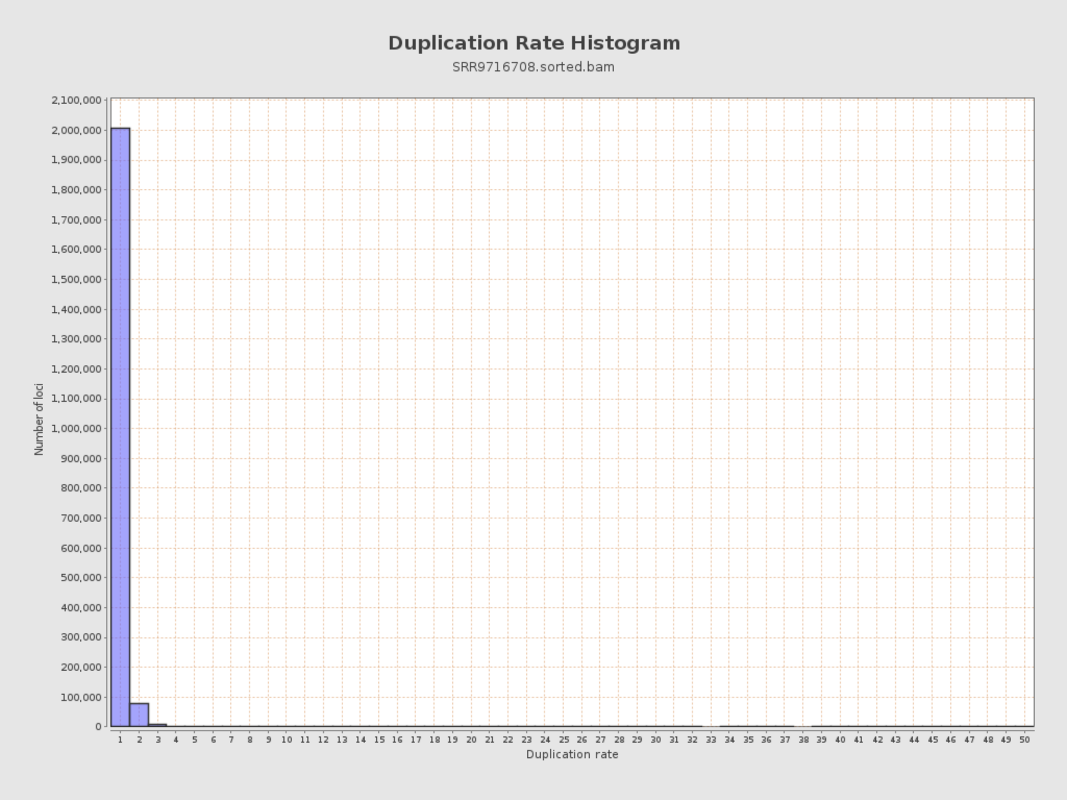
5. Results : Coverage Histogram (0-50X)



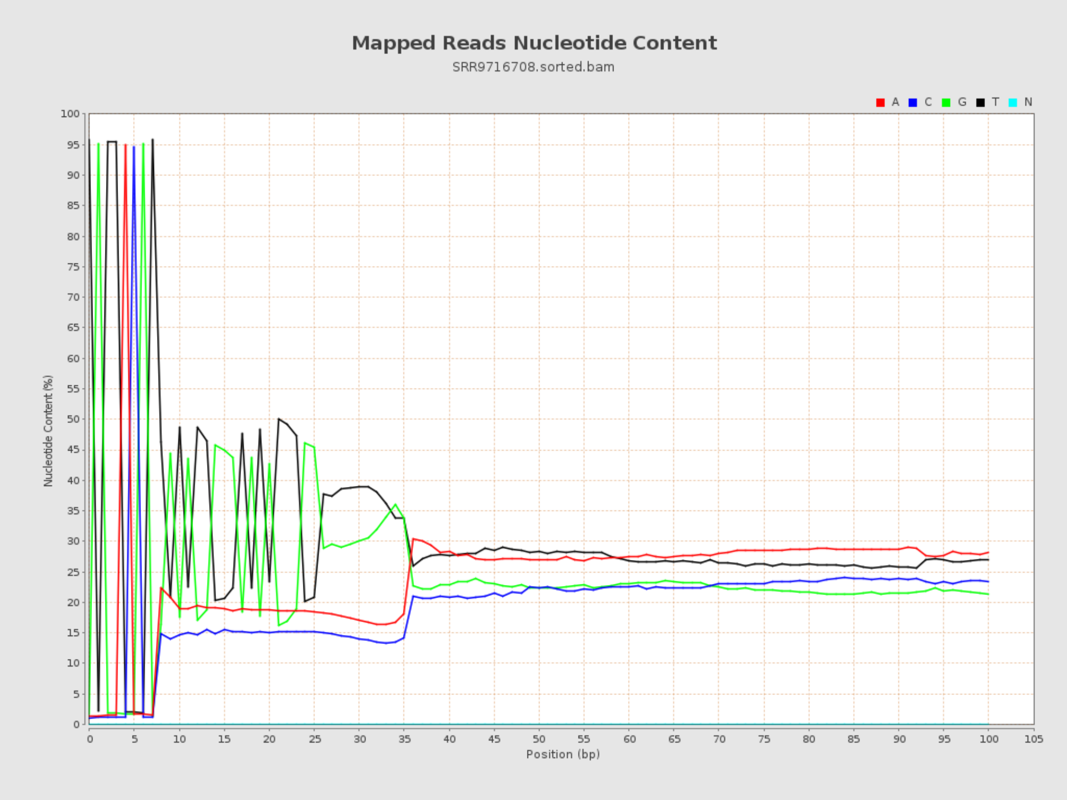
6. Results : Genome Fraction Coverage



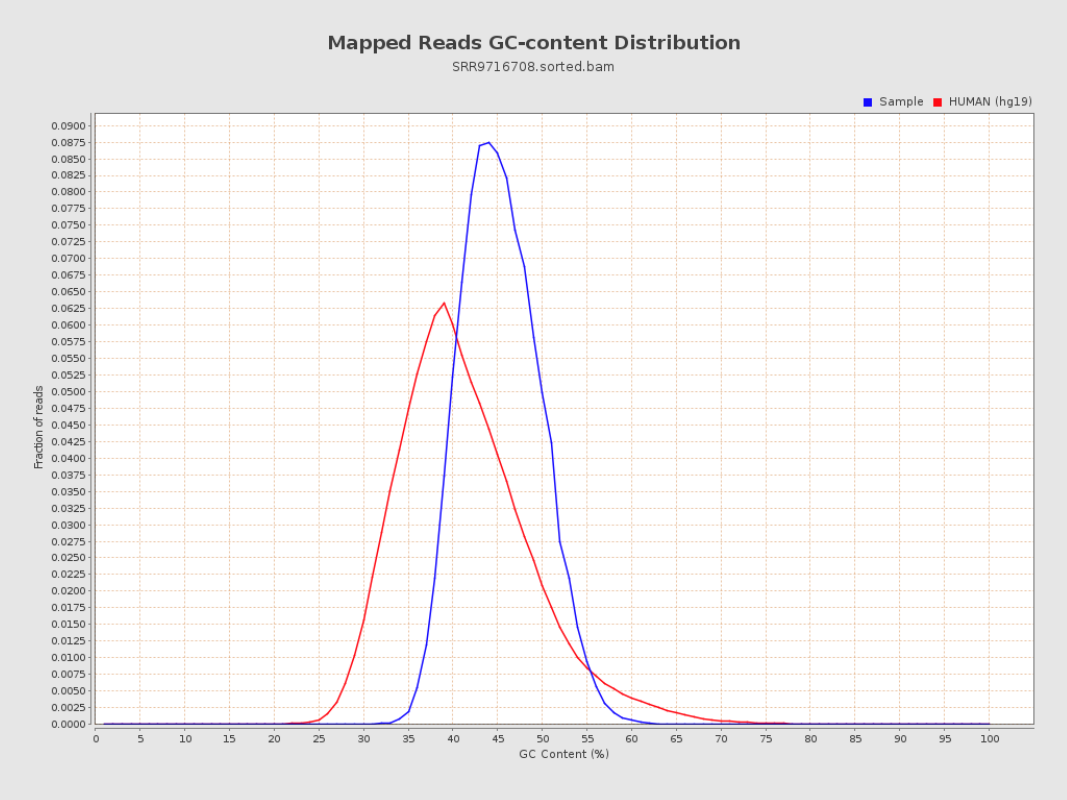
7. Results : Duplication Rate Histogram



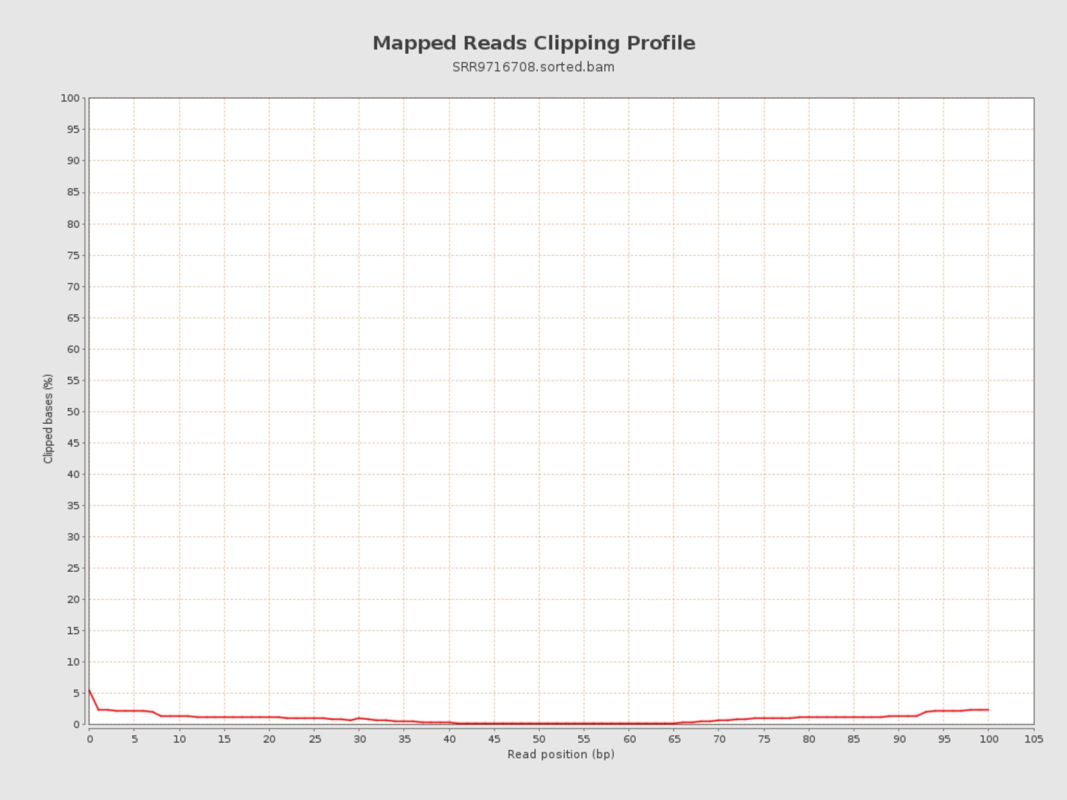
8. Results : Mapped Reads Nucleotide Content



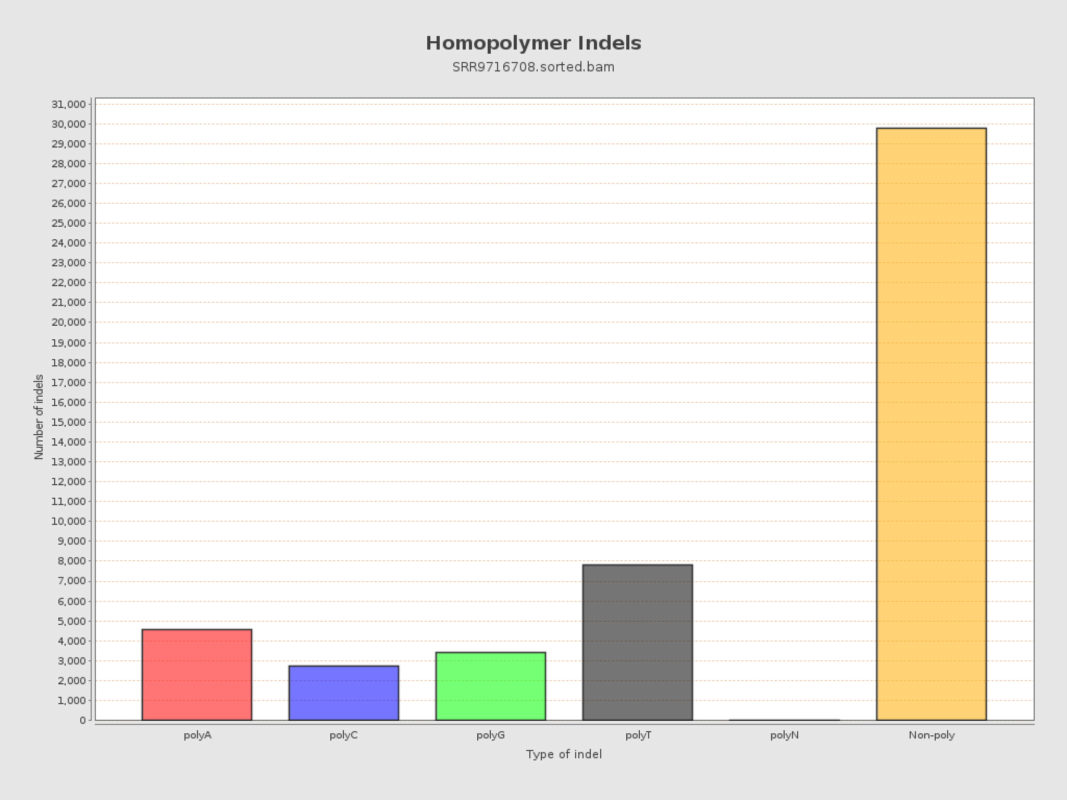
9. Results : Mapped Reads GC-content Distribution



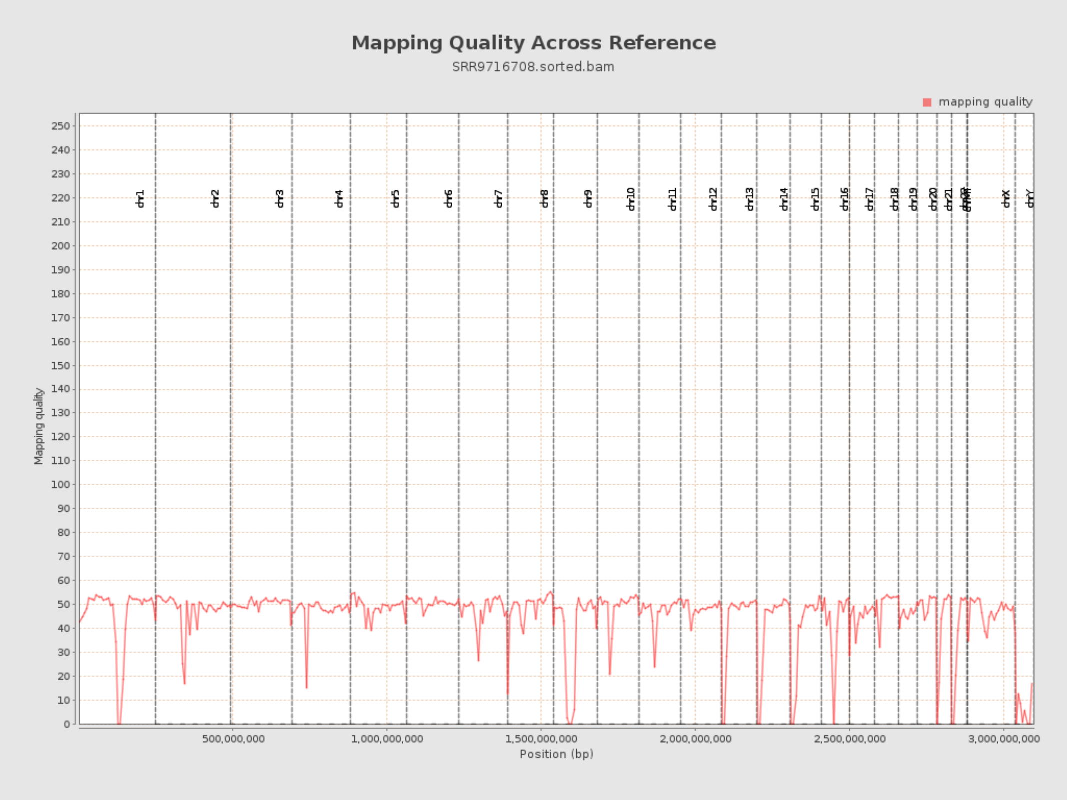
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram