Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/01 22:38:24

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR9716181.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_SRR9716181 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR9716181.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sun Sep 01 22:38:23 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR9716181.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	3,308,474
Mapped reads	2,988,530 / 90.33%
Unmapped reads	319,944 / 9.67%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	12,668 / 0.38%
Read min/max/mean length	30 / 76 / 76.13
Duplicated reads (estimated)	145,930 / 4.41%
Duplication rate	3.65%
Clipped reads	2,992,110 / 90.44%

2.2. ACGT Content

Number/percentage of A's	41,212,371 / 23.96%
Number/percentage of C's	36,101,244 / 20.99%
Number/percentage of T's	54,013,165 / 31.4%
Number/percentage of G's	40,701,954 / 23.66%
Number/percentage of N's	1,273 / 0%
GC Percentage	44.65%

2.3. Coverage

Mean	0.0556

Standard Deviation	0.4069

2.4. Mapping Quality

Mean Mapping Quality	43.97

2.5. Mismatches and indels

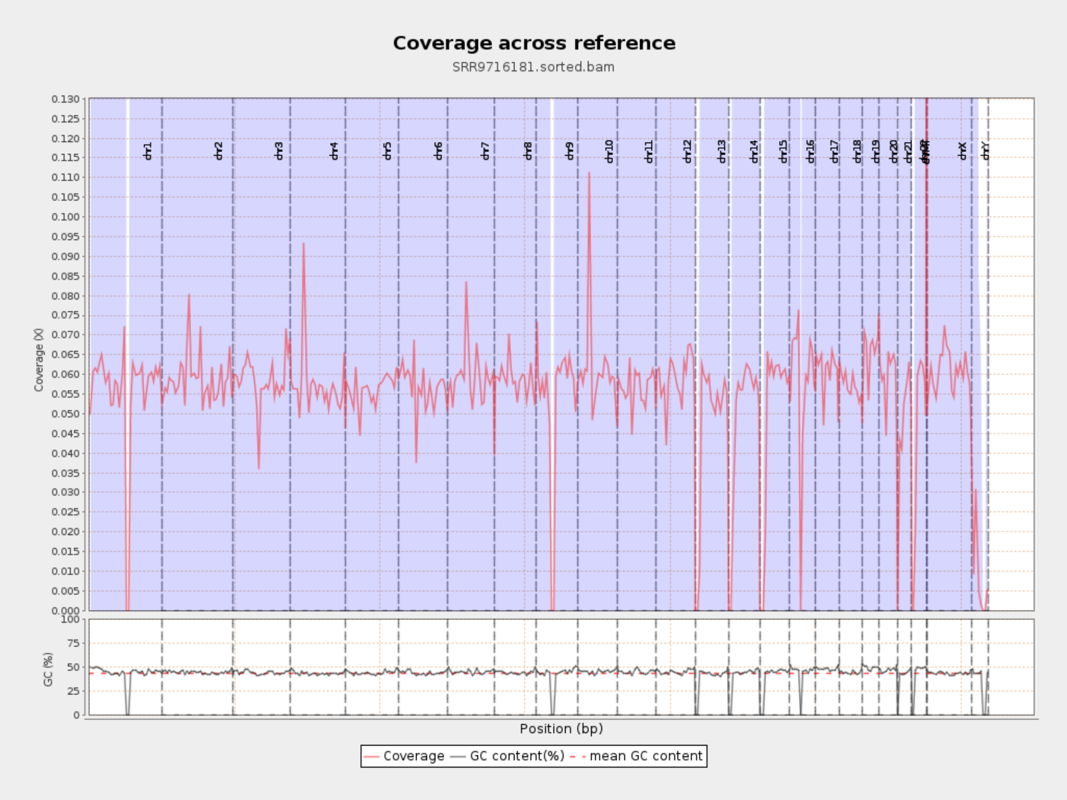
General error rate	0.54%
Mismatches	902,697
Insertions	12,668
Mapped reads with at least one insertion	0.42%
Deletions	33,247
Mapped reads with at least one deletion	1.1%
Homopolymer indels	40.57%

2.6. Chromosome stats

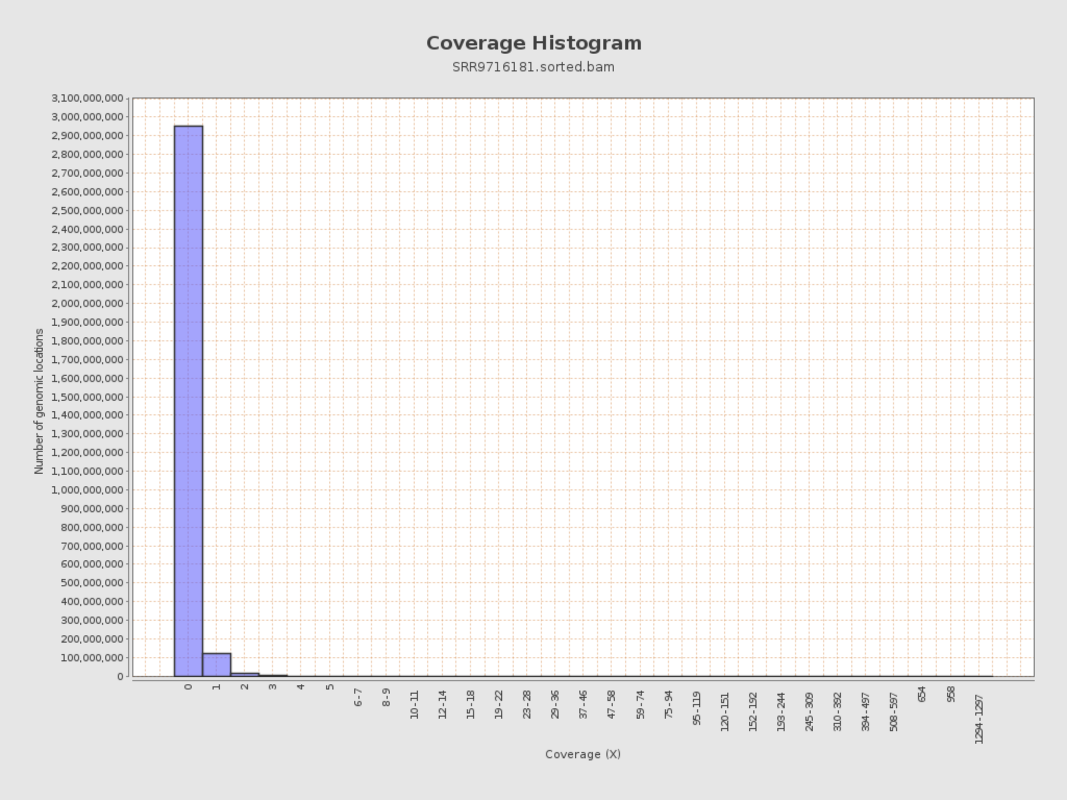
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	13788908	0.0553	0.5572
chr2	243199373	14324253	0.0589	0.6403
chr3	198022430	11567147	0.0584	0.2879
chr4	191154276	10935311	0.0572	0.333
chr5	180915260	10168933	0.0562	0.2777
chr6	171115067	9707789	0.0567	0.3378
chr7	159138663	9504571	0.0597	0.5273

chr8	146364022	8601678	0.0588	0.4197
chr9	141213431	7384883	0.0523	0.3487
chr10	135534747	8324222	0.0614	0.5194
chr11	135006516	7643139	0.0566	0.359
chr12	133851895	7917187	0.0591	0.2922
chr13	115169878	5351365	0.0465	0.253
chr14	107349540	5182885	0.0483	0.2792
chr15	102531392	5054804	0.0493	0.2678
chr16	90354753	5223085	0.0578	0.3205
chr17	81195210	4925039	0.0607	0.3105
chr18	78077248	4486651	0.0575	0.555
chr19	59128983	3883231	0.0657	0.4813
chr20	63025520	3745643	0.0594	0.3007
chr21	48129895	2256720	0.0469	0.3049
chr22	51304566	2147339	0.0419	0.2442
chrMT	16571	4998	0.3016	0.7429
chrX	155270560	9422891	0.0607	0.3217
chrY	59373566	530384	0.0089	0.272

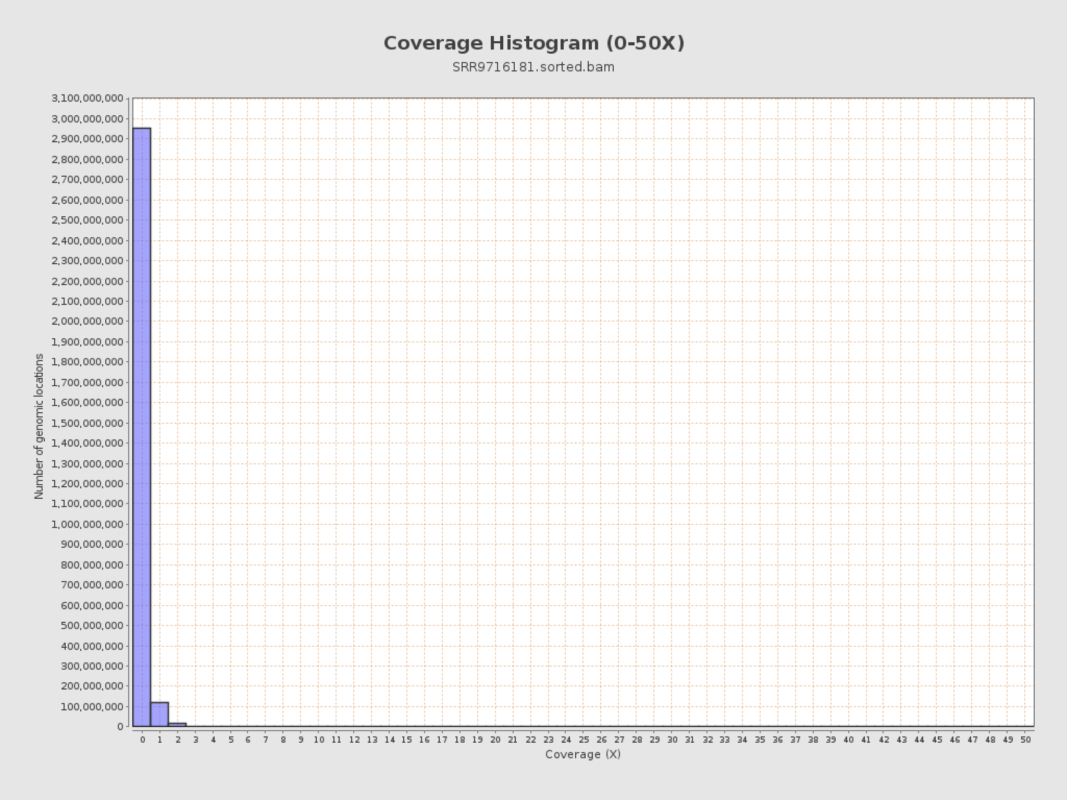
3. Results : Coverage across reference



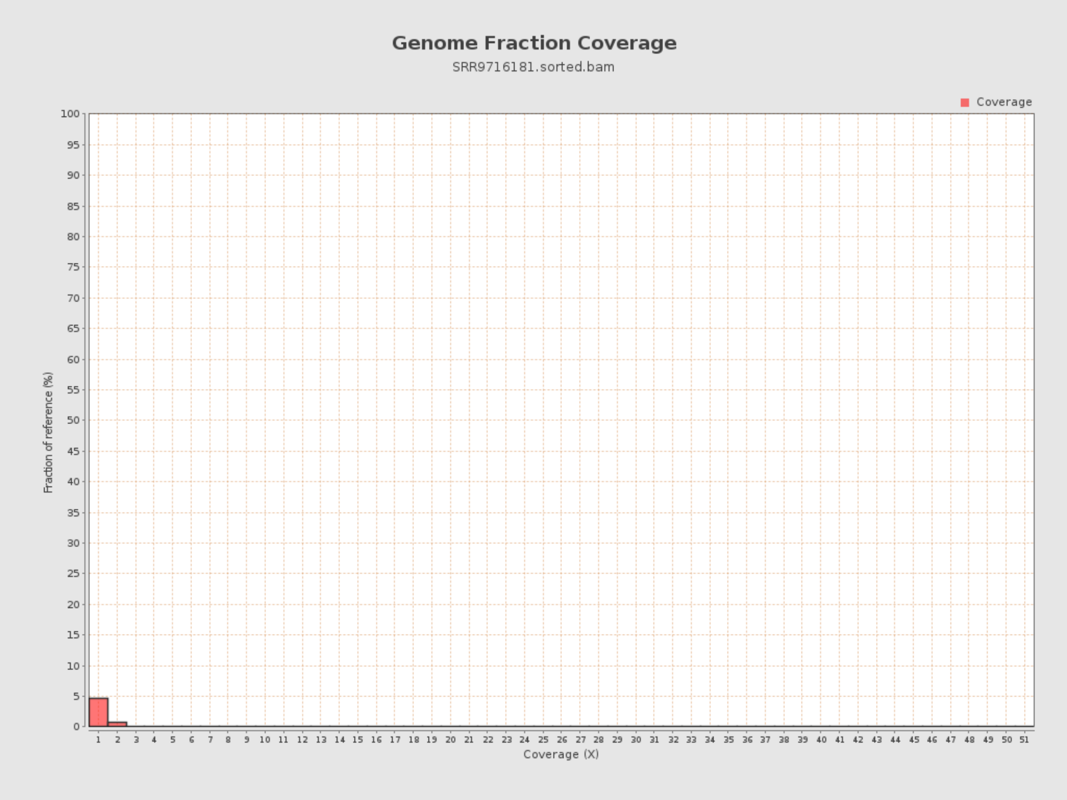
4. Results : Coverage Histogram



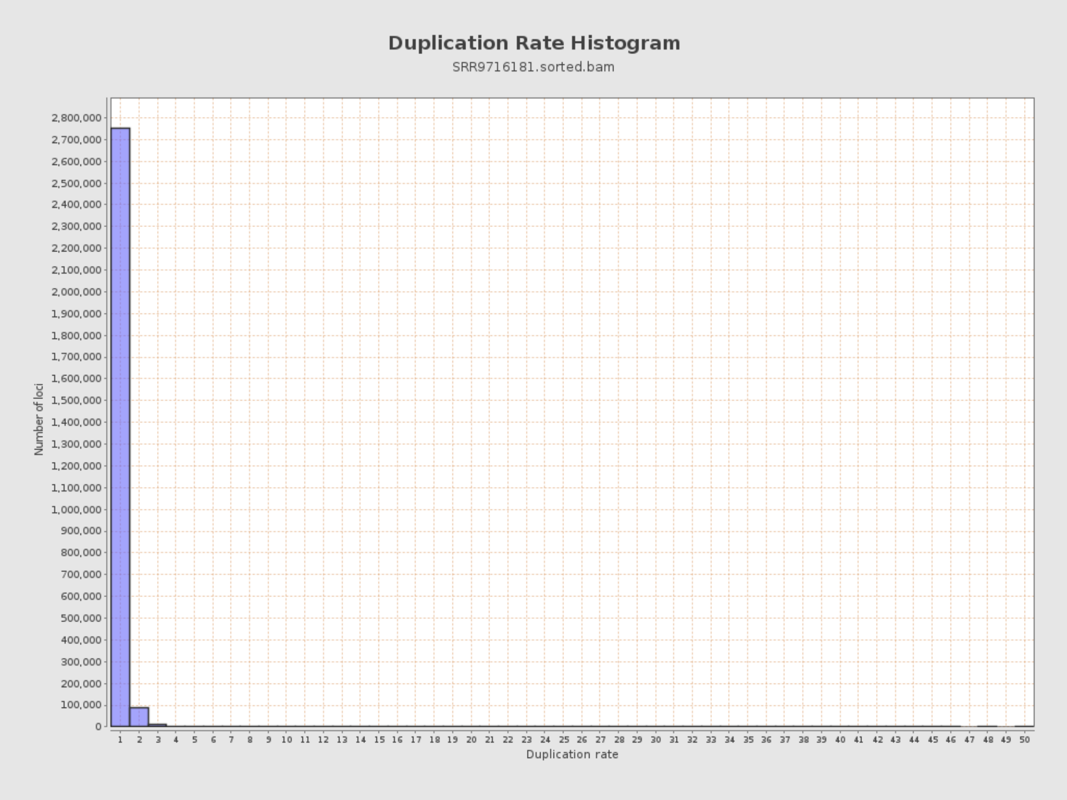
5. Results : Coverage Histogram (0-50X)



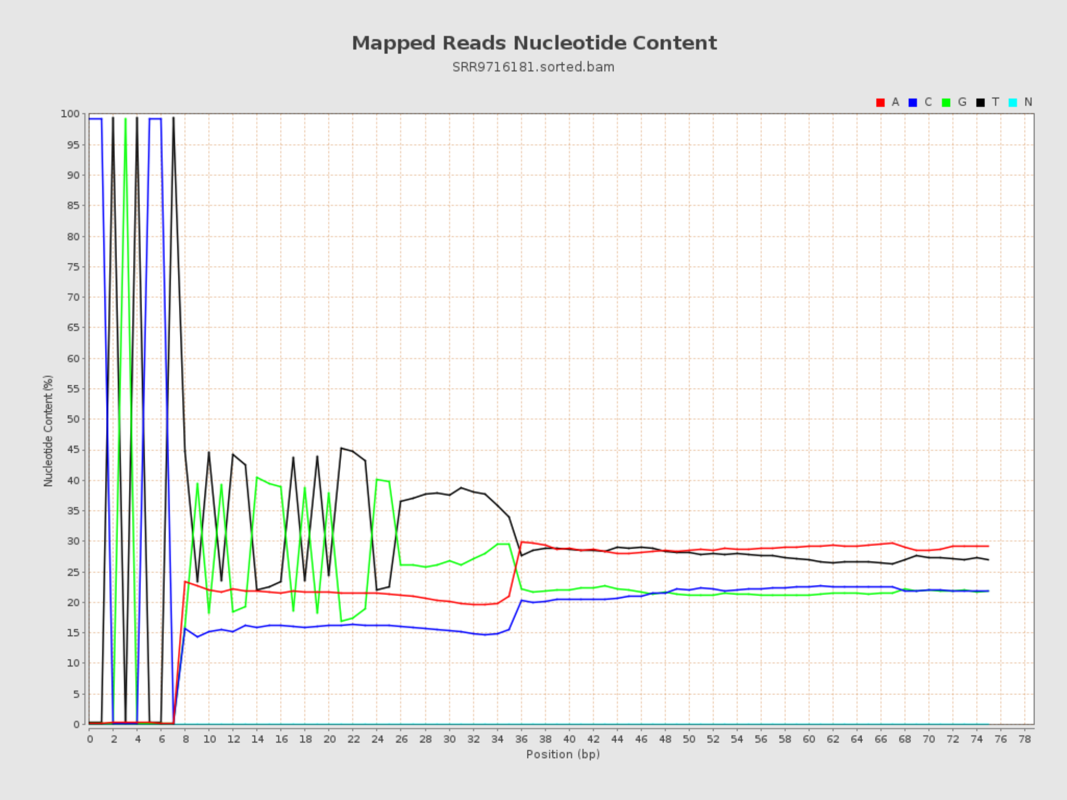
6. Results : Genome Fraction Coverage



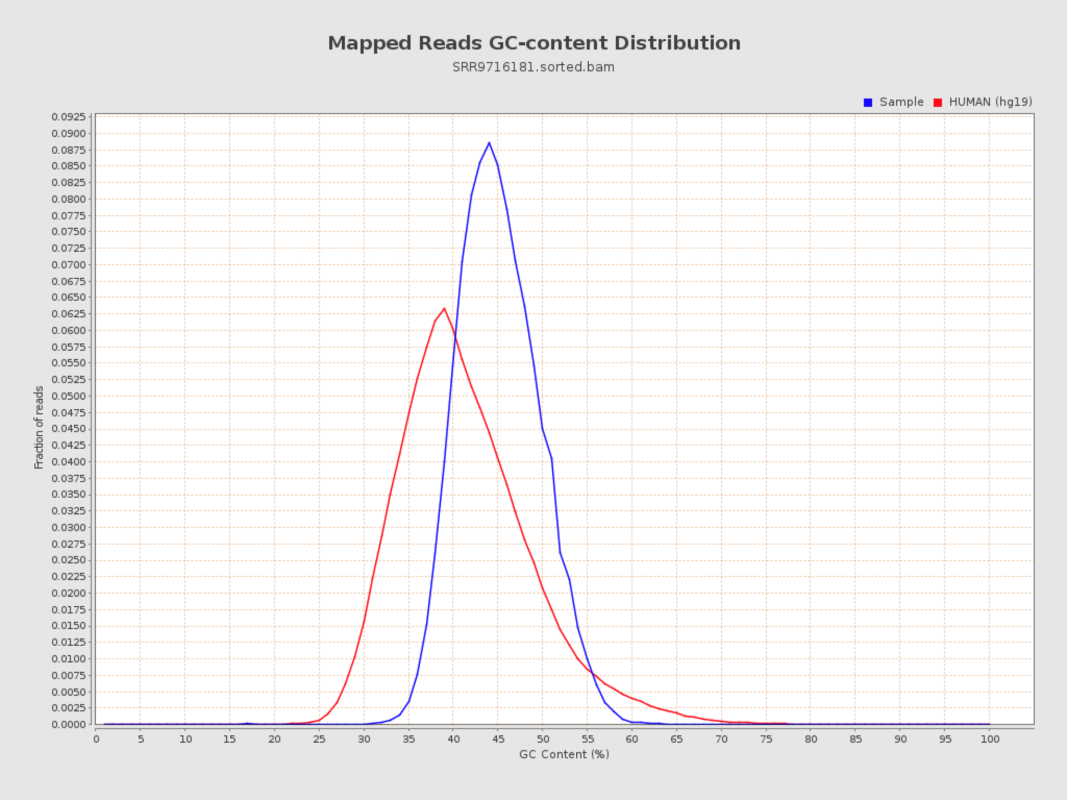
7. Results : Duplication Rate Histogram



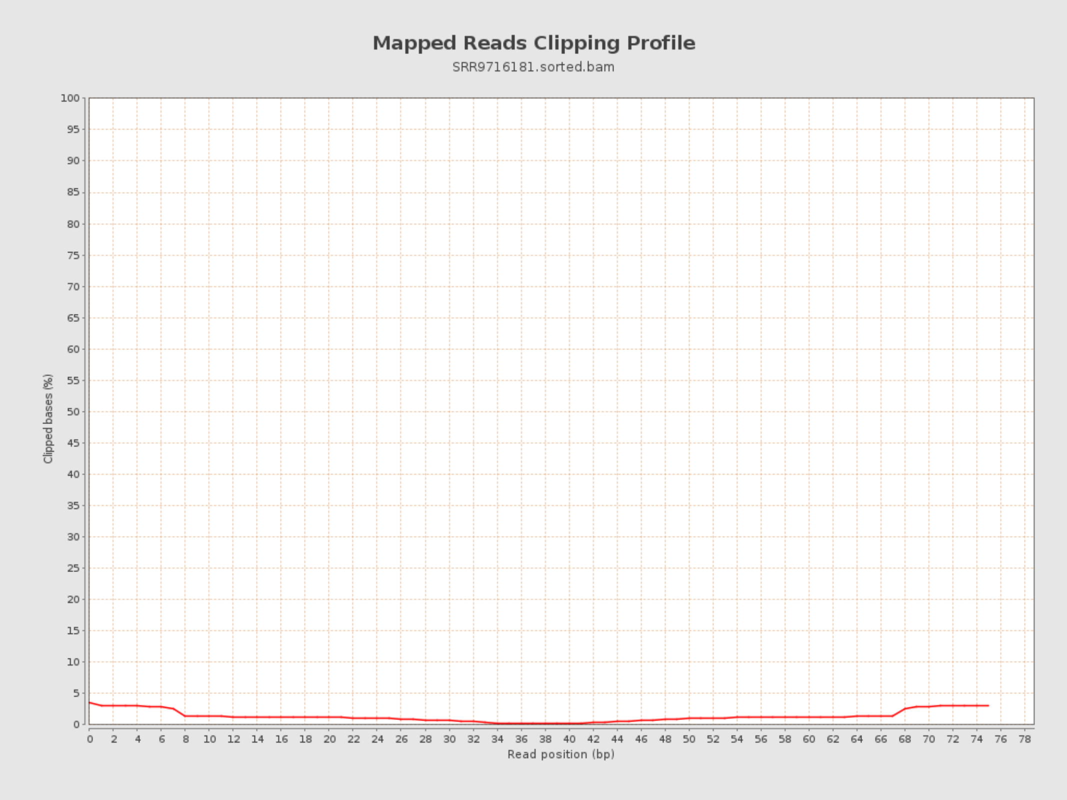
8. Results : Mapped Reads Nucleotide Content



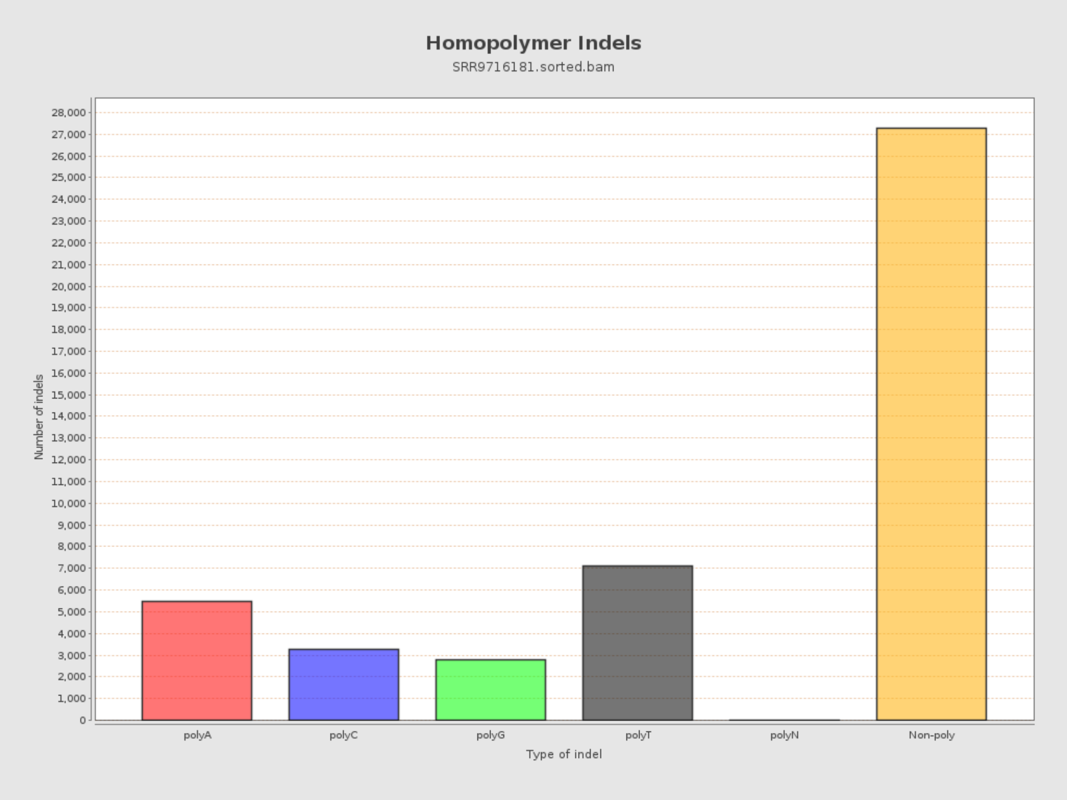
9. Results : Mapped Reads GC-content Distribution



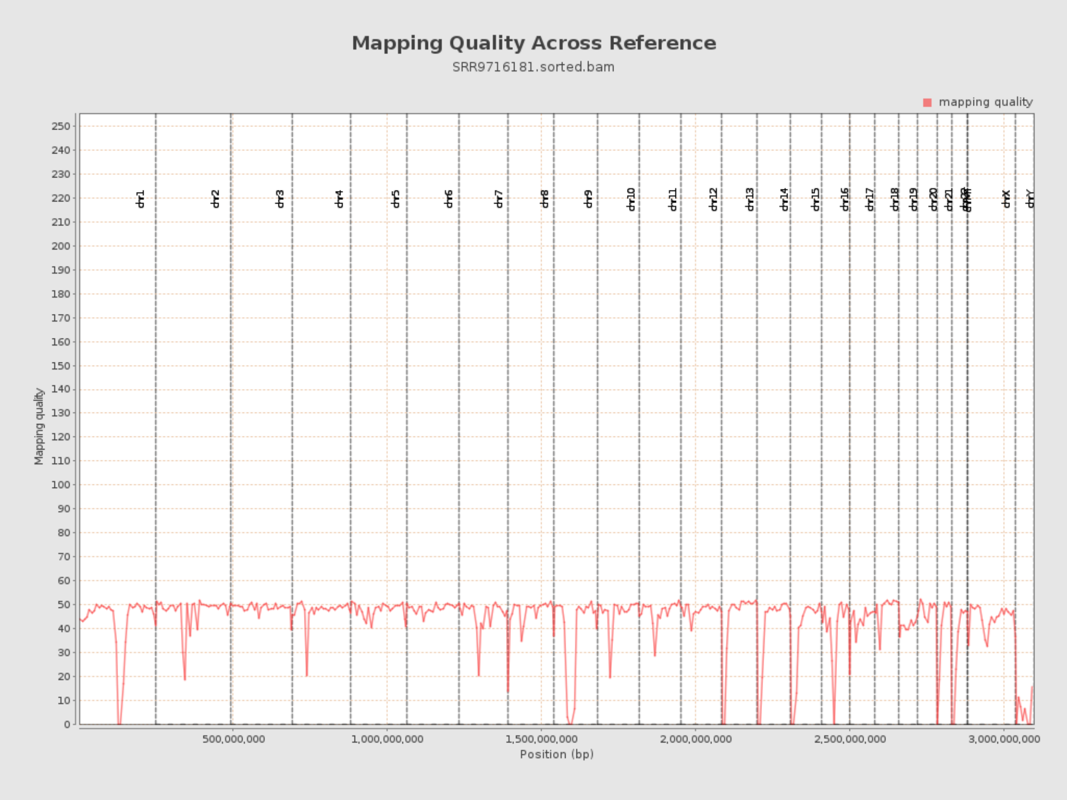
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram